



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 137287

TO: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Sunday, November 14, 2004

Case Serial Number: 09/687864

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Parkin,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Toby Port

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

137287

MS

From: Parkin, Jeffrey
Sent: Saturday, November 06, 2004 4:58 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 09/687,864

RECEIVED
NOV - 8 2004
STIC

Please search SEQ ID NOS.: 12, 13, 15, 17, and 19 from U.S. Serial No. 09/687,864 v. all relevant databases, including interference. Place results on both disk and paper. Thanks!

JSP
AU 1648
REM 3D39
2-0908

http://expoweb1:8001/cgi-bin/expo/GenInfo/snquery.pl?APPL_ID=09687864.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 6472.4 Seconds
(without alignments)
16453.933 Million cell updates/sec

Title: US-09-687-864A-12
Perfect score: 2252
Sequence: 1 agcttgccgcagctgtgta.....ctcgagtgataatctagata 2252

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1470.2	65.3	10000	14 AF038398	AF038398 Simian-Hu
2	1452.6	64.5	2046	6 CQ753919	CQ753919 Sequence
3	1452.6	64.5	2610	6 CQ753921	CQ753921 Sequence
4	1452.6	64.5	9860	14 AF217181	AF217181 Simian-Hu
5	1452.6	64.5	9860	14 STU89134	STU89134 Simian-Hu
6	1452.6	64.5	10501	6 BD161892	BD161892 Nonhuman
7	1448	64.3	9713	14 HIV1U39362	HIV1U39362 Human immun
8	1338.6	59.4	2010	6 CQ753923	CQ753923 Sequence
9	1338.6	59.4	2574	6 CQ753925	CQ753925 Sequence
10	1262	56.0	2553	14 AV247221	AV247221 HIV-1 iso
11	1241.4	55.1	2568	14 AV426111	AV426111 HIV-1 clo
12	1239.8	55.1	2568	14 AV426112	AV426112 HIV-1 clo
13	1238.2	55.0	2568	14 AV426118	AV426118 HIV-1 clo
14	1236.6	54.9	2568	14 AV426110	AV426110 HIV-1 clo
15	1236.6	54.9	2568	14 AV426113	AV426113 HIV-1 clo
16	1236.6	54.9	2568	14 AV426115	AV426115 HIV-1 clo
17	1236.6	54.9	2568	14 AV426117	AV426117 HIV-1 clo
18	1235	54.8	2568	14 AV426114	AV426114 HIV-1 clo
19	1235	54.8	2568	14 AV426116	AV426116 HIV-1 clo

20	1226.8	54.5	3061	14 HIVENVBALA	M63929 Human immun
21	1225.2	54.4	3807	6 AR034235	AR034235 Sequence
22	1225.2	54.4	3807	6 I12144	I12144 Sequence 5
23	1225.2	54.4	3807	6 I28919	I28919 Sequence 5
24	1225.2	54.4	3808	14 HIVBAL1A	M68893 Human immun
25	1224	54.4	2559	14 AY669732	AY669732 HIV-1 iso
26	1223.8	54.3	2547	14 AY426125	AY426125 HIV-1 iso
27	1223.8	54.3	2547	14 AY426127	AY426127 HIV-1 clo
28	1222.2	54.3	2544	14 AY669726	AY669726 HIV-1 iso
29	1222.2	54.3	2547	14 AY426126	AY426126 HIV-1 clo
30	1222.2	54.3	9540	14 HIVJRCFS	M38429 Human immun
31	1221.6	54.2	2568	14 AV247225	AV247225 HIV-1 iso
32	1219	54.1	3211	14 HIVU45960	U45960 Human immun
33	1208.2	53.7	2552	6 I05789	I05789 Sequence 8
34	1207.4	53.6	2559	14 AF025750	AF025750 HIV-1 iso
35	1207.4	53.6	2577	14 AF025763	AF025763 HIV-1 iso
36	1202	53.4	3600	14 HIVBRVA	M1098 Human immun
37	1198	53.2	8896	14 HIVU63632	U63632 HIV-1 iso
38	1197	53.2	1512	6 AX153805	AX153805 Sequence
39	1197	53.2	1512	6 BD017695	BD017695 Assay met
40	1196.8	53.1	2571	14 HIVENVB	L08656 Human immun
41	1196.8	53.1	9074	14 HIVU43096	U43096 Human immun
42	1196	53.1	4273	14 HIVSC	M17450 Human immun
43	1195.4	53.1	2559	14 AV247220	AV247220 HIV-1 iso
44	1195.2	53.1	2565	14 AF025754	AF025754 HIV-1 iso
45	1195.2	53.1	8997	14 AY173952	AY173952 HIV-1 iso

ALIGNMENTS

RESULT 1	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome	10000 bp	DNA	linear	VRL 02-FEB-1998
LOCUS	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome				
DEFINITION	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome				
ACCESSION	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome				
VERSION	AF038398.1	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome				
KEYWORDS		Simian-Human immunodeficiency virus				
SOURCE		Viruses; Retroviridae; Retroviridae; Lentivirus; Primate lentivirus group.				
ORGANISM		Simian-Human immunodeficiency virus				
REFERENCE		1 (bases 1 to 10000)				
AUTHORS		Reimann, K.A., Li, J.T., Voss, G., Lekutis, C., Tenner-Racz, K., Racz, P., Lin, W., Montefiori, D.C., Lee-Parritz, D.E., Lu, Y., Collman, R.G., Sodroski, J. and Letvin, N.L.				
TITLE		An env gene derived from a primary human immunodeficiency virus type 1 isolate confers high in vivo replicative capacity to a chimeric simian/human immunodeficiency virus in rhesus monkeys				
JOURNAL		J. Virol. 70 (5), 3198-3206 (1996)				
MEDLINE		96186751				
PUBMED		8627800				
REFERENCE		2 (bases 1 to 10000)				
AUTHORS		Reimann, K.A., Li, J.T., Voss, G., Lekutis, C., Tenner-Racz, K., Racz, P., Lin, W., Montefiori, D.C., Lee-Parritz, D.E., Lu, Y., Collman, R.G., Sodroski, J. and Letvin, N.L.				
TITLE		Direct Submission				
JOURNAL		Submitted (10-DEC-1997) Human Retrovirology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA				
FEATURES		Location/Qualifiers				
source		1..10000				
		/organism="Simian-Human immunodeficiency virus"				
		/proviral				
		/mol_type="genomic DNA"				
		/strain="SHIV-89.6"				
		/db_xref="taxon:57667"				
LTR		1..301				
repeat_region		1..177				
		/note="5' long terminal repeat"				
misc_feature		178..301				
		/note="R region"				
		178..301				
		/note="U5 region"				

gene	536.. .2068	/product="vpr"
CDS	/gene="gag"	/protein_id="AAB99962.1"
	536.. .2068	/db_xref="GI:2828041"
	/gene="gag"	/translation="MEERPENEGPQRPWDEWVVELEELKEALKHFDPRLLTALG
	/codon_start=1	NHIYNRHGDYLEGAGELIRILQALFMHFRGGCIHSRIGQPGGPNLSAIPPSRML"
	/product="gag"	5948.. .8761
	/protein_id="AAB99958.1"	/gene="tat"
	/db_xref="GI:2828037"	/gene="tat"
	/translation="MGVNSVLGKKADELEKILRLPNGKKYMLKHVVVAANELDRF	join(5948.. .6162,8487.. .8577)
		/codon_start=1
		/product="tat"
		/protein_id="AAB99963.1"
		/db_xref="GI:2828042"
		/translation="MEPVDRLPEWKHPGSKPTACTNICYCKCCFHCQVCFTKALG
		ISYKRRRORRAHQNSQTHQASLSKQSPSQRPDPTGPKQKKVERETETDPVH"
gene	6087.. .8761	
CDS	/gene="rev"	
	join(6087.. .6162,8487.. .8761)	
	/gene="rev"	
	/codon_start=1	
	/product="rev"	
	/protein_id="AAB99964.1"	
	/db_xref="GI:2828043"	
	/translation="MAGRSQSDDEBLIRTVRLIKLYQSNPPPSLEGTRQARRNRRR	
	WRERQRIISRISERILGTYLGRSAEPVPLQLPPLERLTDCNEDCGTSGTGVSQPI	
	LVESTVLESGTKE"	
gene	6179.. .6424	
CDS	/gene="vpu"	
	6179.. .6424	
	/gene="vpu"	
	/codon_start=1	
	/product="vpu"	
	/protein_id="AAB99965.1"	
	/db_xref="GI:2828044"	
	/translation="MQPIQIAIVALVVAIIIVWSVIVVYKILRQKIDRLIDR	
gene	6339.. .8903	
CDS	/gene="env"	
	6339.. .8903	
	/gene="env"	
	/codon_start=1	
	/product="env"	
	/protein_id="AAB99966.1"	
	/db_xref="GI:2828045"	
	/translation="MRVKEYQHLRWGRWGTMLGLMICSATEKLVTVTVYGVVP	
	WREATTILFCASDAXADTEVHNWATHACVTPDPNPQEVVLGNVTENFMKNMVD	
	QMHEDIISLWDESLKPCVKLTPLCLCVTLNLTNLTNTNTKYLISCNTSVITQACPKVSFQPIPI	
	FYITTSIRNMVKKEYALFNRLDVPVIENTNTNTKYLISCNTSVITQACPKVSFQPIPI	
	HYCVPAFMLKCNKTFNGSGPCTNVSTQCTHGIRFVSTQLLNSLAEEDIVIR	
	SENFTDNAKTIIVOLNESVINCTRPNNTRRLSIGPGRAFYARRNIIGDIRQAHCN	
	ISRAKNNTLQOIIVIKLREKPNKTIAFNQSSGGDPEIVMHSFNCGGFFYCNTAQLF	
	NSTWNVTGTTGTEGNDIITLQCRIKOILNMQVKGKAMYAPPIITGOIRCSNITGLL	
	LTRGGNSTETETEIFRPGGDMRDNRSSELYKYKVRIBIPIGIVAPTAKRTVQREK	
	RAVGIGAVFLGFLGAAGSTMGAAVTLTVQARLLSLGIVQQOQLLRALEAQHMLQL	
	TWGIKQIARVLALEYRLDQQLMGICSGKLICTTSPWNVSWSKSVDDIWNMM	
	TMWEERIEDNYTDIYDLLEKSTQOEKNEKLELLELDKASLWNFDTIWMWYIRL	
	PIMTVGLIGLRIYFAVLISIVNRVQGYSPLSFOTLLPASRPPRPGCTEPEGGERDR	
	DRSPLVNGSLAIWDLRSICLSEYHRLDLLIVTRIVELLGRGWEALKYWNLL	
	QYWSQELKNSAVLSLNTATAIABGTDRVIEVQACRAIRHIFRIRQGLERILL"	
gene	8922.. .9713	
CDS	/gene="nef"	
	8922.. .9713	
	/gene="nef"	
	/codon_start=1	
	/product="nef protein"	
	/protein_id="AAB99967.1"	
	/db_xref="GI:2828046"	
	/translation="MGGAISMRRSRPSGDLRQLRLRARGETYGRLLGEVGYQSQSP	
	GLDKGLASLSCEGQYKQGYMNTWRNPAEREKLAAYRKQNMDDIDEDDDLVGVSV	
	RPKVPLRTMSYKLAIDMSHFIEKGGELGIYYSARRHILDIILEKSGIIPDMQDYT	
	SGPGIRYPTKFWLWKLVPVNVSDAEQDEHYLMHPAQTSQWDDPWGEVLANKFDP	
	LAYTEAYVRYPEFBFGSKSGLSEBEVRRRLTARGLLNWDKKETR"	
	9307.. .10000	
LTR		


```
Db 97 AAATGTGGGTCAACAGTCTATTATGGGTACCTGTGTGGAGAGCAACACCACCTCTA 156
Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACACAT 231
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAAT 276
Qy 292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
Db 277 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336
Qy 352 GATGAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTAAATGGCACT 411
Db 337 GATGAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTAAATGGCACT 396
Qy 412 AATTTGAATATCACTAAGAAATACTTAATCCCACTAGTAGCAGCTGGGAAATGATGGAG 471
Db 397 AATTTGAATATCACTAAGAAATACTTAATCCCACTAGTAGCAGCTGGGAAATGATGGAG 456
Qy 472 AAAGGAGAAATAAAAATTTGCTTTTCTATATCAACCAAGCATAAAGAAATAGGTAAG 531
Db 457 GAAGGAGAAATAAAAATTTGCTTTTCTATATCAACCAAGCATAAAGAAATAGGTAAG 516
Qy 532 AAAGAAATGCACTTTTAATAGACTTGATGTAGTACCNAATAGAAATACTTAATACT 591
Db 517 AAAGAAATGCACTTTTAATAGACTTGATGTAGTACCNAATAGAAATACTTAATACT 576
Qy 592 AAGTATAGTTTAATAGTTTAAACACCTCAGTCAATTACAGAGGCTGCCAAAGGTATCC 651
Db 577 AAGTATAGTTTAATAGTTTAAACACCTCAGTCAATTACAGAGGCTGCCAAAGGTATCC 636
Qy 652 TTTCAGCAATTTCCCATATATTGTGTCCCGCTGGGTTTGGCATGTCTAAAGTGAAC 711
Db 637 TTTCAGCAATTTCCCATATATTGTGTCCCGCTGGGTTTGGCATGTCTAAAGTGAAC 696
Qy 712 AATAAGACATTCATGATCAGGACCATGCAACAAATGTGCAGACAGTACATGTACACAT 771
Db 697 AATAAGACATTCATGATCAGGACCATGCAACAAATGTGCAGACAGTACATGTACACAT 756
Qy 772 GGAATTAGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAAC 831
Db 757 GGAATTAGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAAC 816
Qy 832 ATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACATAATAGTACAGCTAAT 891
Db 817 ATAGTAATTAGATCTGAAAAATTTACAGACAATGCTAAAAACATAATAGTACAGCTAAT 876
Qy 892 GAATCTGTAGTAATTAATTTGACAGACCCCAACACATACAGAGGAGGTTATCTATA 951
Db 877 GAATCTGTAGTAATTAATTTGACAGACCCCAACACATACAGAGGAGGTTATCTATA 936
Qy 952 GGACCAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAAGCACAT 1011
Db 937 GGACCAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAAGCACAT 996
Qy 1012 TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACACAGATAGTTTATAAATTAAGA 1071
Db 997 TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACACAGATAGTTTATAAATTAAGA 1056
Qy 1072 GAAAAATTTAGGAATAAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT 1131
Db 1057 GAAAAATTTAGGAATAAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT 1116
Qy 1132 GTAATGCACAGTTTTTAAATTTGGAGGGGAATTTCTTCTACTGTGTAATACAGCAAACTGTTT 1191
Db 1117 GTAATGCACAGTTTTTAAATTTGGAGGGGAATTTTCTACTGTGTAATACAGCAAACTGTTT 1176
Qy 1192 AATAGTACTTGGAAATTTTACTGGAGGGAACAAATGGCACTGAAGGAAATGACATAATCACA 1251
Db 1177 AATAGTACTTGGAAATTTTACTGGAGGGAACAAATGGCACTGAAGGAAATGACATAATCACA 1236
```

```
Qy 1252 CTCCAATGCAGAAATAAAACAAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1311
Db 1237 CTCCAATGCAGAAATAAAACAAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTAT 1296
Qy 1312 GCCCTCCCATCAAGGACAAAATTTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACA 1371
Db 1297 GCCCTCCCATCAAGGACAAAATTTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAACA 1356
Qy 1372 AGAGATGGAGTAATAGTACTAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431
Db 1357 AGAGATGGAGTAATAGTACTAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1416
Qy 1432 ATGAGGACAAATTTGGGAAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA 1491
Db 1417 ATGAGGACAAATTTGGGAAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA 1476
Qy 1492 GGAGTAGCACCCACAGGCAAGAGAGAAAGCAAGTGTCAAAAGAGAAAAGAGGGGGAGG 1550
Db 1477 GGAGTAGCACCCACAGGCAAGAGAGAAAGCAAGTGTCAAAAGAGAAAAGAGGAGTGGG 1535

RESULT 3
CQ753921          2610 bp      DNA      linear      PAT 01-MAR-2004
LOCUS             Sequence 26 from Patent WO2004001051.
DEFINITION        CQ753921
ACCESSION          CQ753921
VERSION            CQ753921.1 GI:44845221
KEYWORDS           Human immunodeficiency virus 1 (HIV-1)
SOURCE             Human immunodeficiency virus 1
ORGANISM            Human immunodeficiency virus 1
                    Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                    lentivirus group.
REFERENCE           1
AUTHORS            Tangy, F., Lorin, C., Mollet, L. and Delebecque, F.
TITLE              Recombinant measles viruses expressing epitopes of antigens of rna
                    viruses - use for the preparation of vaccine compositions
JOURNAL            Patent: WO 2004001051-A 26 31-DEC-2003;
                    INSTITUT PASTEUR (FR)
FEATURES            Location/Qualifiers
                    source
                    1..2610
                    /organism="Human immunodeficiency virus 1"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:11676"

ORIGIN

Query Match      64.5%; Score 1452.6; DB 6; Length 2610;
Best Local Similarity 98.1%; Pred. No. 9e-296;
Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTCTGGGATATTGATGATCTGTAGTGCTACAGAA 111
Db 37 TGGGGGTGGAGATGGGCAACCATGCTCTTGGGATGTTGATGATCTGTAGTGCTACAGAA 96
Qy 112 AAATTTGGGTTCACAGTCTATTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA 171
Db 97 AAATTTGGGTTCACAGTCTATTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTA 156
Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACACAT 231
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAAT 276
Qy 292 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
Db 277 TTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 336
Qy 352 GATGAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTAAATGGCACT 411
Db 337 GATGAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTAAATGGCACT 396
```

```
QY 412 AATTTGAATATCACTAAGAATACCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 471
Db 397 AATTTGAATATCACTAAGAATACCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 456
QY 472 AAAGGAGAAATNAAAAATTCCTCTTCTATATCACCAACAGCATATAGAAATAGGTTAAAG 531
Db 457 GAAGGAGAAATNAAAAATTCCTCTTCTATATCACCAACAGCATATAGAAATAGGTTAAAG 516
QY 532 AAAGAATATGCACCTTTTAAATAGACTTGTAGTACCAATAGAAAATACATAATACT 591
Db 517 AAAGAATATGCACCTTTTAAATAGACTTGTAGTACCAATAGAAAATACATAATACT 576
QY 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCACTATTACACAGGCTCTCCAAAGGTTATCC 651
Db 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCACTATTACACAGGCTCTCCAAAGGTTATCC 636
QY 652 TTTTCAGCAATCCCATACATATTGTGTCCCGCTGGGTTTGGGATGCTTAAGTGTAAAC 711
Db 637 TTTTCAGCAATCCCATACATATTGTGTCCCGCTGGGTTTGGGATGCTTAAGTGTAAAC 696
QY 712 AATAAGACATTCATGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT 771
Db 697 AATAAGACATTCATGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT 756
QY 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 831
Db 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 816
QY 832 ATAGTAATTAGATCTGAATTTTACAGACATGCTTAAACCATTAATAGTACAGCTAAAT 891
Db 817 ATAGTAATTAGATCTGAATTTTACAGACATGCTTAAACCATTAATAGTACAGCTAAAT 876
QY 892 GAATCTGTAGTAATTAATTTGTAAGAACCCCAACAAATACAAAGAAAGGTTATCTATA 951
Db 877 GAATCTGTAGTAATTAATTTGTAAGAACCCCAACAAATACAAAGAAAGGTTATCTATA 936
QY 952 GGACCCAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACAT 1011
Db 937 GGACCCAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGACAAGCACAT 996
QY 1012 TGTAACATTTAGTAGAGCAAAATGGAATAACACATTTTACACAGATAGTTATATAATTAAGA 1071
Db 997 TGTAACATTTAGTAGAGCAAAATGGAATAACACATTTTACACAGATAGTTATATAATTAAGA 1056
QY 1072 GAAAAATTTAGGAATAAAACAAATAGCTTTTAACTCAATCCTCAGGAGGGACCCAGAAATT 1131
Db 1057 GAAAAATTTAGGAATAAAACAAATAGCTTTTAACTCAATCCTCAGGAGGGACCCAGAAATT 1116
QY 1132 GTAATGCACAGTTTAAATTTGGAGGGGAAATTTCTTCTACTGTATATACAGCACAACTGTTT 1191
Db 1117 GTAATGCACAGTTTAAATTTGGAGGGGAAATTTTCTTCTACTGTATATACAGCACAACTGTTT 1176
QY 1192 AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGGCACTGAGAAATGACATATACACA 1251
Db 1177 AATAGTACTTGGAAATGTTACTGGAGGGACAAATGGGCACTGAGAAATGACATATACACA 1236
QY 1252 CTCCAATGCAAGATAAAACAAATTAATAATATGTCGAGAAAGTAGGAAAAGCAATGTAT 1311
Db 1237 CTCCAATGCAAGATAAAACAAATTAATAATATGTCGAGAAAGTAGGAAAAGCAATGTAT 1296
QY 1312 GCCCTCCCATTCACAGGACAAATTAGATGTTTCATCAATATATACAGGCGTCTACTAACA 1371
Db 1297 GCCCTCCCATTCACAGGACAAATTAGATGTTTCATCAATATATACAGGCGTCTACTAACA 1356
QY 1372 AGAGATGGAGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTCGGAGGAGAGAT 1431
Db 1357 AGAGATGGAGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTCGGAGGAGAGAT 1416
QY 1432 ATGAGGACCAATTCGAGAGAGTGAATTTATATAAATATAAGTAGTAAGAAATTTGAACCAATA 1491
Db 1417 ATGAGGACCAATTCGAGAGAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA 1476
```

```
QY 1492 GGAGTAGCACCACCCAGGCAAGAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGAGG 1550
Db 1477 GGAGTAGCACCACCCAGGCAAGAGAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGG 1535

RESULT 4
AP217181 LOCUS 9860 bp RNA linear VRL 01-JAN-2002
DEFINITION Simian-Human immunodeficiency virus SHIV-C2/1, complete genome.
ACCESSION AP217181
VERSION AP217181.1 GI:18026826
KEYWORDS Simian-Human immunodeficiency virus
SOURCE Simian-Human immunodeficiency virus
ORGANISM Simian-Human immunodeficiency virus
VIRUSES; Retrovirdae; Retroviridae; Lentivirus; Primate
REFERENCE 1 (bases 1 to 9860)
AUTHORS Sakai,K., Shinohara,K., Takahashi,E., Ami,Y., Sasaki,Y., Suzuki,Y.,
Nakasone,T. and Honda,M.
TITLE Comparative genetic analysis of simian/human immunodeficiency
viruses (SHIVs) with pathogenic property
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9860)
AUTHORS Sakai,K., Shinohara,K., Takahashi,E. and Honda,M.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1999) AIDS Research Center, National Institute of
Infectious Diseases, Gakuen 4-7-1, Musashimurayama, Tokyo 208-0011,
Japan
FEATURES
Location/Qualifiers
source 1..9860
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic RNA"
/strain="SHIV-C2/1"
/specific_host="cynomolgus monkey"
/db_xref="taxon:57667"
/notes="Obtained from monkey plasma"
misc_feature 1..5938
/notes="derived from SHIVmac239"
LTR 1..301
repeat_region 1..177
/notes="R region"
misc_feature 178..301
/notes="US region"
gene 536..2068
/gene="gag"
536..2068
/gene="gag"
CDS /codon_start=1
/product="gag protein"
/protein_id="AAL55638.1"
/db_xref="GI:18026827"
/translat="MGVRSVLSGKKADELEKIRLPRNGKKKMYLKHVWAANBELDRF
GLAESLLENKGCQKJLSVLAPVPTGSENLSKSYNTVCVWICIHASEKVKHTEAKQ
IEVKHGVETGTTETWPKTRPTAPSGRGNTVPQQIGNYVHLPSPTLNAAVKL
PAPQOQQLREPSQDIAGTSSVDEQIQMYRQNPPIPVGNIRYRWIQLGQCKVR
MYNPNTLIDVKQKPEPFQSVYDRFYKSLRAEQTDAAVKQNMVTTQLLIQANPCKLV
LKLGVNPTLEMLTACQGVGPGQKRLMAELKEALAPVPIPFAAAQQRKPRPIK
CWNGKEGHSAROCRAPRGQCKGCKGMDHVMACKCPDQAGFLGLGPGWKKPRFPMA
QVHGGLIPTAPPEDPAVDLLKMLQKQKQREKQREKPYKEVTEDLLHLNLSLFG
DQ"
<1711..4893
/gene="pol"
<1711..4893
/gene="pol"
/codon_start=1
/product="pol protein"
/protein_id="AAL55639.1"
/db_xref="GI:18026828"
/translat="VLELWERTLCAMQSPKTKMLMKWKNKPCYQMPROTGGFFR
PWSNGKEAPQFPHGSSAGADTNCSPGSGSAKELHAYGQARERKAERKQREALQG
GDRGFAAPQSLWRRRPVVTATGQCPVEVLDTGADDSITVIELGPHYTPKI VGGIG
```

GFINTKEYKNVEIEVLGKRIKGRITMTGDTPIINFGRNLLTALGMSLNFPIAKIYEPVKV
ALKPGDKGPKLKWPLKRIKVALREICEKMEKGOLEEAAPTNPYNTPTFAIKKDK
NKRMILDFRELARVTQDTEVOLGIPHAGLAKRKRIITVLDIGDAVFSIPLDEERQ
YTAFTLPSVNNAPEGKRIYKVLPOGWKGSPIAFQYMRHVLPEFRKANFDVTLVQM
DILIASDRTDLDEHDVVLQKLBNLSIGFSTPEEKFKDDPPFOMMGYELWLPKWKLQ
KIELPQRTVNDIQKLVGLNNAQIYFGIKTKHLRLIRIKHOEDKILKVGKFAKIN
AEYEENKIILSQOEGCYOEGKPLEATVLSQDNQWSYKIHQEDKILKVGKFAKIN
THNGVRLLAHVLOKIGKEAIVTWGOVPKFHLPEUKDQWESQWMTDYQWVTWIPEDPT
STPEPLRVNLKDPKEGETYYTDSCKNQSKGKAGYITDRGDKVKVLSQTTNQ
QAELEAFMALTDSPKANLIVDSQYVYMGIIITGCTPESERLNVNIIEMIKSEIYI
AWPAHKGIGNEIDHLVSGIRQVFLIITGCTPESERLNVNIIEMIKSEIYI
VARQIVDTCDKCHQGEAIGHQANSDLGTQWMDCTHLEGKIIIVAHVASGFTAEVI
POSTGRQTFLLKLACRWPIIHLHTDNGANFASQEVKVMWAGIEHTFGVPLYNPOS
QGVVEAMNHLKQIDIRIQANSVETIIVLMAVHCNFKRGGIGDMTPAERLINMIT
TEQEIQFOQSKNSKFNFRVYREGRDQMKGPGLLWKGEVAILKVGTDIKVFPFR
KAKIIDYGGGKEVDSSSHEDTGEAREVA"

gene

4823. .5467

/gene="vif"

4823. .5467

/gene="vif"

/codon_start=1

/product="vif protein"

/protein_id="AAU55640.1"

/db_xref="GI:18026829"

/translation="MEBEKRWIAVPTWRIPELERMHSILKYLKTKQLQKVCYVPH

FKYGAWMTCSRVIFFLQEGSHLEVQGYHLTPKGLWLSYAVRIIYWSKNFTDVT

NYADILLHSYFFCFTAGEYRRALRGQLLSCCRFPRAHKYQVPSLQYALKVSDVR

SQENPFWKQWRNRRGLRWAKQNSRGDKQKQKPTKGANFPGLAKVLGILA"

5295. .5633

/gene="vpx"

5295. .5633

/gene="vpx"

/codon_start=1

/product="vpx protein"

/protein_id="AAU55641.1"

/db_xref="GI:18026830"

/translation="MSDPRERIPPGNSGEETIGFAFWLNRTVEEINREAVNHLPREL

IFQVQSRWBYWHDQGMSPSYKYRYLCILQKALFMHCKKGCRCGLGEGHAGWRPG

PPPPPPPLA"

5634. .5939

/gene="vpr"

5634. .5939

/gene="vpr"

/codon_start=1

/product="vpr protein"

/protein_id="AAU55642.1"

/db_xref="GI:18026831"

/translation="MEERPPENEGQPQRPEDWVVEVLBELKEELKHPDPRLLTALG

NHIYNRHGDTEGAGELIRILQALFMHFRGGCIHSRIGQPGGPNPLSAIPPSRSL"

5939. .8775

/note="derived from HIV-1"

5948. .8580

/gene="tat"

join(5948. .6162,8487. .8580)

/gene="tat"

/codon_start=1

/product="tat protein"

/protein_id="AAU55643.1"

/db_xref="GI:18026832"

/translation="MEFVDPRLPEWPKHGPSKPKTACTNICYCKKCFHCQVFTTKALG

ISYGRKRRRRRAHQNSQTHQASLSKQSSQPRGDPDTPGPKQKKVRETETDPVHQ

"

6087. .8761

/gene="rev"

join(6087. .6162,8487. .8761)

/gene="rev"

/codon_start=1

/product="rev protein"

/protein_id="AAU55644.1"

/db_xref="GI:18026833"

/translation="MAGRSQSDSEELIRTVRLIKLYQSNPPPSLESTRQARNRRRR

WRERQRIISIRISIRILTYLGRSABPVPLQLPPLRLTLDCNEDCGTSGTGQVGSPOI

LVESPTVLESQTKR"

gene

CDS

6179. .6424

/gene="vpu"

6179. .6424

/gene="vpu"

/codon_start=1

/product="vpu protein"

/protein_id="AAL55645.1"

/db_xref="GI:18026834"

/translation="MQPIQAIIVAVIIAIVVMSIIVIEYRKILRQKIDRLIDR

LIRARSDSGNSEGEISALVEMGVEMGHAPHWDVDDL"

6339. .8948

/gene="env"

6339. .8948

/gene="env"

/codon_start=1

/product="env polyprotein"

/protein_id="AAL55646.1"

/db_xref="GI:18026835"

/translation="MRVKEKYQHLWRMGWRGTMLLGMLMICSATEKLWTVVYGVV

WREATTTFCASDAKAYDTEVHNWATHACVPTDPNPQEVVLGNVTENFNWKNMVD

QMHEDIISLWDESLKPCVKLTPLCVTLNCTNLNTKTNTLTSSWCMGEKIKCS

FIYTSIRNKVKEYALFNRLDVVPVKTNTKYRLISCVTQACPKVSPQPIPI

HYCPAGFALLKCNKNTFNGSGCTNVSTVQCTHGIRPVVSTQLLNGSLAEEDIVR

SEPTDNVTKTIIVOLNESVVINCTNNNTRELSIGPGRAFARRNIIIGDIRQAHN

ISRAKNWTIQQIIVIKLREKFRNTIAFNQSGGDEIVMHSFNCGEFFYCNTPQLP

LSTNWAGTNGTEGNDITLQCRIKQIINWQKVGKAMTAPITGQIKRSRTVQREK

LDGNGNSTETETIIPRGGDMRDNRSELYKYKVRIPIGVAPTRKRRTVQREK

RAVGIGAVFLGFLGAAGSTMGAAASVTLTVQARLLLSGIVQONNLLRAIEAQNMRL

TVNGIKQOLQVIALERYLDRQQMGIGWCSGKLICTTSVPWNVSNKSVDDIWNMM

TMWEEREINDYTDIYDLLEKSTQOENKEKELLELDKWSLWNNFDTITNMLWYIRL

FIMVGLIGLIRIVFVLSIVNRQYSPLSFQTLPLPASRPDRPPEGTEEGEDR

DRGSPVNGSLALIWADRLSLCLFSYHRLRLDLIIVTRTVELLGRRGWEALKYWNLL

QYWSQELNSAVSLQYGWSYFHEAVQVWRSATETTLAGAWGDWETLRRGRWILAI

PRIRQGLELTLL"

8776. .9860

/note="derived from SIVmac239"

8782. .9573

/gene="nef"

8782. .9573

/gene="nef"

/codon_start=1

/product="nef protein"

/protein_id="AAL55647.1"

/db_xref="GI:18026836"

/translation="MGCAISMRSRPSGDLRQLRLRARGETYGRLLGEVEDGYSQSPG

GLDKGLSLSCEQKYNQGYMTPWRPAEREKLAIRYKQNDIDIEEDDLVGVS

RKVPULMTSYKLAIDMSHFIEKGGLEGYIYARRRRIIDYILEKEGIIIPDQDIT

SGGPIRYPKTFGLWKLVPVNVSDAEQDEEHYIMHPAQTSQMDPMPGEVLAWKFDPT

LAYTYEAYVRYPEEFGSKSLSEEVRRRLTARGLLNMADKKETR"

9167. .9860

/note="U3 region"

9684. .9860

/note="R region"

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231

Db 6495 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 6554

Qy 232 GCCTGTGTACCCACAGACACCCCAACCCCAAGAGTGTATTTGGGAAATGTGACAGAAAT 291

ORIGIN

Query Match 64.5%; Score 1452.6; DB 14; Length 9860;

Best Local Similarity 98.1%; Pred. No. 8.4e-296;

Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 52 TGGATCTCGGCTTCGAGATCTATGCTCTTTGGGATATTGATGATCTGTAGTGTACAGAA 111

Db 6375 TGGGGTGGAGATGGGGCACCATGCTCTTTGGGATTTGATGATCTGTAGTGTACAGAA 6434

Qy 112 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6435 AAATTGGGTTCAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 6494

<

Db 6555 GCCTGTGATCCACAGACCCCAACCCACAGAAAGTAGTATTGGGAATGTACAGAAAAT 6614
Qy 292 TTTAACTGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG 351
Db 6615 TTTAACTGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG 6674
Qy 352 GATGAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACT 411
Db 6675 GATGAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACT 6734
Qy 412 AATTGTAATCACTAAGAACTACTTAATCCCACTAGTAGCAGCTGGGAATCATGGAG 471
Db 6735 AATTGTAATCACTAAGAACTACTTAATCCCACTAGTAGCAGCTGGGAATCATGGAG 6794
Qy 472 AAAGGAGAAATAAAAAATTTGCTTTCTTATATCAACCAAGCATAAGAAATAAGGTAAG 531
Db 6795 GAAGGAGAAATAAAAAATTTGCTTTCTTATATCAACCAAGCATAAGAAATAAGGTAAG 6854
Qy 532 AAAGAATATGACATTTTAAATAGACTGTAGTACCAATAGAAATACTAATAACT 591
Db 6855 AAAGAATATGACATTTTAAATAGACTGTAGTACCAATAGAAATACTAATAACT 6914
Qy 592 AAGTATAGGTTAAATAGTTGTAACACCTCACTATTACACAGGCTGTCCAAAGGTATCC 651
Db 6915 AAGTATAGGTTAAATAGTTGTAACACCTCACTATTACACAGGCTGTCCAAAGGTATCC 6974
Qy 652 TTTGAGCAATTCCTCATACATTTATGTGTCGCCGCTGGTTGGGATGCTAAAGTGTAAC 711
Db 6975 TTTGAGCAATTCCTCATACATTTATGTGTCGCCGCTGGTTGGGATGCTAAAGTGTAAC 7034
Qy 712 AATAAGACATTTCAATGATCAGGACCATGACCAAAATGTGACACAGTACAAATGTACACAT 771
Db 7035 AATAAGACATTTCAATGATCAGGACCATGACCAAAATGTGACACAGTACAAATGTACACAT 7094
Qy 772 GGAATTAGGCGAGTGTGCTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGAC 831
Db 7095 GGAATTAGGCGAGTGTGCTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGAC 7154
Qy 832 ATAGTAATTAGATCTGAAATTTTACACAGCAATGCTTAAACCATTAATAGTACAGTAAAT 891
Db 7155 ATAGTAATTAGATCTGAAATTTTACACAGCAATGCTTAAACCATTAATAGTACAGTAAAT 7214
Qy 892 GAATCTGTAGTAATTAATTTGTACAGACCCCAACCAATACAGAGAGAGGTTATCTATA 951
Db 7215 GAATCTGTAGTAATTAATTTGTACAGACCCCAACCAATACAGAGAGAGGTTATCTATA 7274
Qy 952 GGACCCAGGAGAGCATTTTATGCAAGAGAAACATTAATAGGAGATATAAGACAGACAT 1011
Db 7275 GGACCCAGGAGAGCATTTTATGCAAGAGAAACATTAATAGGAGATATAAGACAGACAT 7334
Qy 1012 TGTAAACATTAGTAGACAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAAGA 1071
Db 7335 TGTAAACATTAGTAGACAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAAGA 7394
Qy 1072 GAAAAATTTAGGATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCCCAGAAAT 1131
Db 7395 GAAAAATTTAGGATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGCCCCAGAAAT 7454
Qy 1132 GTAATGACAGATTTTAATTTGTGGAGGGGAATTTCTTCTACTGTATAACAGCAACAATGTTT 1191
Db 7455 GTAATGACAGATTTTAATTTGTGGAGGGGAATTTCTTCTACTGTATAACAGCAACAATGTTT 7514
Qy 1192 AATAGTACTTGGATGTTACTGGGAGGACAAATGGCACTGAAGGAATGACATAATCACA 1251
Db 7515 AATAGTACTTGGATGTTACTGGGAGGACAAATGGCACTGAAGGAATGACATAATCACA 7574
Qy 1252 CTCAATGCAAGATAAAACAAATTAATAATATGTCAGAGAAAGTAGGAAAAGCAATGTAT 1311
Db 7575 CTCAATGCAAGATAAAACAAATTAATAATATGTCAGAGAAAGTAGGAAAAGCAATGTAT 7634
Qy 1312 GCCCTCCCATCATCAGGACAAATTAGATGTTCAATCAAAATATTACAGGCTGCTACTAACA 1371

Db 7635 GCCCTCCCATCATCAGGACAAATTAGATGTTCAAAATATTACAGGCTGCTACTAACA 7694
Qy 1372 AGAGATGAGGTAATAGTACTAGACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAT 1431
Db 7695 AGAGATGAGGTAATAGTACTAGACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAT 7754
Qy 1432 ATGAGGACAAATTTGGAGAAAGTGAATTAATATAAATATAAAGTAGTAAGATTGAACCAATA 1491
Db 7755 ATGAGGACAAATTTGGAGAAAGTGAATTAATATAAATATAAAGTAGTAAGATTGAACCAATA 7814
Qy 1492 GGAGTAGACCCACCCAGGCAAGAGAGAAAGCAAGTGCAGAGAGAAAAGAGGGGGAGG 1550
Db 7815 GGAGTAGACCCACCCAGGCAAGAGAGAAAGCAAGTGCAGAGAGAAAAGAGGGGGAGG 7873

RESULT 5
SIU89134
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PubMed
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
source
source
source
LTR
misc_feature
misc_feature
gene

SIU89134
Simian-Human immunodeficiency virus strain SHIV-89.6P, complete genome.
U89134
U89134.1 GI:2108163
Simian-Human immunodeficiency virus
Simian-Human immunodeficiency virus
Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 9860)
Karlsson,G.B., Halloran,M., Li,J., Park,I.W., Gomila,R.,
Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.
Characterization of molecularly cloned simian-human
immunodeficiency viruses causing rapid CD4+ lymphocyte depletion in
rhesus monkeys
J. Virol. 71 (6), 4218-4225 (1997)
97296224
9151808
2 (bases 1 to 9860)
Karlsson,G.B., Halloran,M., Li,J., Park,I., Gomila,R.,
Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.
Direct Submission
Submitted (10-FEB-1997) Human Retrovirology, Dana-Farber Cancer
Institute, 44 Binney Street, Boston, MA 02115, USA
Location/Qualifiers
1. .9860
/organism="Simian-Human immunodeficiency virus"
/proviral
/mol_type="genomic DNA"
/strain="SHIV-89.6P"
/db_xref="taxon:57667"
/clone="SHIV-89.6KB9"
1. .5946
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/notes="derived from SIV"
5947. .8778
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/notes="derived from HIV-1"
8779. .9860
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/notes="derived from SIV"
1. .301
/notes="5' LTR"
1. .177
/note="R region"
178. .301
/note="U5 region"
536. .2068
/gene="gag"

Best Local Similarity 98.1%; Pred. No. 8.4e-296; Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;			
Qy	52	TGGATCTCGGCTTCGAGATCTATGCTCTCTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	6375	TGGGGTGGAGATGGGACCATGCTCTCTGGGATGTTGATGATCTGTAGTGCTACAGAA	6434
Qy	112	AAATGTGGGTCAAGTCTATTATGGGGTACTCTGTGGAGAGAACCAACCACTCTTA	171
Db	6435	AAATGTGGGTCAAGTCTATTATGGGGTACTCTGTGGAGAGAACCAACCACTCTTA	6494
Qy	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	6495	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAGAACTAGTATTGGGAAATGTGACAGAAAAT	291
Db	6555	GCCTGTGTACCCACAGACCCCAACCCACAGAACTAGTATTGGGAAATGTGACAGAAAAT	6614
Qy	292	TTTAACTGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG	351
Db	6615	TTTAACTGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG	6674
Qy	352	GATGAAGCCTTAAGCCATGTTTAAATTAACCCACTCTGTGTTACTTTAAATTCACAT	411
Db	6675	GATGAAGCCTTAAGCCATGTTTAAATTAACCCACTCTGTGTTACTTTAAATTCACAT	6734
Qy	412	AAATTGAATATCACTAAGAACTACTTAATCCACTAGTAGCAGCTGGGAAATGATGGAG	471
Db	6735	AAATTGAATATCACTAAGAACTACTTAATCCACTAGTAGCAGCTGGGAAATGATGGAG	6794
Qy	472	AAAGGAGAAATAAAAAATGCTCTTTCTATATCAACCAAGCATATAAGAAATAAGGTAAG	531
Db	6795	AAAGGAGAAATAAAAAATGCTCTTTCTATATCAACCAAGCATATAAGAAATAAGGTAAG	6854
Qy	532	AAAGAAATGCACCTTTTAAATAGACTTGATGATGATGATGATGATGATGATGATGATGAT	591
Db	6855	AAAGAAATGCACCTTTTAAATAGACTTGATGATGATGATGATGATGATGATGATGATGAT	6914
Qy	592	AAGTATAGGTTAATAAGTTGAACACCTCAGTCAATACACAGGCTGCTCCAAAGGTATCC	651
Db	6915	AAGTATAGGTTAATAAGTTGAACACCTCAGTCAATACACAGGCTGCTCCAAAGGTATCC	6974
Qy	652	TTTCAGCAATCCCATACATTAATTTGTGTCGGCTGGGTTTGGATGCTGCTGCTGCTGCTG	711
Db	6975	TTTCAGCAATCCCATACATTAATTTGTGTCGGCTGGGTTTGGATGCTGCTGCTGCTGCTG	7034
Qy	712	AATAAGACATTCATGATCAGGACCATGACAAATGTGACACAGTACATGATGACAT	771
Db	7035	AATAAGACATTCATGATCAGGACCATGACAAATGTGACACAGTACATGATGACAT	7094
Qy	772	GGAATTAGGCGCAGTGTGCTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGAC	831
Db	7095	GGAATTAGGCGCAGTGTGCTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGAC	7154
Qy	832	ATAGTAATTAGATCTGAAAAATTTTACAGACAAATGCTAAAAACCAATAATAGTACAGCTAAAT	891
Db	7155	ATAGTAATTAGATCTGAAAAATTTTACAGACAAATGCTAAAAACCAATAATAGTACAGCTAAAT	7214
Qy	892	GAATCTGTAGTAATTAATTGTACAGACCCCAACCAATATACAGAAAGGTTTATCTATA	951
Db	7215	GAATCTGTAGTAATTAATTGTACAGACCCCAACCAATATACAGAAAGGTTTATCTATA	7274
Qy	952	GGACCGGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGCAAGCACAT	1011
Db	7275	GGACCGGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGCAAGCACAT	7334
Qy	1012	TGTAACATTAGTAGAGCAAAATGGAATAACATTTTACACAGATAGTTTATAAAATTAAGA	1071
Db	7335	TGTAACATTAGTAGAGCAAAATGGAATAACATTTTACACAGATAGTTTATAAAATTAAGA	7394
Qy	1072	GAATAATTTAGGAATAAAACATATAGCCTTTAATCAATCTCCTCAGGAGGGGACCCGAAATT	1131

Db	7395	GAATAATTTAGGAATAAAACATATAGCCTTTAATCAATCTCCTCAGGAGGGGCCAGAAATT	7454
Qy	1132	GTAATGCACAGTTTAAATTTGAGAGGGGAAATTTCTTACTGTATATACAGCACAACTGTTT	1191
Db	7455	GTAATGCACAGTTTAAATTTGAGAGGGGAAATTTCTTACTGTATATACAGCACAACTGTTT	7514
Qy	1192	AATAGTACTTTGGAATGTTTACTTGGAGGACAAATGGCACTGAGGAAATGACATATATCA	1251
Db	7515	AATAGTACTTTGGAATGTTTACTTGGAGGACAAATGGCACTGAGGAAATGACATATATCA	7574
Qy	1252	CTCAATGTCAGAAATAAAACAAATTTATAAATATGTCGAGAGAAAGTAGGAAAGCAATGTAT	1311
Db	7575	CTCAATGTCAGAAATAAAACAAATTTATAAATATGTCGAGAGAAAGTAGGAAAGCAATGTAT	7634
Qy	1312	GCCCTCCCATCATCAGGACAAATTTAGATGTTTCATCAATATATACAGGCTGCTACTAACA	1371
Db	7635	GCCCTCCCATCATCAGGACAAATTTAGATGTTTCATCAATATATACAGGCTGCTACTAACA	7694
Qy	1372	AGAGATGGAGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAT	1431
Db	7695	AGAGATGGAGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAT	7754
Qy	1432	ATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAATAGTAGTAAGAAATTTGAACCAATA	1491
Db	7755	ATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAATAGTAGTAAGAAATTTGAACCAATA	7814
Qy	1492	GGAGTAGCACCCACCAGGCAAGAGAGAACAGTGCAGGAGAGAGAGAGAGAGAGAGAGG	1550
Db	7815	GGAGTAGCACCCACCAGGCAAGAGAGAACAGTGCAGGAGAGAGAGAGAGAGAGAGAGG	7873
RESULT 6			
LOCUS	BD161892	10501 bp	DNA linear PAT 17-JAN-2003
DEFINITION	Nonhuman primate model of acquired immunodeficiency syndrome.		
ACCESSION	BD161892		
VERSION	BD161892.1	GI:27867650	
KEYWORDS	JP 2002159296-A/1.		
SOURCE	Simian-Human immunodeficiency virus		
ORGANISM	Simian-Human immunodeficiency virus		
REFERENCE	1. (bases 1 to 10501)		
AUTHORS	Shinohara, K., Sakai, K. and Honda, M.		
TITLE	Nonhuman primate model of acquired immunodeficiency syndrome		
JOURNAL	Patent: JP 2002159296-A 1 04-JUN-2002;		
COMMENT	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH		
OS	Simian-human immunodeficiency virus		
PN	JP 2002159296-A/1		
PD	04-JUN-2002		
PF	27-NOV-2000 JP 2000360274		
PI	KATSUAKI SHINOHARA, KOJI SAKAI MITSUO HONDA		
PC	C12N15/09,A01K67/027,C12N7/00,C12N7/02,G01N33/15,G01N33/50//		
PC	G01N33/569,		
PC	(C12N7/00,C12N1:93),(C12N7/02,C12N1:93),C12N15/00 CC genomic		
DNA	strains='SHIV-C2/1'		
CC	derived from SiVmac239		
CC	5' long terminal repeat		
CC	U3 region		
CC	R region		
CC	U5 region		
CC	gag		
CC	pol		
CC	vif		
CC	vpx		
CC	vpr		
CC	tat derived from HIV-1		
CC	rev		
CC	vpu		
CC	env		

ACCESSION	U039362 M96155	CDS	
VERSION	U039362.2 GI:9409797		
KEYWORDS			
SOURCE	Human immunodeficiency virus 1 (HIV-1)		
ORGANISM	Human immunodeficiency virus 1		
	Viruses: Retroid viruses; Retroviridae; Lentivirus; Primate		
	lentivirus group.		
REFERENCE	1 (bases 1 to 5029)		
AUTHORS	Collman,R.G. and Yoon,H.L.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 5030 to 9713)		
AUTHORS	Kim,F.M., Kolson,D.L., Balliet,J.W., Srinivasan,A. and Collman,R.G.		
TITLE	V3-independent determinants of macrophage tropism in a primary		
	human immunodeficiency virus type 1 isolate		
JOURNAL	J. Virol. 69 (3), 1755-1761 (1995)		
MEDLINE	95156606		
PUBMED	7853514		
REFERENCE	3 (bases 1 to 9713)		
AUTHORS	Collman,R., Balliet,J.W., Gregory,S.A., Friedman,H., Kolson,D.L.,		
	Nathanson,N. and Srinivasan,A.		
TITLE	An infectious molecular clone of an unusual macrophage-tropic and		
	highly cytopathic strain of human immunodeficiency virus type 1		
JOURNAL	J. Virol. 66 (12), 7517-7521 (1992)		
MEDLINE	93059708		
PUBMED	1433527		
REMARK	Describes the isolation of the full-length clone and virus strain		
	89.6		
REFERENCE	4 (bases 1 to 9713)	gene	
AUTHORS	Collman,R.G.	CDS	
TITLE	Direct Submission		
JOURNAL	Submitted (24-OCT-1995) Ronald G. Collman, Pulmonary & Critical		
	Care Division, University of Pennsylvania, 522 Johnson Pavilion,		
	3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA		
REFERENCE	5 (bases 1 to 9713)		
AUTHORS	Collman,R.G.	gene	
TITLE	Direct Submission	CDS	
JOURNAL	Submitted (24-JUN-2000) Ronald G. Collman, Pulmonary & Critical		
	Care Division, University of Pennsylvania, 522 Johnson Pavilion,		
	3610 Hamilton Walk, Philadelphia, PA 19104-6060, USA		
REMARK	Sequence updated by submitter		
COMMENT	On Jul 24, 2000 this sequence version replaced gi:1055029.		
FEATURES	Location/Qualifiers		
source	1..9713		
	/organism="Human immunodeficiency virus 1"		
	/proviral		
	/mol_type="genomic DNA"		
	/strain="89_6"		
	/db_xref="taxon:11676"		
	/clone_lib="subgenomic lambda phage library of HMW"		
	/note="from short-term culture in mixed peripheral blood		
	mononuclear cells."		
LTR	1..634		
	/note="5' LTR"		
	/citation=[1]		
gene	789..2291		
	/gene="gag"		
CDS	789..2291		
	/gene="gag"		
	/citation=[1]		
	/codon_start=1		
	/product="GAG polyprotein precursor"		
	/protein_id="AAA81036.1"		
	/db_xref="GI:1055030"		
	/translation="MGARASVLGGELDRWEKIRLPGGKKYKLIKHIVASRELRF		
	AVNPSLTSGCRIQLQSSLTGSEELKSLYNTVATLYCVHQRLEVDKTEALD		
	KIEEONKSKKAADATGNSSQVSPFIVQNTQGMVHQALSPRLNAAWKVE		
	EKAPSPVIMFSALESGATFDLNTMLNTVGGHQAQMQLKETINEEAASWDLHPV		
	QAGVPACQMRPGSDIAGTSTLQEQIGWMTNNPPIPVGEIYKRWIILGNKIVRM		
	YSPSLDIKQPKPEFRDYDRFYKTLRAEQASQEVKNWMTETLLVONANPDCKTIL		
	KALGPGATLEEMWTACQGVGGPHKARVLAEAMSVQVTSATIMMQRGNRQRTKVC		
	PNCCKEGHAKNCRAPRKGKWCCKGCHQMKDCTERQANFLGKIWPCHKRPGNFLQ		
	SRPEPTAPPEPSFRGEEITTTTSQKQEPIDKELYPLASIRLSLFGNDPSSQ"		
	2084..5095		
	/gene="vif"		
	/citation=[2]		
	/product="REV protein"		
	/protein_id="AAA81041.1"		
	/db_xref="GI:1055035"		
	/translation="MAGSGSDDELLKTVBLIKFLYOSPPSLGTTGTRQARNRRRR		
	RERQRQISERILFTLGRFEPVPLPLPLEKLLDNCNDCSTGTQGVGSPQIL		
	VESPAILEPGTKE"		
	2084..5095		
	/gene="pol"		
	<2084..5095		
	/gene="pol"		
	/citation=[1]		
	/codon_start=1		
	/product="POL polyprotein precursor"		
	/protein_id="AAA81037.1"		
	/db_xref="GI:1055031"		
	/translation="FFRENLAFFPGQKAREFSSEQTRANSPTTRRELQVWGDNNISSEA		
	GADRGTVLSFPQITLWQRPLVTKVGGQLKEALLDTCADDTVLEDSLPGRWPKPM		
	ETVGGFTIKVQYQIDIEIGCHAKAGTVLVGPTVNIIGRNLLTQIGCTLNFPISPI		
	ETVPKLGKMGDPKVKWOMPLTEEKIKALVEICTEMEKEGKISKIGPENPVNTVFAI		
	KKKSTWRKLVDFRELNKRQDFWEVOLGIPHPAGLKKKXSVTVLDVGDAYFSPVLD		
	EDFRKYATFTIPSINNETPGIRYQNVLPQGWKSPAIQSSMTKILBFFFRKQNPDIIV		
	IYQYMDLYVGSLEIIGQHRAKIEDLRHLLKMGFTTPDKHQKPEPFLMAYEVLHPD		
	KWTQPIVLPEKDSWTNDIQKLVKLWASQIVAGIRKQKCLLGRGKLTATVTVPL		
	TEAELELAENREILKEPVGVYDPTKDLIAELQKOGQOWTYOIOBPYKNTKTKG		
	YARWGAHTNDVKOLTEAVOKIATESIVIMGKTPKFLPIOKETWEAMWTDVQATWI		
	PEWFFVNTPLVKLWYLEKEPIVGAETFFYDGAANRDTKSGAGYVTDGRQKVSL		
	ADTTNQKTELQAIHLAQDSLEVNIVTDSQIAGIIOAQPKDSELSVSIIEQLIK		
	KERYLAWVPAHKIGGNEQDKLVKSAGIRKVLFDGIDKAOEHEKHYHTNWRWASD		
	FNLPVVAKEIVASCNKQKGEAMHQVDSPGIWLQDCTHLEKGLVILVAHVASGY		
	IEAEVIPAETGOETAYFLLLAGRWPKVTIHTDNGSNFTSTTVKAACWAGIKQSPFGI		
	PYNQSQGVSSMKNELKIIIGVORDQAEHLKTAQMAVFIHNRKRGKIGYSAGER		
	IVDLIASDIQKELQKITKIQNFRVYRDSRDLPLWKGPALKLWKGEANVIQDNSDI		
	KVPRRRKAKIIRDKYQWAGDDCVASRODED"		
	5040..5618		
	/gene="vif"		
	<5040..5618		
	/gene="vif"		
	/citation=[2]		
	/codon_start=1		
	/product="VIF protein"		
	/protein_id="AAA81038.1"		
	/db_xref="GI:1055032"		
	/translation="MENRWQVNIWQVDRMEIRTWKSLVKHHMYISGKAKGWSYRHHY		
	ESTNPRISSEVHIPLGDALVVTYTWLHTGERDWHLGQGVSIEMRKRYSTQVDPGL		
	ADRLTHLYYDFCSDSAIRKSIHLGIVSPSCYEQAGHNKVGSLQYLALAAALTPRRIK		
	PPFSPVTKLTDNRWKPQTKGHRGSHMTGTH"		
	5558..5848		
	/gene="vpr"		
	5558..5848		
	/gene="vpr"		
	/citation=[2]		
	/codon_start=1		
	/product="VPR protein"		
	/protein_id="AAA81039.1"		
	/db_xref="GI:1055033"		
	/translation="MEQAPEDQGPQREPYNDWTLELLELNKNEAVRHFPRIWLHSLGQ		
	HIYTYGDTWTGVEALIRLQQLFIHFIRIGRHSRIGIIQORRTNRGASKS"		
	5829..8458		
	/gene="tat"		
	join(5829..6042,8370..8458)		
	/gene="tat"		
	/citation=[2]		
	/codon_start=1		
	/product="TAT protein"		
	/protein_id="AAA81040.1"		
	/db_xref="GI:1055034"		
	/translation="MEPVNPSLEPWKHGPGSQPKTACTNICYCKKCCFHCQACFITKGLG		
	ISYGRKKRRQRPRRPQDSQTHQVSLSKPSSQPRGDPFGKQKKKVERETETDPVH"		
	5968..8642		
	/gene="rev"		
	join(5968..6042,8370..8642)		
	/gene="rev"		
	/citation=[2]		
	/codon_start=1		
	/product="REV protein"		
	/protein_id="AAA81041.1"		
	/db_xref="GI:1055035"		
	/translation="MAGSGSDDELLKTVBLIKFLYOSPPSLGTTGTRQARNRRRR		
	RERQRQISERILFTLGRFEPVPLPLPLEKLLDNCNDCSTGTQGVGSPQIL		
	VESPAILEPGTKE"		

KEYWORDS	Human immunodeficiency virus 1 (HIV-1)
SOURCE	Human immunodeficiency virus 1
ORGANISM	Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE	1
AUTHORS	Tang, F., Lorin, C., Mollet, L. and Delebecque, F.
TITLE	Recombinant measles viruses expressing epitopes of antigens of rna viruses - use for the preparation of vaccine compositions
JOURNAL	Patent: WO 2004001051-A 30 31-DEC-2003;
INSTITUT	INSTITUT PASTEUR (PR)
FEATURES	Location/Qualifiers
source	1..2574
	/organism="Human immunodeficiency virus 1"
	/mol_type="unassigned DNA"
	/db_xref="taxon:11676"
ORIGIN	
Query Match	59.4%; Score 1338.6; DB 6; Length 2574;
Best Local Similarity	94.3%; Pred. No. 9.7e-272;
Matches 1414; Conservative	0; Mismatches 49; Indels 36; Gaps 1.
Qy	52 TGGATCTCGGCTTCGAGATCTATGCTCTTGGGATATTGATGATCTGTAGTCTACAGAA 111
Db	37 TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTCTACAGAA 96
Qy	112 AAATTGTGGGTACAGTCTATTATGGGGTACTCTGTGGAGAGAACCAACCACTCTA 171
Db	97 AAATTGTGGGTACAGTCTATTATGGGGTACTCTGTGGAGAGAACCAACCACTCTA 156
Qy	172 TTTTGTGCATCAGATGCTTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231
Db	157 TTTTGTGCATCAGATGCTTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 216
Qy	232 GCCTGTGTACCACAGACCCCAACCCACAGAGTAGTATTGGGNAATGTACAGAAAT 291
Db	217 GCCTGTGTACCACAGACCCCAACCCACAGAGTAGTATTGGGNAATGTACAGAAAT 276
Qy	292 TTTTAAACATGTGGAATAATTAACATGGTAGATCAGATGCATGAGGATATAATCAGTTATGG 351
Db	277 TTTTAAACATGTGGAATAATTAACATGGTAGATCAGATGCATGAGGATATAATCAGTTATGG 336
Qy	352 GATGAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTCCTTAAATGTCAC 411
Db	337 GATGAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTCCTTAAATGTCAC 396
Qy	412 AATTGGAATATCATGAAGATACACTAATCCACTAGTAGCAGCTGGGGAATGATGAG 471
Db	397 AATTGGAATATCATGAAGATACACTAATCTCTACTAGTAGCAGCTGGGGAATGATGAG 456
Qy	472 AAGGAGAAATAAATAATTCCTTTCTATATCACCACAGCATGAAGAAATAAGGTAAG 531
Db	457 GAAGAGAAATAAATAATTCCTTTCTATATCACCACAGCATGAAGAAATAAGGTAAG 516
Qy	532 AAAGAATATGCACATTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT 591
Db	517 AAAGAATATGCACATTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAATAACT 576
Qy	592 AAGTATAGGTTAATAAGTTGTAAACACCTCAGTCAATACACAGGCCCTGTCCAAAGGTATCC 651
Db	577 AAGTATAGGTTAATAAGTTGTAAACACCTCAGTCAATACACAGGCCCTGTCCAAAGGTATCC 636
Qy	652 TTTTCAGCCAAATCCCATACATTATTGTGTCGGCTGGGTTTGGCATGCTAAAGGTATAC 711
Db	637 TTTTCAGCCAAATCCCATACATTATTGTGTCGGCTGGGTTTGGCATGCTAAAGGTATAC 696
Qy	712 AATAAGACATTCATAGGATCAGGACCATGCACAAATGTGCAGCACAGTACAAATGTACACAT 771
Db	697 AATAAGACATTCATAGGATCAGGACCATGCACAAATGTGCAGCACAGTACAAATGTACACAT 756
Qy	772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAAC 831
Db	757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAAC 816

JOURNAL	Submitted (04-MAR-2003) NCID/DASTLR/HARB/VETS, Centers for Disease Control & Prevention, 1600 Clifton Rd., Mail Stop G-19, Atlanta, GA 30333, USA
FEATURES	Location/Qualifiers
source	1. .2553 /organism="Human immunodeficiency virus 1" /proviral /mol_type="genomic DNA" /isolate="81NJ" /db_xref="taxon:11676" /country="USA: New Jersey" /note="sampled in 1981 subtype: B" <1. .2553 /gene="env" 1. .2553 /gene="env" /note="gp160" /codon_start=1 /product="envelope glycoprotein" /protein_id="AAP37149.1" /db_xref="GI:30794653"
gene	/translation="MRVKEIRKNYOHRLRWGTMILGILMICSAAEKLWTVYGVPPV KEATTLPCASDAKAYDTEVHNWATHACVPTDNPQSVLVLENVTENEMKNWVEQ MHEDIISLDQSLKFCVKLTPLCVTLNCTDLRNATNTSSSGTNERGEIKNCSFNIT TSIRDKVQKELAFYKLDVPIIDNDNTTTSYRLISCNTSVITQACPKVSFPPIPHYC TPAGFAILKCDKKEFGTGPCTNVSTQCTGIRFVSTVQLLLNGSLAEVEEVIKSDN FKDNTAKIIVLKRLEQNGNTIIVFNQSSGDPPEIVTHSFNCGGFFVYCDSTQLPNST AKWNTLQIVLKRLEQNGNTIIVFNQSSGDPPEIVTHSFNCGGFFVYCDSTQLPNST WNVTGNSNTEGNTILTPCRIKQIINWQEVGKAMYPPIRGQIRCSNITGLLLTR DGNNESETEIPFGGDMRNRSELYKIKVKEIPELPGVAPTAKRVRQREKRAVG IGAVPLFGAAGSMTLTVQARLLLSIVQOQNLLRAIEAQHLLQLTVWG IKQOLRAVLERYLKDQQLGIGWCSGKLICTTVPWNWSNKSLSDKIWNNTWME WERENNTSLITLIEESQOENKEBELLELKWASLWNWFDITKWLVIKIPMI VGLVGLRIVPAVLSIVNRVQYSPLSFOTELPAPRGPDRPEGTEEBGGRDRRS BLVDGLALFVWLRLSLCLPSYHRLRDLILVTRIVELLGRGHEVLKYNWLLQYWS QELKNSVSLNATIAIABGTRDVIEWQRTCRALLHPIRIRQGLERALL"
CDS	
ORIGIN	
Query Match	56.0%; Score 1262; DB 14; Length 2553;
Best Local Similarity	91.9%; Pred. No. 1.4e-255;
Matches 1370; Conservative	0; Mismatches 105; Indels 15; Gaps 3;
QY	64 TCGAGATCTATGCTCCTGGGATATGATGATCTGTAGTGCTACAGAAAAATTTGGGTC 123
Db	
QY	46 TGGGGCACCATGCTCCTGGGATATTGATGATCTGTAGTGCTGACAGAAAAATTTGGGTC 105
Db	
QY	124 ACAGTCTATTATGGGGTACCTGTGGAGAGAGCAACCCACCTCTATTTTGTGCATCA 183
Db	
QY	106 ACAGTCTATTATGGGGTACCTGTGGAGAGAGCAACCCACCTCTATTTTGTGCATCA 165
Db	
QY	184 GATGCTAAAGCCTATGATACAGGTACATATATTTGGGGCACACATGCTGTGTACCC 243
Db	
QY	166 GATGCTAAAGCATATGATACAGGTACATATATTTGGGGCACACATGCTGTGTACCC 225
Db	
QY	244 ACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303
Db	
QY	226 ACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 285
Db	
QY	304 AAAAAATACATGGTATGATGATGAGGATATTAATCAGTTTATGGATGAAGGCCTA 363
Db	
QY	286 AAAAAATACATGGTATGATGATGAGGATATTAATCAGTTTATGGATGAAGGCCTA 345
Db	
QY	364 AAGCCATGTGTAATAATTAACCCCATCTGTGTGTACTTTTAAATTTGACATAATTC 423
Db	
QY	346 AAGCCATGTGTAATAATTAACCCCATCTGTGTGTACTTTTAAATTTGACATAATTC 399
Db	
QY	424 ACTAAGAATCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA 483
Db	
QY	400 ---AGGAATGCTACTAATACCACTAGTAGTAGCGGGGAAACGATGGAGAGAGGAGAAATA 456
Db	
QY	484 AAAAAATGCTCTTCTTATATACCAACAGCATAGAAATTAAGTTAAAGAGAAATATGCA 543
Db	

RESULT 11
AY426111

LOCUS AY426111 2568 bp DNA linear VRL 28-JUN-2004
DEFINITION HIV-1 clone BaL-lp isolate BaL from USA envelope glycoprotein (env)
gene, complete cds.

ACCESSION AY426111

VERSION AY426111.1 GI:37962967

KEYWORDS

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1 (HIV-1)

Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate

lenticivirus group.

1 (bases 1 to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Intrinsic Obstacles to Human Immunodeficiency Virus Type 1

Coreceptor Switching

J. Virol. 78 (14), 7565-7574 (2004)

PUBLISHED 15220431

2 (bases 1 to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Direct Submission

Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research

Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

Location/Qualifiers

1..2568

/organism="Human immunodeficiency virus 1"

/proviral

/mol_type="genomic DNA"

/isolate="BaL"

/isolation_source="RSX4 mutant of BaL isolated after

multiple passages in CXCR4 expressing cells"

/db_xref="taxon:11676"

/clone="BaL-lp"

/country="USA"

1..2568

/gene="env"

1..2568

/gene="env"

/codon_start=1

/product="envelope glycoprotein"

/protein_id="AA05835.1"

/db_xref="GI:37962968"

/translation="MRVKEKYQHLWRWGRWGTMLLGLMIGCSATEKLWTVVYGVV

WKEATTFPCASDAKAYDETVHNWATHACVPDPNPOBEVLENVTENFNWKNMVE

OMHEDIISLDQSLKPCVKLTPLCVTLNCTDLRNTNGDNTTSSREMGGGMBKN

CSFKITIRGKQVEYALFYKLDIVPDDNNSNRYRLISCNTSVITQACPKISEPI

PIHYCAPAGFAILKCKDFNGKPCSNVSTVQCTHGIRPVVSTQLLNGSLAEVV

INSENFADNAKTIIVQLMESVEINCTRNPNTRKSIHIGPRGALYTKIKIGIRQAH

CNLSRAKNWDTLTKIVIKLEQFGNKTIVFKHSSGGDPEIVTHSPFCGGEFFYCNSTQ

LFSNTWNTDESNNTVENNTITLPCRKIQINWQKVRAMYPPIRGQIRCSNITG

LLTRDGGPDNKTVEFRPGGDMRDNRSLEYKVKVKEIPLGVAPTKAKRRVVORE

KRAVIGAVLLGFLAAGSTMGASMTLTVOARLLLSGIVQOQNNLLRAIEAQHLLQ

LTWVGILQARLVAVERLYRDLQGLIGWCSGKLCITVAVPWNASWNSKLNKLWKN

MTWMEDEINNTSIIIVSLIBESQOQEKNELELDKWSLWNFEITEWLYIK

IFMITIGLIGLIRIVFVSLIMNRVQGYSPLSFQTHLPASRGPDPGIEBEGGERD

RDRSGLVNGLSLALWDLRLSCLFSYHRLRLDLIVTRIVELLGRRGWEALKYWNWL

LQWSEQLKNSAVSLNLNATAIAVAEGTDRVIEVVGACRAIRHPRIRQGLERILL"

ORIGIN

Query Match 55.1%; Score 1241.4; DB 14; Length 2568;

Best Local Similarity 90.0%; Pred. No. 3e-251;

Matches 1355; Conservative 0; Mismatches 141; Indels 9; Gaps 2;

52 TGGATCTCGGCTCGAGATCTATGCTCCTTGGGATATTCATGATCTGTAGTCTCAGAA 111

37 TGGGGGTGAGATGGGGCCATGCTCCTTGGGATGTTGATGATCTGTAGTCTCAGAA 96

112 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA 171

97 AAATTGTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA 156

172 TTTTGTGCATCAGTCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACAT 231

157 TTTTGTGCATCAGTCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACAT 216

232 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291

217 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAT 276

292 TTTAACATGTGGAAAAATPAAACATGGTATGATGATGATGATGATGATGATGATGAT 351

277 TTTAACATGTGGAAAAATPAAACATGGTATGATGATGATGATGATGATGATGATGAT 336

352 GATGAAGCCCTAAGCCATGTGTAATAATTAACCCCACTCTGTGTACCTTTAAATGCACT 411

337 GATCAAGCCCTAAGCCATGTGTAATAATTAACCCCACTCTGTGTACCTTTAAATGCACT 396

412 AATTGGAATATCACTA-----AGAAATCTACTAATCCCACTAGTAGCAGCTGGGGAATG 465

397 GATTGAGGATATCTACTAATGGGATGACACTAATACCACTAGTAGTAGCAGGGAATG 456

466 ATGGAGAAAGAGAAATAAAAAATTTGCTCTTTCTATATACCAAGCATTAAGAAATAG 525

457 ATGGGGGAGAGAAATGAAAAATTTGCTCTTTCAAAATCACCACAAACATAGAGGTAG 516

526 GTAAAGAAAGATATGCACTTTTAAATAGACTGTGATGTAGTACCAATAGAAATACTAAT 585

517 GTGCAGAAAGAAATATGCACTTTTAAATAGACTGTGATGTAGTACCAATAGAAATAGT 576

586 AATACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAG 645

577 AATAATAGATATAGGTTGATTAAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAG 636

646 GTATCCTTTAGCCCAATTTCCCATACATTTATGTGTGCCGGTGGTGTTCGATGTCTAAG 705

637 ATATCCTTTAGCCCAATTTCCCATACATTTATGTGTGCCGGTGGTGTTCGATGTCTAAG 696

706 TGTAAACATAGACATTTCAATGGATCAGGACCATGCAAAATGTGTCAGACAGTACAAATGT 765

697 TGTAAAGATAGAAAGTTTCAATGGAAAGGACCATGTTCAAAATGTGTCAGACAGTACAAATGT 756

766 ACACATGGAATTTAGGCCAGTGGTGTCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA 825

757 ACACATGGAATTTAGGCCAGTGGTGTCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA 816

826 GAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGTCTTAAACCATTAATAGTACAG 885

817 GAAGAGGTAGTAATTTAGATCTGAAATTTTCGCGGCAATGTCTTAAACCATTAATAGTACAG 876

886 CTAATAGTACTGTAGTATTAATTTGTACAGACCCCAACCAATACAGAGAGAGAGTTA 945

877 CTGAATGAATCTGTAGAAATTAATTTGTACAGACCCCAACCAATACAGAGAGAGAGTTA 936

946 TCTATAGGACACGAGGAGAGCATTTTATGCAAGAGAAACATTAATAGGAGATATAAGACAA 1005

937 CATATAGGACACGAGGAGCATTTATACACAGGAGAAATTAATAGGAGATATAAGACAA 996

1006 GCACATTTGATATTTAGTAGACAAAAATGGAATAACATTTTACACAGATAGTTTATAAAA 1065

997 GCACATTTGATATTTAGTAGACAAAAATGGAATAACATTTTAAATAAGATAGTTTATAAAA 1056

1066 TTAAGAGAAAAATTTAGGATTAAGAAATTAAGTCTTTTAAATCAATCTCAGAGGGGACCA 1125

1057 TTAAGAGAAAAATTTAGGATTAAGAAATTAAGTCTTTTAAATCAATCTCAGAGGGGACCA 1116

1126 GAAATTTGAAATGCACAGATTTTAAATTTGTGGAGGGGAATTTCTTACTGTAAATACAGACAA 1185

1117 GAAATTTGACGACACAGATTTTAAATTTGTGGAGGGGAATTTTCTACTGTAAATCAACACAA 1176

1186 CTGTTTAAATAGTACTTGGAAATGTTTACTGGAGGGAACAAATGGGCACTGAAGGAAATGACATA 1245

1177 CTGTTTAAATAGTACTTGGAAATGTTTACTGAAGAGTCAAAATTAACACTGTAGAAAAATACACA 1236

1246 ATCACATCCCATGAGATTAAGAAATTAAGTCTTGTGAGAGAGTGTGAGAGAAATGACATA 1305

1237 ATCACATCCCATGAGATTAAGAAATTAAGTCTTGTGAGAGAGTGTGAGAGAAATGACATA 1296

1306 ATGTATGCCCTTCCCATCACAGGACAAATTTAGATGTTCATCAAAATTTACAGGGCTGCTA 1365

Db 1297 ATGTATGCCCTCCCATCAGAGACAAATAGATGTTTCATCAATATTACAGGGCTGCTA 1356
Qy 1366 CTAACAAGAGATGGAGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACTCGGAGCA 1425
Db 1357 TTAACAGAGATGGTGG---TCCAGAGGACAACAAGCCGAGGCTTCAGACTGGAGA 1413
Qy 1426 GGAGATATGAGGACAATTTGGAGAGTGAATATATAAATAAAGTAGTAAGAATTGAA 1485
Db 1414 CGAGATATGAGGACAATTTGGAGAGTGAATATATAAATAAAGTAGTAAGAATTGAA 1473
Qy 1486 CCAATAGGAGTACCAACCCAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1545
Db 1474 CCAATAGGAGTACCAACCCAGGCAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGCA 1533
Qy 1546 GGAGG 1550
Db 1534 GTGGG 1538

RESULT 12
AY426112
LOCUS AY426112 2568 bp DNA linear VRL 28-JUN-2004
DEFINITION HIV-1 clone Bal-1A isolate Bal from USA envelope glycoprotein (env)
gene, complete cds.
ACCESSION AY426112
VERSION AY426112.1 GI:37962969
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate
REFERENCE 1 (bases 1 to 2568)
AUTHORS Pastore, C., Ramos, A. and Mosier, D. E.
TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
CORRECTOR Switching
J. Virol. 78 (14), 7565-7574 (2004)
JOURNAL 15220431
PUBMED 2 (bases 1 to 2568)
REFERENCE Pastore, C., Ramos, A. and Mosier, D. E.
AUTHORS Direct Submission
TITLE Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
JOURNAL Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
LOCATION/Qualifiers
FEATURES
1. .2568
source /organism="Human immunodeficiency virus 1"
/proviral
/mol_type="genomic DNA"
/isolate="Bal"
/isolation_source="R5X4 mutant of Bal isolated after
multiple passages in CXCR4 expressing cells"
/db_xref="taxon:11676"
/clone="Bal-1A"
/country="USA"
1. .2568
gene /gene="env"
1. .2568
CDS /gene="env"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AA05836.1"
/db_xref="GI:37962970"
/translation="NRVKEKYHWRWGWGTMGLGLMIGCSATEKLWTVVYGVVP
WKEATTLFCASDAKAYDTEHNVATHACVPTDPNPOEVELENVTENPMWKNMVE
QNHEDIISLDQSLKPCVKLTPCLVTLNCTDLRTNNGNDNTSSRSMGGGEMKN
CSFKLITIRGVQKEYALFYKLDIVPDINNNSNRRLISCVITQACPKISPEPI
PHYCAPAGFALKCKDKKFGKPCSVQCTGHGIRPVVSTQLLNGSLAEVEV
IRSEFNADNAKTIIVQLNESVEINCRPNNTKSHIGPGRALYTKIKIGDIRQAH
CNLSRAKNDTLNKIVIKLREOFGNKTVFVHSSGDPDEIVHNSFNCGEPPYCNSTQ
LPNSTWNTVEESNVTVENTITLPCRIKQIINWOKVGRMAYAPIRGICSSNITG
LLLTDDGDPEDNKTVEFRPGGDMRDNRSELYKYKVKBELGVAPTKARVVORE
KXAVGIGAVFLGLLGAAGSTMGAASMTLVQARLLLSGIVQOONLLRAIEAQHLLR
LTVMGIKQARVLAVERYLRDQQLLGIWGCSGKLICTTAVPMNASWSNKSINKINDN

MTWMEWDREINNYTSIIYSLEESNQOQKNEQELLELDKWASLWNWPFITBWLWIK
IPIMIGLIGLIRIVFSLSIMNRVQGYSPLSFQTHLPASRPPRGIGIBEGGERD
RDRSRLVNGSLALWDLRLSLCFSYHRLRDLILVTRIVELLGLRRGWALKYWNWL
LQYMQELKNSAVSLNATAITAVAGTDRVIEVQGCACRAIRHIPPRIQGLERILL"
ORIGIN
Query Match 55.1%; Score 1239.8; DB 14; Length 2568;
Best Local Similarity 90.0%; Pred. No. 6.6e-251;
Matches 1354; Conservative 0; Mismatches 142; Indels 9; Gaps 2;
Qy 52 TGGATCTCGGCTTCAGATCTATGCTCTTGGGATATTGATGATCTGTAGTCTCAGAA 111
Db 37 TGGGGTGGAGATGGGGCACCATGCTCTTGGGATGTTGATGATCTGTAGTCTCAGAA 96
Qy 112 AAATTTGTGGGTCAACAGTCTATTATTTGGGTACCTGTGTGGAGAGAGCAACACCACCTCTA 171
Db 97 AAATTTGTGGGTCAACAGTCTATTATTTGGGTACCTGTGTGGAGAGAGCAACACCACCTCTA 156
Qy 172 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 157 TTTTGTGATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATCTGCAGAGAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGAAAATGTGCAGAAAAT 276
Qy 292 TTTAACATGTGAAAAATAACAATGCTAGATCAGATGATGAGGATATATTCAGTTTATGG 351
Db 277 TTTAACATGTGAAAAATAACAATGCTAGAGACAGATGATGAGGATATATTCAGTTTATGG 336
Qy 352 GATGAAAGCTTAAAGCCATGTGTAAAAATTAACCCACCTCTGTGTACTTTTAAATTCACCT 411
Db 337 GATCAAAAGCCTAAAGCCATGTGTAAAAATTAACCCACCTCTGTGTACTTTTAAATTCACCT 396
Qy 412 AATTTGAATATCACTA-----AGAACTACTACTACTCCACTAGTAGGAGCTGGGGAATG 465
Db 397 GATTTGAGGAATCACTAATGAGGAATGACACTAATACCACTAGTAGTAGGAGGAAATG 456
Qy 466 ATGAGAGAGAGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCAATAAGAAATAG 525
Db 457 ATGGGGGGAGAGAAATGAAAAATTTGCTCTTTCAAAATCACCACACATAAGAGGTAAG 516
Qy 526 GTAAAGAGAGAAATATGCACCTTTTAAATAGACTGTGATGATGATGATGATGATGATGATGAT 585
Db 517 GTGCAGAGAGAAATATGCACCTTTTAAATAGACTGTGATGATGATGATGATGATGATGATGAT 576
Qy 586 AATCTAGTATAGGTAAATAGTTGTAACTCAGTCACTTACACAGGCTGCTCCAGAG 645
Db 577 AATAATAGATATAGGTTGATAGTTGTAACTCAGTCACTTACACAGGCTGCTCCAGAG 636
Qy 646 GTATCTTTTACGCCCAATTTCCCATACATTTATTTGTCCTGGCTGGGTTTTCGATGCTAAAG 705
Db 637 ATATCTTTGAGCCAATTTCCCATACATTTATTTGTCCTGGCTGGGTTTTCGATGCTAAAG 696
Qy 706 TGTAAACAATAGACATTCATAGGATCAGGACCATGCAAAATGTCAGCAAGTACATATGT 765
Db 697 TGTAAAGATAAGAGTTCAATTTGGAAGAGGACCATGTTTCAAAAGTTCAGCAAGTACATATGT 756
Qy 766 ACACATGGAATTTAGGCCAGTGTGCACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTTAGGCCAGTGTGCACTCAACTGCTGTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAAAATTTACAGACAAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAAAAATTTTCGGGACCAATGCTTAAACCATATAGTACAG 876
Qy 886 CTAATAGTATCTGTAGTAAATTAATTTGTAAGAGCCCAACAAATATCAAGAGAGAGTTA 945
Db 877 CTGAATGAATCTGTAGAAATTAATTTGTAAGAGCCCAACAAATATCAAGAGAGAGTTA 936
Qy 946 TCTATAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
Db 937 CATATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 996

QY	1006	GCACATTGTAACATTAGTAGACCAAAATCGAATAACACATTTTACAACAGATAGTTATAAAA	1065
DB	997	GCACATTGTAACCTTAGTAGACCAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAA	1056
QY	1066	TTAAGAGAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGACCCA	1125
DB	1057	TTAAGAGAACAAATTTGGGAATAAAACAATAGTCTTTAAGCATTCCTCAGGAGGGACCCA	1116
QY	1126	GAATTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTCCTTACTGTAAATACACACAA	1185
DB	1117	GAATTGTCACACACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAAATTCACACAA	1176
QY	1186	CTGTTTAAATAGTACTTGAATGTTACTCGAGGAGCAAAATGGCACGTAAGGAAATGACATA	1245
DB	1177	CTGTTTAAATAGTACTTGAATGTTACTGAAAGAGTCAAAATAACACTGTAGAAAATAACACA	1236
QY	1246	ATCACATCCCAATGCAGATAAAACAAATTTATAATATGTGCGAGAAAGTAGGAAAAGCA	1305
DB	1237	ATCACATCCCAATGCAGATAAAACAAATTTATAATATGTGCGAGAAAGTAGGAAAAGCA	1296
QY	1306	ATGATATGCCCTCCCATACAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTGCTA	1365
DB	1297	ATGATATGCCCTCCCATACAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTGCTA	1356
QY	1366	CTAACAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTCGAGGA	1425
DB	1357	TTAACAGAGATGGTGG---TCCAGAGGACACAAGCCGAGGTCTTCAGACCTCGAGGA	1413
QY	1426	GGAGATATGAGGACAAATTTGAGAGAGTGAATTTATATAATAATAAAGTAGTAAGAAATTGAA	1485
DB	1414	GGAGATATGAGGACAAATTTGAGAGAGTGAATTTATATAATAATAAAGTAGTAAGAAATTGAA	1473
QY	1486	CCAATAGGATAGACCCCAACAGGGCAAGAGAGAGAACAGTGCACAAAGAGAAAAAGAGGG	1545
DB	1474	CCAATAGGATAGACCCCAACAGGGCAAGAGAGAGAGTGTGTCAGAGAGAAAAAGAGCA	1533
QY	1546	GGAGG 1550	
DB	1534	GTGGG 1538	

RESULT 13	
LOCUS	AY426118
DEFINITION	HIV-1 clone Bal-4p isolate Bal from USA envelope glycoprotein (env)
ACCESSION	AY426118
VERSION	AY426118.1
KEYWORDS	GI:37962981
SOURCE	Human immunodeficiency virus 1 (HIV-1)
ORGANISM	Human immunodeficiency virus 1 (HIV-1)
REFERENCE	Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
AUTHORS	1 (bases 1 to 2568)
TITLE	Pastore, C., Ramos, A. and Mosier, D.E.
JOURNAL	Intrinsic Obsacles to Human Immunodeficiency Virus Type 1
PUBLISHED	Coreceptor Switching
REFERENCE	J. Virol. 78 (14), 7565-7574 (2004)
AUTHORS	15220431
TITLE	2 (bases 1 to 2568)
JOURNAL	Pastore, C., Ramos, A. and Mosier, D.E.
PUBLISHED	Direct Submission
AUTHORS	Submitted (02-Oct-2003)
TITLE	Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
JOURNAL	Location/Qualifiers
FEATURES	1..2568
source	/organism="Human immunodeficiency virus 1"
	/proliferal
	/mol_type="genomic DNA"
	/isolate="Bal"
	/isolation_source="RSX4 mutant of Bal isolated after
	multiple passages in CXCR4 expressing cells"

gene	/db_xref="taxon:11676"
CDS	/clone="Bal-4p"
	/count="USA"
	1..2568
	/gene="env"
	1..2568
	/gene="env"
	/codon_start=1
	/product="envelope glycoprotein"
	/protein_id="AAR05842.1"
	/db_xref="GI:37962982"
	/translation="MRVKERYQHLWRGWRGTMGLMLMI CSA TEKLVTVTYVGVV
	WKEATITLFCASDAKAYDEVHNVWATHACVPTDENPOSELENTENFNMKNMNV
	QMHDIISLWQSLKPCVKLPCLVTLCTDLNRNATNDNTTSSSREMMGGGGMKN
	CSFKITNIRCKVOKEYALFYKLDIVIPIDNNNNRYRLISNTSVITQACPKISPEPI
	PIHYCAPAGFALLCKCKFKNGKPCSNVSVQCTHGRPVVSTQLLNGSLAESEV
	IRSNFADNAKTIIVOLNESVEINCTRNNTNRHSIHIGPRALYITTKIGIDIRQAH
	CNLRKAWNDTLNKIVIKLREQFGNKTIVFKHSSGGDEIVTHSPNCGEFPYCSNQ
	LFNSTWNVTESSNNTVENNTITLPCRIMQIIMMOKVGRAMYAPPVIRQIIRCSNITG
	LLLRDGGPDNKTVEPRPGGDMRDNWRSLEYKVKVILBPLGAPVTKAKRVVQRE
	KRAGIGAVFGLFGLGAAGSTWGAASMTLTVOARLLLSGIVQOONNLLRAIEAQHLLQ
	LTWGIKOLQARVLAVERYLRDQQLGLIWWGSGKLICTTAVPWNASWNSKSLKIDN
	MTMWEDEINNYTSIIYSLEBESQOEKNEQELLELDKWLAWNWFETBWLWYIK
	IFIMTIGLILGRIVFVSLIMNRVQGYSPLSFQTHLPASGRDPRPGIEEBEGWNL
	RDRSGLVNGSLALIWDDLRLCLFVYHRLRDLILLIVTRIVELLGRGWEALKYWNL
	LQYKSQELKNSAVSLNATAJAVAEGRDRIEVEVQGCACRAIRHIRPRIRQGLERILL"
ORIGIN	
	Query Match 55.0%; Score 1238.2; DB 14; Length 2568;
	Best Local Similarity 89.9%; Pred. No. 1.4e-250;
	Matches 1353; Conservative 0; Mismatches 143; Indels 9; Gaps 2;
QY	52 TGGATCTCGCTTCAGATCTATGCTCTCTGGGATATGATGATCTGTAGTCTACAGAA 111
DB	37 TGGGGGTGGAGATGGGGCACCCTCTCTGGGATGTTGATGATCTGTAGTCTACAGAA 96
QY	112 AAAATTTGGGTGCACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 171
DB	97 AAAATTTGGGTGCACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 156
QY	172 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231
DB	157 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 216
QY	232 GCTGTGTACCCACAGAGCCCAACCAAGAGAGTAGTATTGGGAAATGTGCAGAGAAAT 291
DB	217 GCTGTGTACCCACAGAGCCCAACCAAGAGAGTAGTATTGGGAAATGTGCAGAGAAAT 276
QY	292 TTTAACTGTGGAAAAATAACATGTTAGATCAGATGCGATGAGGATATATCATGTTTATGG 351
DB	277 TTTAACTGTGGAAAAATAACATGTTAGATCAGATGCGATGAGGATATATCATGTTTATGG 336
QY	352 GATGAAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTGTTACTTTAAATGCACT 411
DB	337 GATCAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTGTTACTTTAAATGCACT 396
QY	412 AATTTGA-----ATATCACTAAGATACTACTTAATCCCACTAGTAGCAGCTGGGAAATG 465
DB	397 AATTTGA-----ATATCACTAAGATACTACTTAATCCCACTAGTAGCAGCTGGGAAATG 456
QY	466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCATAGAGAAATAAG 525
DB	457 ATGGGGGAGGAGAAATGAAAAATTTGCTCTTTTCAAAATCACCACAAACATAAGAGGTAAG 516
QY	526 GTAAAGAGAGAAATATGCACTTTTAAATAGACTGTATGATGATGATGATGATGATGATGAT 585
DB	517 GTGAGAGAGAAATATGCACTTTTAAATAGACTGTATGATGATGATGATGATGATGATGAT 576
QY	586 AATACCTAGTATAGGTTAATAAGTTTAACTCACTCACTCACTCACTCACTCACTCACTCACT 645
DB	577 AATAATAGATATAGGTTGATAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTA 636
QY	646 GTATCTTTTACGCCAATTTCCCATACATATTATGTGTCGCCGCTGGGTTTGGATGCTAAAG 705

Db 637 ATATCTTTGAGCAATTCACATATATGTCGCCCGCTGTTTGGATCTCAAAG 696
QY 706 TGTAAACAATAAGACATTCATATGATCAGGACCAATGACAAATGTCAGCAGTACAAATGT 765
Db 697 TGTAAAGATAAGAGTTCATATGGAAGGACCATGTTCAAATGTCAGCAGTACAAATGT 756
QY 766 ACATATGGAATATAGGCGAGTGTGTCATCAATCTCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACATATGGGATATAGGCGAGTGTGTCATCAATCTCTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATATATATGATCTGAAATTTTACAGACAATGCTTAACCAATATATAGTACAG 885
Db 817 GAAGAGGTATATATGATCCGAAATTTTGGGCAATATGCTTAACCAATATATAGTACAG 876
QY 886 CTAATATGAATCTGTAGTAATTAATGTCACAGACCCCAACAAATCAAGAAAGAGGTTA 945
Db 877 CTGAATGAATCTGTAGAAATTAATGTCACAGACCCCAACAAATCAAGAAAGAGTATA 936
QY 946 TCTATAGGACCGAGGAGAGCATTTTATGCAAGAGAAACATATATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCGAGGAGAGCATTTATACAAAGGAAATATATAGGAGATATAGACAA 996
QY 1006 GCACATTTGAACATATATAGTACGCAAAATGGAATGACACTTTTAAATAAATAGTTATAAA 1065
Db 997 GCACATTTGAACCTTATAGTACGCAAAATGGAATGACACTTTTAAATAAATAGTTATAAA 1056
QY 1066 TTAAGAGAAATTTTATAGGAAATTAACAAATAGCTTTAAATCAATCTCTCAGAGGGACCCA 1125
Db 1057 TTAAGAGAAATTTTATAGGAAATTAACAAATAGCTTTTAAAGATCTCTCAGAGGGACCCA 1116
QY 1126 GAAATTTGTAATGACAGTTTTTAAATGTCAGGGGAAATCTTCTATGTTAATACAGACAA 1185
Db 1117 GAAATTTGTCAGGACAGTTTTTAAATGTCAGGGGAAATTTTCTATGTTAATCAACACAA 1176
QY 1186 CTGTTTAATAGTACTTGGAAATGTTACTGAGGAGCAAAATGGCACTGAAGAAATGACATA 1245
Db 1177 CTGTTTAATAGTACTTGGAAATGTTACTGAGGAGTCAATTAACACTGTAGAAATTAACACA 1236
QY 1246 ATCACACTCCAATGACAGATAAAACAAATATTAATATATGTCAGAGAAAGTACGAAAGCA 1305
Db 1237 ATCACACTCCATGACAGATAAAACAAATATTAACATGTGGCAGAAAGTACGAAAGCA 1296
QY 1306 ATGTATGCCCTCCCATCAGGACAAATATAGATGTTTCATCAAAATATACAGGGCTGCTA 1365
Db 1297 ATGTATGCCCTCCCATCAGGACAAATATAGATGTTTCATCAAAATATACAGGGCTGCTA 1356
QY 1366 CTAACAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTCTTCAGACTGGAGGA 1425
Db 1357 TTAACAGAGATGGTGG---TCCAGAGGACAAACAGACCGAGGTCTTCAGACTGGAGGA 1413
QY 1426 GGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGAAATTGAA 1485
Db 1414 GGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGAAATTGAA 1473
QY 1486 CCAATAGGATGAGACCCCAAGGCAAGAGAGAAACAGTGCACAAAGAGAAAAAGAGGG 1545
Db 1474 CCAATAGGATGAGACCCCAAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAAGAGCA 1533
QY 1546 GGAGG 1550
Db 1534 GTGGG 1538

RESULT 14
AY426110
LOCUS
DEFINITION
HIV-1 isolate BaL from USA envelope glycoprotein (env) gene,
complete cds.
ACCESSION
AY426110
VERSION
AY426110.1
KEYWORDS
Human immunodeficiency virus 1 (HIV-1)

ORGANISM
Human immunodeficiency virus 1
Viruses; Retroviridae; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE
1 (bases 1 to 2568)
AUTHORS
Pastore, C., Ramos, A. and Mosier, D.E.
TITLE
Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
Coreceptor Switching
J. Virol. 78 (14), 7565-7574 (2004)
PUBMED
15220431
REFERENCE
2 (bases 1 to 2568)
AUTHORS
Pastore, C., Ramos, A. and Mosier, D.E.
TITLE
Direct Submission
Submitted (02-Oct-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
LOCATION/Qualifiers
1. .2568
/organism="Human immunodeficiency virus 1"
/proviral
/mol_type="genomic DNA"
/isolate="BaL"
/db_xref="taxon:11676"
/country="USA"
1. .2568
/gene="env"
1. .2568
/gene="env"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AA05834.1"
/db_xref="GI:37962966"
/translation="MRVKEKYOHLMRWGRWGTMLLGLMIMICSATEKLVVTVYGVV
WKEATTTTFCSADAKAYDEVHNWATHACVPTDPNPOEVELENTENFNMNKNVVE
QKHEDIIISLWQSLKPCVKLTPLCTVLTACTDLNRATNGDNTTSSSRMGGEKMN
CSFKITNIRGKQKEVALFYELDIVPTDNNNNRRLISNTVTSITQACPKISPEPI
PIHYCAPAGAILKCKDKKFKGKPCSNVSTVQCTHGRPVVSTOLLGSLAEERVV
IRSENFADNAKTLIVQLNEVEINCTRENNTKRSIHGIPGPRALVTGELIGDIRAH
LNSRAKWNDDTLKIVIKLRFQGNKTIKFRHSSGSDPEIVTHSFNCGGEFFYCNSTQ
LFNSTWNTYESNNTVNTTLPCKRIQINMWQKVGAMYPAPPIRGQICSSNTIG
KRAVGIGAVFLGFLGAGSTWGAASMTLTVOARLLSGIVQQNNLSTAEQAQHLQ
LTVGKIKOLQARVLAVERYLRDQQLGLTWGSGKLICTTAVPMNASWSNKSINKLWDN
MTWMDREINNTYSIIYSLIEESQNKREKQELLELDKWSLUNWFEITBWLWYIK
IFPMIGGLIGLRIVFSLISIMNRVQYSPUSFQHLFPASGRPPGPGGIESEGBRD
RDRSLRGLVSLALIDRLSLCLFSYHRLRDLIVTRIVELLRRGRGHEALKYWNWL
LQYWSQLKNSAVSLNATAVAEBGTDRVIEVQGACRAIRHPRIRQGLERILL"

Query Match 54.9%; Score 1236.6; DB 14; Length 2568;
Best Local Similarity 89.8%; Pred. No. 3.1e-250;
Matches 1352; Conservative 0; Mismatches 144; Indels 9; Gaps 2;
QY 52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111
Db 37 TGGGGGTGGAGTGGGGACCATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 96
QY 112 AAATTTGGGTCCAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA 171
Db 97 AAATTTGGGTCCAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA 156
QY 172 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231
Db 157 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 216
QY 232 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAT 276
QY 292 TTTTAACTGTGGAAAAATAACATGTTAGTACAGATGTCATGAGGATATATATGTTATGG 351
Db 277 TTTTAACTGTGGAAAAATAACATGTTAGTACAGATGTCATGAGGATATATATGTTATGG 336
QY 352 GATGAAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTTAAATTCAC 411

Db 337 GATCAAGCCCTAAAGCCATGTGTAAAAATTAACTCCACTCTGTGTACTTTTAAATTGCACT 396

Qy 412 AATTGA-----ATATCACTAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGAATG 465

Db 397 GATTTGAGGAATGCTACTAATGGGAATGACACTAATACCACTAGTAGTAGCAGGGAATG 456

Qy 466 ATGGAGAAGGAGAAATAAAAAATTCCTTTCTATATCACACAAGCATAGAATAAG 525

Db 457 ATGGGGGAGGAGAAATGAAANAATTCCTTTTCAANAATCACCAANAATAGAGGTAAAG 516

Qy 526 GTAAAGAAGAATATGCACTTTTAAATAGACTTGATGTAGTAGTACCAATAGAAAATACTAAT 585

Db 517 GTGCAGAAAGAATATGCACTTTTATGAACCTTGATATAGTACCAATAGATAAATAAGT 576

Qy 586 AATACCTAAGTATAGTTAATAGTTGTAACACCTCAGTCATTACACAGCCTGTCCAAAG 645

Db 577 AATAATAGATATAGTTGTAATAGTTGTAACACCTCAGTCATTACACAGCCTGTCCAAAG 636

Qy 646 GTATCCTTTGAGCCCAATCCCATACATTATGTGTCGCGCTGGGTTTGGCATGCTAAAG 705

Db 637 ATATCCTTTGAGCCCAATCCCATACATTATGTGTCGCGCTGGGTTTGGCATGCTAAAG 696

Qy 706 TGTAAACAATAGACATTCAAATGGATCAGGACCATGCACAAAATGTGAGCACAGTACAATGT 765

Db 697 TGTAAAGATAAGAACTTCAATGGAAGAGGACCATGTTCAAATGTGAGCACAGTACAATGT 756

Qy 766 ACACATGGAATAGGCCAGTGTGTCAACTCACTGCTGTTTAAATGGCAGTCTAGCAGAA 825

Db 757 ACACATGGATTAGGCCAGTGTATCAACTCACTGCTGTTTAAATGGCAGTCTAGCAGAA 816

Qy 826 GAAGACATAGTAATTAGATCTGAAAATTTTACAGACAATGCTTAAACCATATAGTACAG 885

Db 817 GAAGAGGTAGTAATTAGATCCGAAAATTTTCGGGCAATGCTTAAACCATATAGTACAG 876

Qy 886 CTAATATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAGAGAAAGTTA 945

Db 877 CTGAATGAATCTGTAGAAATTAATTTGTACAAGACCCCAACAATACAGAAAGTATA 936

Qy 946 TCTATAGNACGAGGAGAGCATTTTATGCAAGAAGAAACATATAGGAGATATAGACAA 1005

Db 937 CATATAGGACGAGGAGAGCATTTATATACAGAGGAGAAATATAGGAGATATAGACAA 996

Qy 1006 GCACATTTGAACATTAGTAGACAAAATGGAATAACACTTTTACACAGATAGTTATAAAA 1065

Db 997 GCACATTTGAACCTTAGTAGACAAAATGGAATGACACTTTTAAATAGATAGTTATAAAA 1056

Qy 1066 TTAAGAGAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCTCAGGAGGGACCCA 1125

Db 1057 TTAAGAGAACAAATTTGGGAATAAAACAATAGTCTTTAAGCAATCTCAGGAGGGACCCA 1116

Qy 1126 GAAATTTGAATGCACAGTTTTTAATTTGTGGAGGGAAATCTTCTACTGTAAATACAGACNA 1185

Db 1117 GAAATTTGTGACGCACACAGTTTTTAATTTGTGGAGGGAAATTTTCTACTGTAAATCAACACAA 1176

Qy 1186 CTGTTTAAATAGTACTTGAATGTTACTGAGGAGCAAAATGGCACTTGAAGGAATGACATA 1245

Db 1177 CTGTTTAAATAGTACTTGAATGTTACTGAAAGAGTCAATTAACACTGTAGAAAATACACA 1236

Qy 1246 ATCACACTCCAATGCAGATAAAACAATAATATAATATGTGCAGAAAGTAGGAAAGCA 1305

Db 1237 ATCACACTCCCATGCAGATAAAACAATAATATAACATGTGCAGAAAGTAGGAAAGCA 1296

Qy 1306 ATGTATGCCCTCCCATGCAGACAAATTAGATGTTTCAATCAATATTAACAGGCTGCTA 1365

Db 1297 ATGTATGCCCTCCCATGCAGACAAATTAGATGTTTCAATCAATATTAACAGGCTGCTA 1356

Qy 1366 CTAACAAGATGGAGGTAAATAGTACTGAGACTGAGACTGAGACTCTTTCAGACTGGAGGA 1425

Db 1357 TTAACAAGAGATGGTGG-----TCCAGAGGACAAACAGACCGAGGTCTTTCAGACTGGAGGA 1413

Qy 1426 GGAGATATAGGAGCAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGAATTGAA 1485

Db 1414 GGAGATATAGGAGCAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGAATTGAA 1473

Qy 1486 CCAATAGGATAGCACCCACCAGGCAAGAGAGAAACAGTGCAAAGAGAAAAAGAGGG 1545

Db 1474 CCAATAGGATAGCACCCACCAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAAGAGCA 1533

Qy 1546 GGAGG 1550

Db 1534 GTGGG 1538

RESULT 15

AY426113

LOCUS

DEFINITION

AY426113

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .2568

/organism="Human immunodeficiency virus 1"

/proviral

/mol_type="genomic DNA"

/isolate="Bal"

/isolation_source="RSX4 mutant of Bal isolated after multiple passages in CXCR4 expressing cells"

/db_xref="taxon:11676"

/clone="Bal-1B"

/country="USA"

1. .2568

/gene="env"

1. .2568

/gene="env"

/codon_start=1

/product="envelope glycoprotein"

/protein_id="BAR05837.1"

/db_xref="GI:37962972"

/translation="MRVKEKYQHLNRWRMGTMLLGMLMICSATEKLVVTVYGVV

WKEATTLFCASDAKAYDEVHNVWATHACVPTDPNQEVELENTFNFMKNMNV

OMHEDIISLWQSLKPCVKLPTCLVTLNCTDLRNTNGDNTNTSSRMMGGEMKN

CSFKITTIIRGKVOKEVALFYKLDIVIPIDNNNNRRLISCNSTVITQACPISEPI

PIHYCAPAGAILCKDKKFKNGKPCSNVSTVQCTHGRIPVSTOLLGSLAEDEV

IRSENPAKATIIIVQLNESVEINCRPNNTKSIHIGPGKIVYTGKIGDIRQAH

CNLSAKWNTDLNKIVIKLRQFGNKTIVFRHSSGGDEPIVTHSFCGGEFYCNSTQ

LFNSTWNTTEESNNTVENTTILPCRIKQIINMWKVGAMTYAPPPIRGQICSSNIT

LLLTRDGGPENKTEVFRPGGDMRDNRSLEYKYVKVIEPLVAPTKAKRRVVQRE

KRAVGIGAVLLGFLGAAGSTWGAASMTLTVOARLSGLIVQQNNLLRAIEAQHLLQ

LTVNGIKOLQARVLAVERYLRDQOLGIGWGSGLICTTAVPNWASWNSKLNKIWDN

MTWMDREINNTYSIIIVLSIESNQKEQELLEDKWSLWNSWFEITWLAAYIK

IFPMIIGLIGLIRIVFVLSIMNRVRQGSPLSFQTHLPASRGPPRGGIEBEGGERD

RDRSRLVYSLGRLVLDLRLSLFSLHRLDLLLIVTRIVELLGRGWEAKYWNVL

LQYWSQELKNSAVSLNATATAVAEGTDRVIEVQVQACRAIRHPRIRQGLERILL"

ORIGIN

Query Match 54.9%; Score 1236.6; DB 14; Length 2568;

Best Local Similarity 89.8%; Pred. No. 3.1e-250;

Matches 1352; Conservative 0; Mismatches 144; Indels 9; Gaps 2;

QY 52 TGGATCTCGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAA 111
Db 37 TGGGGTGGAGATGGGGCCACCATGCTCCTTGGGATGTTGATGATCTGTAGTCTACAGAA 96
QY 112 AAATTTGTGGGTACACAGTCTATTATATGGGTACCTGTGTGGAGAGAGCAACCACTCTA 171
Db 97 AAATTTGTGGGTACACAGTCTATTATATGGGTACCTGTGTGGAGAGAGCAACCACTCTA 156
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
QY 232 GCTGTGTACCCACAGAGCCCAACCCACCAAGAGTAGTATTGGGAAAATGTGACAGAAAT 291
Db 217 GCTGTGTACCCACAGAGCCCAACCCACCAAGAGTAGTATTGGGAAAATGTGACAGAAAT 276
QY 292 TTTTAAATGCTGGAATAAATGCTGTAGATCAGATGAGGATATATCAATGTTTATGG 351
Db 277 TTTTAAATGCTGGAATAAATGCTGTAGATGAGGATATATCAATGTTTATGG 336
QY 352 GATGAAAGCCTAAAGCCTATGCTGTAATAATTAACCCCACTCTGTGTACTTTAAATTCGACT 411
Db 337 GATCAAGCCTAAAGCCTATGCTGTAATAATTAACCTCTGTGTACTTTAAATTCGACT 396
QY 412 AATTTGAATATCACTA-----AGAACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 397 GATTTGAGGAATFACTACTAATGGGAATGACACTAATACCCTAGTAGTAGCAGGGAATG 456
QY 466 ATGGAGAAGGAGAAATAAATAATGCTCTTTCTATATCACCACCAAGCATAGAATAAG 525
Db 457 ATGGGGGGAGGAATAAATAATGCTCTTTCTAATCACCACCAAGCATAGAATAAG 516
QY 526 GTPAAGAAAGAAATATGCACTTTTAAATAGACTGTAGTAGTACCAATAGAAAATCTAAT 585
Db 517 GTGCAGAAAGAAATATGCACTTTTAAATAGACTGTAGTAGTACCAATAGATAATAGT 576
QY 586 AATACTAGTATAGTTAATAGTTGTAACACTCAGTCAATTTACACAGCCCTGTCAAAG 645
Db 577 AATAATAGTATAGTTGTAATAGTTGTAACACTCAGTCAATTTACACAGCCCTGTCAAAG 636
QY 646 GTATCTCTTTCAGCCAAATCCCATACATATTGTCCTCCGGCTGGGTTTGCAGTCTAAAG 705
Db 637 ATATCTTTTGACCAATTCCTCATATATTGTCCTCCGGCTGGGTTTGCAGTCTAAAG 696
QY 706 TGTAAACAATAGACATTTCAATGGATCAGGACCATGCACAAATGTCTCAGCACAGTACAATGT 765
Db 697 TGTAAAGATAAGAGTTCAATGGAAGAGGACCATGTTCAAATGTCTCAGCACAGTACAATGT 756
QY 766 ACACATGGAAATTTAGGCCAGTGTGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGGAATTTAGGCCAGTGTGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATAGTAATTTAGATCTGAAAATTTTCAGACAAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCCGAAAATTTTCGGGCAATGCTTAAACCATATAGTACAG 876
QY 886 CTAAATGAATCTGTAGTAATTTATGTAAGACCCCAACAATAACAGAGAGAGGTTA 945
Db 877 CTGAATGAATCTGTAGTAATTTATGTAAGACCCCAACAATAACAGAGAGAGTATA 936
QY 946 TCTATAGGACGAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACGAGGAGAGAAATATATATACAGGAAAATAATAGGAGATATAAGACAA 996
QY 1006 GCACATTTGACATTTAGTAGCAAAATGGAATACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGACCTTAGTAGCAAAATGGAATGACCTTTTAAATAGATAGTTATAAAA 1056
QY 1066 TTAAGAGAAAATTTAGGAATTAACAAATAGCCTTTTAAATCAATCCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAATTTGGGAAATAAACAATAGTCTTTAAGCATTCCTCAGGAGGGACCCA 1116
QY 1126 GAAATTTGATGCA CAGTTTTTAAATTTGTTGGAGGGGAATTTCTTCTACTGTAATACAGCAAA 1185

Db 1117 GAAATTTGTGAGCACA CAGTTTTTAAATTTGTGGAGGGGAATTTTCTACTGTAAATTCACACAA 1176
QY 1186 CTGTTTAAATAGTACTTTGGAATGTTTACTGGAGGGACAAAATGGCACTGAAGGAAATGACATA 1245
Db 1177 CTGTTTAAATAGTACTTTGGAATGTTTACTGGAAGGTCAAAATACACTGTAGAAAATAACACA 1236
QY 1246 ATCACACTCCCAATGAGAAATAAAAACAAATTTATAATATGTGGCAGAAAAGTAGGAAAAGCA 1305
Db 1237 ATCACACTCCCAATGAGAAATAAAAACAAATTTATAAACATGTGGCAGAAAAGTAGGAAAAGCA 1296
QY 1306 ATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCAATCAATATTTACAGGGCTGCTA 1365
Db 1297 ATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCAATCAATATTTACAGGGCTGCTA 1356
QY 1366 CTAAACAAGAGATGGAGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGAGCTTGGAGGA 1425
Db 1357 TTAAACAAGAGATGGTGG---TCCAGAGGACAAACAGACCGAGGTCTTTCAGAGCTTGGAGGA 1413
QY 1426 GGAGATATGAGGGACAAATTTGGAGAAAGTGAATTTATATAATAATAATAAGTAGTAAGAAATTGAA 1485
Db 1414 GGAGATATGAGGGACAAATTTGGAGAAAGTGAATTTATATAATAATAATAAGTAGTAAGAAATTGAA 1473
QY 1486 CCAATAGGAGTAGCACCCACCCAGGCAAGAGAGAAACAGTGCACAGAGAGAAAAGAGGG 1545
Db 1474 CCATTTAGGAGTAGCACCCACCCAGGCAAGAGAGAAAGAGTGGTGCAGAGAGAAAAGAGCA 1533
QY 1546 GGAGG 1550
Db 1534 GTGGG 1538

Search completed: November 12, 2004, 07:54:24

Job time : 6478.4 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 15:28:44 ; Search time 738.71 Seconds
(without alignments)
16003.167 Million cell updates/sec

Title: US-09-687-864A-12
Perfect score: 2252
Sequence: 1 aagcttgccgcatgtgta.....ctcgagtataatctagata 2252

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2252	100.0	2252	4	Aaf82928 HIV-1 gp1
2	2153.8	95.6	2209	4	Aaf82929 HIV-1 gp1
3	1880	83.5	2070	4	Aaf82930 HIV-1 gp1
4	1786.4	79.3	2028	4	Aaf82931 HIV-1 gp1
5	1452.6	64.5	2046	12	ACA63265 HIV-1 imm
6	1452.6	64.5	2610	12	ACA63266 HIV-1 imm
7	1448	64.3	2051	10	Aal56171 HIV trunc
8	1448	64.3	2562	10	Aal56170 Human imm
9	1338.6	59.4	2010	12	ACA63267 HIV-1 imm
10	1338.6	59.4	2574	12	ACA63268 HIV-1 imm
11	1225.2	54.4	3806	2	Aax04767 Env gene
12	1225.2	54.4	3807	2	Aat58551 Human imm
13	1222.2	54.3	9540	12	ADO52562 Human imm
14	1222.2	54.3	9540	12	ADP20074 Human imm
15	1218.8	54.1	3807	2	Aaql14753 HIV-1 BA-
16	1206.6	53.6	2553	1	Aan80949 HIV prote
17	1198	53.2	2612	12	ADJ92821 Human imm
18	1198	53.2	8896	12	ADP20082 Human imm
19	1197	53.2	1512	5	Aaf87100 HIV-1 gp1
20	1179.8	52.4	1422	1	ADP74731 HIV-1 iso
21	1173.4	52.1	4527	2	Aat33899 HIV-1 SP3

ALIGNMENTS

RESULT 1

AAf82928	AAf82928 standard; cDNA; 2252 BP.
XX	XX
AC	AAf82928;
XX	XX
DT	11-SEP-2003 (revised)
DT	29-JUN-2001 (first entry)
XX	XX
DE	HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
XX	XX
KW	Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW	acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW	HIV-1; gp120; human; CD154; fusion protein; ss.
OS	Human immunodeficiency virus 1.
OS	Homo sapiens.
XX	XX
PH	Key
FT	CDS
FT	Location/Qualifiers
FT	13..2252
FT	/*tag= a
FT	13..72
FT	/*tag= b
FT	/note= "synthetic secretory signal peptide"
FT	73..1542
FT	/*tag= c
FT	/note= "HIV-1 gp120 domain coding sequence"
FT	1543..1593
FT	/*tag= d
FT	/note= "[Gly4Ser]3 linker coding sequence"
FT	1594..2252
FT	/*tag= e
FT	/note= "human CD154 long form extracellular domain coding sequence"
XX	XX
PN	WO200126608-A2.
XX	XX
PD	19-APR-2001.
XX	XX
PF	13-OCT-2000; 2000WO-US028414.
XX	XX
PR	14-OCT-1999; 99US-0159690P.
XX	XX
PA	(LEDB/) LEDBETTER J A.

Db 1741 GATATTAATGTTAAACAAAGAGGAGCAGCAAGAAAGAAAACAGCTTTGAAATGCAAAAAGT 1800
Qy 1801 GATCAGAACTCTCAAAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAAAACAACATCT 1860
Db 1801 GATCAGAACTCTCAAAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAAAACAACATCT 1860
Qy 1861 GTGTTACAGTGGCTGAAAAGGATACATACCATGAGCAACAACCTTGTAAACCTTGGAA 1920
Db 1861 GTGTTACAGTGGCTGAAAAGGATACATACCATGAGCAACAACCTTGTAAACCTTGGAA 1920
Qy 1921 AATGGGAAACAGCTGACCGCTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACC 1980
Db 1921 AATGGGAAACAGCTGACCGCTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACC 1980
Qy 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCCTAAAG 2040
Db 1981 TTCTGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCCTAAAG 2040
Qy 2041 TCCCCGGTAGATTTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTTCGGCCAAA 2100
Db 2041 TCCCCGGTAGATTTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTTCGGCCAAA 2100
Qy 2101 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCCAGGTCTTCG 2160
Db 2101 CCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACCCAGGTCTTCG 2160
Qy 2161 GTGTTTGTCAATGTGACTGATCCAAAGCAAGTGAGCCATGGCTTCACGTCCTTT 2220
Db 2161 GTGTTTGTCAATGTGACTGATCCAAAGCAAGTGAGCCATGGCTTCACGTCCTTT 2220
Qy 2221 GCCTTACTCAAACTCGAGTGATAATCTAGATA 2252
Db 2221 GCCTTACTCAAACTCGAGTGATAATCTAGATA 2252

RESULT 2
AAAF82929
ID AAF82929 standard; cDNA; 2209 BP.
AC AAF82929;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX
DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX
OS Human immunodeficiency virus 1.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 13..2209
FT /tag= a
FT sig_peptide 13..72
FT /tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1551
FT /tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 1552..2209
FT /tag= e
FT /note= "human CD154 long form extracellular domain coding sequence"
XX
PN WO200126608-A2.
XX
PD 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028414.
PF XX
XX 14-OCT-1999; 99US-0159690P.
PR XX
XX (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
PA
XX Ledbetter JA, Hayden-Ledbetter MS;
XX
XX WPI; 2001-281790/29.
DR P-PSDB; AAB62334.
XX
PT DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.
PT
XX Example 1; Fig 3A; 55pp; English.
PS
XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 long form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;
SQ
Query Match 95.6%; Score 2153.8; DB 4; Length 2209;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 2; Indels 42; Gaps 1;
Qy 1 AAGCTTGGCGGCATCTGTATACCTCTCAGCTGTAGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGGCATCTGTATACCTCTCAGCTGTAGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGG 120
Db 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGG 120
Qy 121 GTCAGATCTATTATGGGGTACCTGTGGAGAGAACCAACCACCTCTATTTTTGTGCA 180
Db 121 GTCAGATCTATTATGGGGTACCTGTGGAGAGAACCAACCACCTCTATTTTTGTGCA 180
Qy 181 TCAGATGCTAAAGCCTATGATACAGGTACATATATTTGGGCCACACATCCCTGTGTA 240
Db 181 TCAGATGCTAAAGCCTATGATACAGGTACATATATTTGGGCCACACATCCCTGTGTA 240
Qy 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTG 300
Db 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTG 300
Qy 301 TGGAAAAATAACATGGTAGATCAGATGAGGATATAATCAGTTTATGGGATGAAGC 360
Db 301 TGGAAAAATAACATGGTAGATCAGATGAGGATATAATCAGTTTATGGGATGAAGC 360
Qy 361 CTAAGCCATGTGTAATAATTAACCCCTCTGTGTACTTTTAAATTTGACATAATTTGAAT 420
Db 361 CTAAGCCATGTGTAATAATTAACCCCTCTGTGTACTTTTAAATTTGACATAATTTGAAT 420
Qy 421 ATCCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGAGAA 480
Db 421 ATCCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGAGAA 480
Qy 481 ATAAAAAATTTGCTCTTTCTTATATACCCACAGCATAAAGAAATAGGTAAGAAAGATAT 540
Db 481 ATAAAAAATTTGCTCTTTCTTATATACCCACAGCATAAAGAAATAGGTAAGAAAGATAT 540
Qy 541 GCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATCTAATAACTAAGTATAGG 600
Db 541 GCACCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAAATCTAATAACTAAGTATAGG 600

```
QY 601 TTAATAAGTGTGTAACACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCCTTTTCAGCCA 660
Db 601 TTAATAAGTGTGTAACACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCCTTTTCAGCCA 660
QY 661 ATTCCCATACATTATTGTGTCCCGCGCTGGGTTCGGATGCTAAAGCTGTAAACAATAAGACA 720
Db 661 ATTCCCATACATTATTGTGTCCCGCGCTGGGTTCGGATGCTAAAGCTGTAAACAATAAGACA 720
QY 721 TTCAATGGATCAGGACCAATGCAAAATGTTCAGCA CAGTACAAATGTACACATGGAATTAGG 780
Db 721 TTCAATGGATCAGGACCAATGCAAAATGTTCAGCA CAGTACAAATGTACACATGGAATTAGG 780
QY 781 CCAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT 840
Db 781 CCAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT 840
QY 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACATAATAGTAGTACAGCTAAATGAAATCTGTA 900
Db 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACATAATAGTAGTACAGCTAAATGAAATCTGTA 900
QY 901 GTAATTAATTTGTAAGAGCCCAACAACTAATACAGAGAGGTTATCTATAGGACCAAGG 960
Db 901 GTAATTAATTTGTAAGAGCCCAACAACTAATACAGAGAGGTTATCTATAGGACCAAGG 960
QY 961 AGAGCATTTTATGCAAGAGAACATAATAGGAGATATAAGACAAGCACATTTGTAACATT 1020
Db 961 AGAGCATTTTATGCAAGAGAACATAATAGGAGATATAAGACAAGCACATTTGTAACATT 1020
QY 1021 AGTAGAGCAAAATGGAATAAACACTTTTCAACAGATAGTTTATAAAATTAAGAGAAAAATTT 1080
Db 1021 AGTAGAGCAAAATGGAATAAACACTTTTCAACAGATAGTTTATAAAATTAAGAGAAAAATTT 1080
QY 1081 AGGAATAAAACAATAGCCTTTTAACTCAATCTCAGAGAGGACCCAGAAATTTGTAATGCAC 1140
Db 1081 AGGAATAAAACAATAGCCTTTTAACTCAATCTCAGAGAGGACCCAGAAATTTGTAATGCAC 1140
QY 1141 AGTTTAAATTTGAGAGGGAATTTCTTACTGTAATACAGCACACTGTTTAAATAGTACT 1200
Db 1141 AGTTTAAATTTGAGAGGGAATTTCTTACTGTAATACAGCACACTGTTTAAATAGTACT 1200
QY 1201 TCGAATGTTACTGAGAGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC 1260
Db 1201 TCGAATGTTACTGAGAGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC 1260
QY 1261 AGAATAAAACAATTAATAATTTGTCGACGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
Db 1261 AGAATAAAACAATTAATAATTTGTCGACGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
QY 1321 ATCAGAGCAAAATTAGATGTTTCATCAAAATATTACAGGCGTCTACTAACAGAGATGGA 1380
Db 1321 ATCAGAGCAAAATTAGATGTTTCATCAAAATATTACAGGCGTCTACTAACAGAGATGGA 1380
QY 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTTAGAGGAGGAGATATAGGGAC 1440
Db 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTTAGAGGAGGAGATATAGGGAC 1440
QY 1441 AATTGAGAGTGAATTATATAATAATAAAGTATAGTAAGTAAGTAACCAATAGGATAGCA 1500
Db 1441 AATTGAGAGTGAATTATATAATAATAAAGTATAGTAAGTAAGTAACCAATAGGATAGCA 1500
QY 1501 CCCACAGGGCAAGAGAGACGTCGCAAGGAAAAAGAGAGGGGGCGGTTTCAGGA 1560
Db 1501 CCCACAGGGCAAGAGAGACGTCGCAAGGAAAAAGAGAGGGGGCGGTTTCAGGA 1560
QY 1561 GGTGAGGTTCTGGAGGTGGCGGATCGGATCCGAAGGTTCGACAAAGATAGAAGATGAA 1620
Db 1561 GGTGAGGTTCTGGAGGTGGCGGATCGGATCCGAAGGTTCGACAAAGATAGAAGATGAA 1620
QY 1621 AGGAATCTTCATGAAGATTTTGTATTTATCATGTAAGAAACGATACAGAGATGCAACACAGGAA 1680
Db 1621 AGGAATCTTCATGAAGATTTTGTATTTATCATGTAAGAAACGATACAGAGATGCAACACAGGAA 1680
QY 1579 AGGAATCTTCATGAAGATTTTGTATTTATCATGTAAGAAACGATACAGAGATGCAACACAGGAA 1638
Db 1579 AGGAATCTTCATGAAGATTTTGTATTTATCATGTAAGAAACGATACAGAGATGCAACACAGGAA 1638
```

```
QY 1681 AGATCCCTTATCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAG 1740
Db 1639 AGATCCCTTATCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAG 1698
QY 1741 GATATAATGTTTAAACAAAGAGGAGACGAAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGT 1800
Db 1699 GATATAATGTTTAAACAAAGAGGAGACGAAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGT 1758
QY 1801 GATCAGATCTCAAAATTCGCGGCACATGCTCATAGTGGAGCCAGCAGTAAACACATCT 1860
Db 1759 GATCAGATCTCAAAATTCGCGGCACATGCTCATAGTGGAGCCAGCAGTAAACACATCT 1818
QY 1861 GTGTACAGTGGGCTGAAAAAGAGTACTTACACCATGAGCAACAACTTGGTAAACCCCTGGAA 1920
Db 1819 GTGTACAGTGGGCTGAAAAAGAGTACTTACACCATGAGCAACAACTTGGTAAACCCCTGGAA 1878
QY 1921 AATGGAAAAACAGCTGACCGTTTAAAGACAAGGACTCTTATATATATATGCCCCAAGTCACC 1980
Db 1879 AATGGAAAAACAGCTGACCGTTTAAAGACAAGGACTCTTATATATATATGCCCCAAGTCACC 1938
QY 1981 TTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTCTAAAG 2040
Db 1939 TTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTCTAAAG 1998
QY 2041 TCCCCCGGTAGATTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCAGTTTCCGCCAAA 2100
Db 1999 TCCCCCGGTAGATTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCAGTTTCCGCCAAA 2058
QY 2101 CTTGCGGGCAACAAATCCATTCACCTTGGAGAGAGTATTTGAAATTCGAACCCAGGTCCTCG 2160
Db 2059 CTTGCGGGCAACAAATCCATTCACCTTGGAGAGAGTATTTGAAATTCGAACCCAGGTCCTCG 2118
QY 2161 GTGTTTGTCAATGTGACTGATCCAGCCAGTCAAGCTGAGCCATGCGCTTCACGTCCTTT 2220
Db 2119 GTGTTTGTCAATGTGACTGATCCAGCCAGTCAAGCTGAGCCATGCGCTTCACGTCCTTT 2178
QY 2221 GGTCTACTCAAACTCGAGTGAATACTTAGAT 2251
Db 2179 GGTCTACTCAAACTCGAGTGAATACTTAGAT 2209
RESULT 3
AAP82930
ID AAP82930 standard; cDNA; 2070 BP.
XX
AC AAP82930;
XX
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX
DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
XX
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX
OS Human immunodeficiency virus 1.
OS Homo sapiens.
XX
FH Key
CDS Location/Qualifiers
FT 13..2070
FT /*tag= a
FT sig_peptide 13..72
FT /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /*tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1593
FT /*tag= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 1594..2070
FT /*tag= e
```

FT	/note= "human CD154 short form extracellular domain
FT	coding sequence"
FW	
FW	WO200126608-A2.
PD	19-APR-2001.
XX	
XX	13-OCT-2000; 2000WO-US028414.
XX	
XX	14-OCT-1999; 99US-0159690P.
XX	
XX	(LEDB/) LEDBETTER J A.
PA	(HAYD/) HAYDEN-LEDBETTER M S.
PA	
XX	
PI	Ledbetter JA, Hayden-Ledbetter MS;
XX	
XX	WPI; 2001-281790/29.
DR	P-PSDB; AAB62335.
DR	
XX	
XX	DNA vaccine for improving antigen-specific humoral and cellular immune
PT	responses, comprising one or more antigens linked to a domain that binds
PT	at least one receptor.
XX	
XX	Example 1; Fig 3B; 55pp; English.
PS	
XX	
CC	The invention provides a vaccine comprising one or more antigens linked
CC	to a domain that binds at least one receptor to improve the antigen-
CC	specific humoral and cellular immune response. The DNA vaccines induce
CC	strong antigen-specific humoral and cellular immune responses. The
CC	vaccine can be use against acquired immunodeficiency syndrome (AIDS). The
CC	present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC	short form extracellular domain fusion protein linked by (Gly4Ser)3
CC	linker. (Updated on 11-SEP-2003 to standardise OS field)
XX	
XX	
SQ	Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;
Query Match 83.5%; Score 1880; DB 4; Length 2070;	
Best Local Similarity 92.0%; Pred. No. 0;	
Matches 2070; Conservative 0; Mismatches 0; Indels 180; Gaps 1	
QY	1 AAGCTTGCGCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG
DB	1 AAGCTTGCGCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG
QY	61 GCTTTCAGATCTATGCTCCCTGGGATATTGATCTCTAGTGCTACAGAAAAATTGTGG
DB	61 GCTTTCAGATCTATGCTCCCTGGGATATTGATCTCTAGTGCTACAGAAAAATTGTGG
QY	121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCA
DB	121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCA
QY	181 TCAGATGCTTAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTA
DB	181 TCAGATGCTTAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTA
QY	241 CCCACAGACCCCAACCCACAGAAGTAGTATTGGGAATGTGACAGAAAAATTTTAACTG
DB	241 CCCACAGACCCCAACCCACAGAAGTAGTATTGGGAATGTGACAGAAAAATTTTAACTG
QY	301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTTATGGGATGAAAGC
DB	301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTTATGGGATGAAAGC
QY	361 CTAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTAAATTGCCTAAATTTGAAT
DB	361 CTAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTAAATTGCCTAAATTTGAAT
QY	421 ATCAGCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGTAGGAGAAAGGAA
DB	421 ATCAGCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGTAGGAGAAAGGAA
QY	481 ATAAAAAATTTGCTCTTTCTATATCACCACAGCATAAGGAATAGGTAAGGAAGAATAAT
DB	481 ATAAAAAATTTGCTCTTTCTATATCACCACAGCATAAGGAATAGGTAAGGAAGAATAAT

Db 1561 GGTGGAGGTTCTGGAGGTGGCGGATCGGATCC----- 1592
Qy 1621 AGGAATCTTCATGAAGATTTTGTATTCATGAACGATACAGAGTCAACACAGGAGAA 1680
Db 1593 ----- 1592
Qy 1681 AGATCCTTATCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAG 1740
Db 1593 ----- 1592
Qy 1741 GATATAATGTTAAACAAAGAGAGAGAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGT 1800
Db 1593 -----AGAAAAACAGCTTTGAAATGCAAAAAGGT 1620
Qy 1801 GATCAGAAATCCTCAAAATTGGCGCACATGTCTAAGTGGAGGCGAGTAAACACATCT 1860
Db 1621 GATCAGAAATCCTCAAAATTGGCGCACATGTCTAAGTGGAGGCGAGTAAACACATCT 1680
Qy 1861 GTGTTACAGTGGGCTGAAAAAGGATACTACACATGAGCAACAACTTGGTAACCTGGAA 1920
Db 1681 GTGTTACAGTGGGCTGAAAAAGGATACTACACATGAGCAACAACTTGGTAACCTGGAA 1740
Qy 1921 AATGGGAACAGCTACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980
Db 1741 AATGGGAACAGCTACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACC 1800
Qy 1981 TTCCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTCAAG 2040
Db 1801 TTCCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTCAAG 1860
Qy 2041 TCCCGCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAA 2100
Db 1861 TCCCGCGGTAGATTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAA 1920
Qy 2101 CTTTCGGGCAACAAATCCATTCACATTGGGAGAGTATTGAAATGCAACAGGCTGCTCG 2160
Db 1921 CTTTCGGGCAACAAATCCATTCACATTGGGAGAGTATTGAAATGCAACAGGCTGCTCG 1980
Qy 2161 GTGTTGTCAATGTGACTGATCCAGCCCAAGTGAGCCATGGCAGCTGGCTTACGTCCTTT 2220
Db 1981 GTGTTGTCAATGTGACTGATCCAGCCCAAGTGAGCCATGGCAGCTGGCTTACGTCCTTT 2040
Qy 2221 GCCTTACTCAAACTCGAGTGATAATCTAGA 2250
Db 2041 GCCTTACTCAAACTCGAGTGATAATCTAGA 2070

RESULT 4

ID AAF82931 standard; cDNA; 2028 BP.
XX AAF82931;
AC AAF82931;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 13..2028
FT CDS /*tag= a
FT sig_peptide 13..72 /*tag= b
FT /*notes= "synthetic secretory signal peptide"
FT misc_feature 73..1542 /*tag= c

misc_feature /note= "HIV-1 gp120 domain coding sequence"
FT 1543..1551 /*tag= d
FT /note= "ProAspPro linker coding sequence"
FT 1552..2028 /*tag= e
FT /note= "human CD154 short form extracellular domain coding sequence"
XX WO200126608-A2.
PN 19-APR-2001.
XX 13-OCT-2000; 2000WO-US028414.
XX 14-OCT-1999; 99US-0159690P.
XX (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
XX Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
DR P-PSDB; AAB62336.
XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.
PT Example 1; Fig 3B; 55pp; English.
CC The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;
SQ Query Match 79.3%; Score 1786.4; DB 4; Length 2028;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 6; Indels 222; Gaps 1;
Qy 1 AAGCTTGGCGGATCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGGATCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGG 120
Db 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGG 120
Qy 121 GTCAGAGTCTATTATGGGGTACCTGTGGGAGAGCAACCCACCTCTATTTTGTGCA 180
Db 121 GTCAGAGTCTATTATGGGGTACCTGTGGGAGAGCAACCCACCTCTATTTTGTGCA 180
Qy 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCTGTGTA 240
Db 181 TCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCTGTGTA 240
Qy 241 CCCACAGACCCCAACCCACAGAGTATGTTGGGAAATGTGACAGAAAAATTTAACATG 300
Db 241 CCCACAGACCCCAACCCACAGAGTATGTTGGGAAATGTGACAGAAAAATTTAACATG 300
Qy 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Db 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Qy 361 CTAAGCCCATGTGTAATAATTAACCCCTCTGTTTAAATTTGCACTAATTTGAAT 420
Db 361 CTAAGCCCATGTGTAATAATTAACCCCTCTGTTTAAATTTGCACTAATTTGAAT 420

QY 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAGAGAAAGGAGAA 480
DB 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAGAGAAAGGAGAA 480
QY 481 ATAAAAAATTTGCTCTTCTTATATCACCACCAAGCATAGAAATAAGGTAAGAAAGAAATAT 540
DB 481 ATAAAAAATTTGCTCTTCTTATATCACCACCAAGCATAGAAATAAGGTAAGAAAGAAATAT 540
QY 541 GCACCTTTTAAATAGAGCTTGATGTAGTACCACATAGAAAATACATAAATACTAAAGTATAGG 600
DB 541 GCACCTTTTAAATAGAGCTTGATGTAGTACCACATAGAAAATACATAAATACTAAAGTATAGG 600
QY 601 TTAATAAGTTGTAACACCTCAGTCATTAACAGAGCTGTCCAAAGGTATCCTTTTCAGCCA 660
DB 601 TTAATAAGTTGTAACACCTCAGTCATTAACAGAGCTGTCCAAAGGTATCCTTTTCAGCCA 660
QY 661 ATTTCCCATACATATTGTGTCCCGCTGGTGTGGATCTAAAGTGTAAACAATAAGACA 720
DB 661 ATTTCCCATACATATTGTGTCCCGCTGGTGTGGATCTAAAGTGTAAACAATAAGACA 720
QY 721 TTCAATGATCAGGACCAATGCAAAATGTACGACACAGTACAAATGTACACATGGAATTAGG 780
DB 721 TTCAATGATCAGGACCAATGCAAAATGTACGACACAGTACAAATGTACACATGGAATTAGG 780
QY 781 CCAGTGGTGTCAACTCACTGCTGTAAATGCGAGTCTAGCAGAGAAAGACATAGTAATT 840
DB 781 CCAGTGGTGTCAACTCACTGCTGTAAATGCGAGTCTAGCAGAGAAAGACATAGTAATT 840
QY 841 AGATCTGAAATTTTACAGACAAATGCTAAACCAATAAGTACAGCTAAATGAATCTGTA 900
DB 841 AGATCTGAAATTTTACAGACAAATGCTAAACCAATAAGTACAGCTAAATGAATCTGTA 900
QY 901 GTAAATTAATTTGACAGACCCCAACCAATACAGAGAGGTTATCTATAGGACAGGG 960
DB 901 GTAAATTAATTTGACAGACCCCAACCAATACAGAGAGGTTATCTATAGGACAGGG 960
QY 961 AGAGCATTTTATGCAAGAGAAACATAATAGAGATATAAGACAAGCAATGTAAACATT 1020
DB 961 AGAGCATTTTATGCAAGAGAAACATAATAGAGATATAAGACAAGCAATGTAAACATT 1020
QY 1021 AGTAGCAGAAATGCAATTAACACTTTACACAGATAGTTATTAATTAAGAGAAATTT 1080
DB 1021 AGTAGCAGAAATGCAATTAACACTTTACACAGATAGTTATTAATTAAGAGAAATTT 1080
QY 1081 AGGAATAAAACAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATGTAAATGCAC 1140
DB 1081 AGGAATAAAACAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATGTAAATGCAC 1140
QY 1141 AGTTTAAATTTGGAGGGGAATTTCTTCTACTGTAATACAGCAAACTGTTTAAATAGTACT 1200
DB 1141 AGTTTAAATTTGGAGGGGAATTTCTTCTACTGTAATACAGCAAACTGTTTAAATAGTACT 1200
QY 1201 TGGAAATTTAGTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC 1260
DB 1201 TGGAAATTTAGTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACACTCCAATGC 1260
QY 1261 AGAATAAAACAATTTAATAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
DB 1261 AGAATAAAACAATTTAATAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
QY 1321 ATCAGAGCAAAATTTAGATGTTTCATCAATATTTACAGGGCTGCTACTAACAGAGATGGA 1380
DB 1321 ATCAGAGCAAAATTTAGATGTTTCATCAATATTTACAGGGCTGCTACTAACAGAGATGGA 1380
QY 1381 GGTAAATAGTACGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGAC 1440
DB 1381 GGTAAATAGTACGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGAC 1440
QY 1441 AATTCGAGAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500
DB 1441 AATTCGAGAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500

QY 1501 CCCACGAGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGGGGAGCGGTTTCAGGA 1560
DB 1501 CCCACGAGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGCGG----- 1546
QY 1561 GGTGAGGTTCTGGAGGTGGCGGATCGGATCCAAGAAGGTTTGGACAAGATAGAAGATGAA 1620
DB 1547 ----- 1546
QY 1621 AGGAATCTTCATGAAGATTTTGTATTTCATGAANAACGATACAGAGATGCAACAACAGGAGAA 1680
DB 1547 ----- 1546
QY 1681 AGATCCTTATCCTTACTGAACTGTGAGAGATTAANAAGCCAGTTTGAAGGCTTTGTGAAG 1740
DB 1547 ----- 1546
QY 1741 GATATAATGTTTAAACAAAAGAGAGAGAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGT 1800
DB 1547 -----ATCCAGAAAAACAGCTTTGAAATGCAAAAAGGT 1578
QY 1801 GATCAGAAATCTCAAATTTGCGGCACATGTCTATAAGTGAAGGCCAGCAGTAAACCAACATCT 1860
DB 1579 GATCAGAAATCTCAAATTTGCGGCACATGTCTATAAGTGAAGGCCAGCAGTAAACCAACATCT 1638
QY 1861 GTGTTACAGTGGGCTGAAAAAGGATATACACCATGAGCAACAACCTTGGTAAACCTGGAA 1920
DB 1639 GTGTTACAGTGGGCTGAAAAAGGATATACACCATGAGCAACAACCTTGGTAAACCTGGAA 1698
QY 1921 AATGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980
DB 1699 AATGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1758
QY 1981 TTCTGTTTCCAAATCGGGAAGCTTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAG 2040
DB 1759 TTCTGTTTCCAAATCGGGAAGCTTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAG 1818
QY 2041 TCCCCCGTAGATTCGAGAGAAATCTTACTCAGAGTGCAAAATACCACAGTTCGCCCAA 2100
DB 1819 TCCCCCGTAGATTCGAGAGAAATCTTACTCAGAGTGCAAAATACCACAGTTCGCCCAA 1878
QY 2101 CCTTCGCGGCAACAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCG 2160
DB 1879 CCTTCGCGGCAACAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCG 1938
QY 2161 GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAAGCCATGGCAGTTCGCTTCACTGCTTT 2220
DB 1939 GTGTTTGTCAATGTGACTGATCCAAGCCAAGTGAAGCCATGGCAGTTCGCTTCACTGCTTT 1998
QY 2221 GGCTTACTCAAACTCGAGTGAATCTAGA 2250
DB 1999 GGCTTACTCAAACTCGAGTGAATCTAGA 2028

RESULT 5
ACA63265

ID ACA63265 standard; DNA; 2046 BP.

AC ACA63265;

XX AC

XX AC

DT 22-APR-2004 (first entry)

XX HIV-1 immunogenic sequence #1.

XX Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;

XX immunogenic; virucide; ds.

XX Human immunodeficiency virus type 1.

XX WO2004001051-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-EP007146.

XX WO2004001051-A2.
PN XX
PD 31-DEC-2003.
XX 20-JUN-2003; 2003WO-EP007146.
XX PF
XX 20-JUN-2002; 2002EP-00291550.
PR XX
XX (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Tangy F, Lorin C, Mollet L, Delebecque F;
XX WPI; 2004-082508/08.
DR XX
XX
PT New recombinant mononegavirales measles virus expressing a heterologous
PT amino acid, useful for preparing immunogenic or vaccine composition for
PT the prophylaxis or treatment of measles.
XX
XX Disclosure; Fig 16C; Opp; English.
PS
XX The present invention relates to a recombinant mononegavirales measles
CC virus expressing a heterologous amino acid, which is capable of eliciting
CC a humoral and/or cellular immune response against the heterologous amino
CC acid sequence including in individuals having pre-existing measles virus
CC immunity. The recombinant virus is useful for preparing immunogenic or
CC vaccine composition for the prophylaxis or treatment of measles. The
CC present sequence is a HIV immunogenic sequence shown in the
CC exemplification of the invention
XX
SQ Sequence 2610 BP; 885 A; 442 C; 643 G; 640 T; 0 U; 0 Other;
Query Match 64.5%; Score 1452.6; DB 12; Length 2610;
Best Local Similarity 98.1%; Pred. No. 5.8e-296;
Matches 1470; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 52 TGGATCTCGGCTTCGAGATCTATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAA 111
DB |||
QY 37 TGGGGGTGGAGATGGGGCACCACATGCTCTCTGGGATGTTGATGATCTGTAGTGTACAGAA 96
DB |||
QY 112 AAATTTGGGTGCACAGTCTATTATGGGTACCTGTGGGATGATGATGATGATGATGATGATGAT 171
DB |||
QY 97 AAATTTGGGTGCACAGTCTATTATGGGTACCTGTGGGATGATGATGATGATGATGATGATGAT 156
DB |||
QY 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACAT 231
DB |||
QY 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACAT 216
DB |||
QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGGTAGTATTGGGAAATGTGACAGAAAT 291
DB |||
QY 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGGTAGTATTGGGAAATGTGACAGAAAT 276
DB |||
QY 292 TTTTACATGTGAAAATAAATGCTTTTAAATTTAAACCCCACTCTGTGTTACTTTTAAATTTGCACT 351
DB |||
QY 277 TTTTACATGTGAAAATAAATGCTTTTAAATTTAAACCCCACTCTGTGTTACTTTTAAATTTGCACT 336
DB |||
QY 352 GATGAAAGCCTAAAGCCATGTTGTAATTTAAATTTAAACCCCACTCTGTGTTACTTTTAAATTTGCACT 411
DB |||
QY 337 GATGAAAGCCTAAAGCCATGTTGTAATTTAAATTTAAACCCCACTCTGTGTTACTTTTAAATTTGCACT 396
DB |||
QY 412 AATTTGAATATCCTAAGAAATCTACTAATCCCACTAGTGTAGGAGTGGGGAATGTAGAG 471
DB |||
QY 397 AATTTGAATATCCTAAGAAATCTACTAATCCCACTAGTGTAGGAGTGGGGAATGTAGAG 456
DB |||
QY 472 AAAGAGAAATATAAATTTGCTTTCTTATATACCAACAGCATTAAGAAATAGTAAAG 531
DB |||
QY 457 GAAGAGAAATATAAATTTGCTTTCTTATATACCAACAGCATTAAGAAATAGTAAAG 516
DB |||
QY 532 AAAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCAATAGAAATTAATAATACT 591
DB |||
QY 517 AAAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCAATAGAAATTAATAATACT 576
DB |||

RESULT 7
AAL56171
ID AAL56171 standard; DNA; 2051 BP.
XX
AC AAL56171;
XX
DT 11-MAR-2004 (first entry)
XX

QY 592 AAGTATAGTTAATAGTTTGTAAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCC 651
DB |||
QY 577 AAGTATAGTTAATAGTTTGTAAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCC 636
DB |||
QY 652 TTTTCAGCCAAATTTCCCATACATTTATTGTGTCCTGGGCTGGGTTTGCATGCTAAAGTGTAAAC 711
DB |||
QY 637 TTTTCAGCCAAATTTCCCATACATTTATTGTGTCCTGGGCTGGGTTTGCATGCTAAAGTGTAAAC 696
DB |||
QY 712 AATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGACACAGTACAATGTATACAT 771
DB |||
QY 697 AATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGACACAGTACAATGTATACAT 756
DB |||
QY 772 GGAATTAGCCAGTGGTGTCTCACTCACTGCTGTTAAATGGCAGTCTTACGACAGAAAGAC 831
DB |||
QY 757 GGAATTAGCCAGTGGTGTCTCACTCACTGCTGTTAAATGGCAGTCTTACGACAGAAAGAC 816
DB |||
QY 832 ATAGTAATTTAGATCTGAAAAATTTTCACACACAAATGCTAAAAACCATTAATAGTACAGCTAAAT 891
DB |||
QY 817 ATAGTAATTTAGATCTGAAAAATTTTCACACACAAATGCTAAAAACCATTAATAGTACAGCTAAAT 876
DB |||
QY 892 GAATCTGTAGTAATTTAATTTGTACAAGACCCCAACCAATACAAGAAAGGTTATCTATA 951
DB |||
QY 877 GAATCTGTAGTAATTTAATTTGTACAAGACCCCAACCAATACAAGAAAGGTTATCTATA 936
DB |||
QY 952 GGACAGGAGGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAGACACAGCAT 1011
DB |||
QY 937 GGACAGGAGGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATAGACACAGCAT 996
DB |||
QY 1012 TGTAACTATTAGTAGAGCAAAATGGAATAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1071
DB |||
QY 997 TGTAACTATTAGTAGAGCAAAATGGAATAAATGGAATGGAATGGAATGGAATGGAATGGAAT 1056
DB |||
QY 1072 GAAAAATTTAGGAATTAATAATAGCCTTTTAAATCAATCCTCAGGAGGAGCCAGCAATTT 1131
DB |||
QY 1057 GAAAAATTTAGGAATTAATAATAGCCTTTTAAATCAATCCTCAGGAGGAGCCAGCAATTT 1116
DB |||
QY 1132 GTAATGCACAGTCTTTAATTTGGAGGGGAAATTTCTTCTACTGTATATACAGCACAACCTGTTT 1191
DB |||
QY 1117 GTAATGCACAGTCTTTAATTTGGAGGGGAAATTTTCTTCTACTGTATATACAGCACAACCTGTTT 1176
DB |||
QY 1192 AATAGTACTTGGAAATGTTTACTTGGAGGGGCAAAATGGCCTAGAGGAAATGACATAATCACA 1251
DB |||
QY 1177 AATAGTACTTGGAAATGTTTCTTGGAGGGGCAAAATGGCCTAGAGGAAATGACATAATCACA 1236
DB |||
QY 1252 CTCCAATGCAGATAAATAAATAATTTATAATATGTTGGCAGAAAGTAGGAAAGCAATGTAT 1311
DB |||
QY 1237 CTCCAATGCAGATAAATAAATAATTTATAATATGTTGGCAGAAAGTAGGAAAGCAATGTAT 1296
DB |||
QY 1312 GCCCTCCCATCAGAGCAAAATTTAGATGTTTCATCAAAATTTTACAGGCTGTCTACTAACA 1371
DB |||
QY 1297 GCCCTCCCATCAGAGCAAAATTTAGATGTTTCATCAAAATTTTACAGGCTGTCTACTAACA 1356
DB |||
QY 1372 AGAGATGAGGATTAATAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 1431
DB |||
QY 1357 AGAGATGAGGATTAATAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 1416
DB |||
QY 1432 ATGAGGGCAATTTGGAGAAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA 1491
DB |||
QY 1417 ATGAGGGCAATTTGGAGAAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA 1476
DB |||
QY 1492 GGAGTAGCACCACCCAGGGCAAGAGAAAGACAGTGTCAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1550
DB |||
QY 1477 GGAGTAGCACCACCCAGGGCAAGAGAAAGACAGTGTCAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1535
DB |||

DE HIV truncated envelope glycoprotein 160 coding sequence.
XX HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;
KW gene; ds; anti-HIV; truncated.
XX Human immunodeficiency virus.
OS
FH Key Location/Qualifiers
FT 1..2001
FT /*tag= a
FT /product= "truncated gp 160"
XX WO2003077838-A2.
XX
XX 25-SEP-2003.
XX
XX 05-MAR-2002; 2002WO-US007144.
XX
XX 05-MAR-2002; 2002WO-US007144.
XX (NAME-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.
XX
XX Dimitrov DS, Chow Y, Phogat SK, Broder CC;
XX
XX WPI: 2003-779074/73.
XX P-PSDB; ABU64219.
XX
XX New HIV antigenic composition comprising an HIV envelope glycoprotein 160
XX having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
XX subunit useful for protecting a human from HIV infection.
XX
XX Disclosure; Page 62-63; 65pp; English.
XX
XX The present invention relates to an HIV antigenic composition, comprising
XX an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
XX subunit, where the carboxy-terminal end of gp120 is covalently linked
XX through a peptide linker of at least 5 amino acids, to the amino-terminal
XX end of gp41. The HIV antigenic composition is useful for protecting a
XX human from HIV infection, potentially in the form of a vaccine. The
XX present sequence is the HIV truncated gp160 coding sequence
XX
SQ Sequence 2051 BP; 749 A; 333 C; 467 G; 502 T; 0 U; 0 Other;

Query Match 64.3%; Score 1448; DB 10; Length 2051;
Best Local Similarity 99.1%; Pred. No. 5.1e-295;
Matches 1467; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 74 TGCTCCTTGGGATATTGATGATCTGTAGTGCT---ACAGAAAAATTGTGGGTACAGTCT 130
DB 53 TGCTCCTTGGGATTTGATGATCTGTAGTGCTGCAAGAAAAACGTGGGTCAAACT 112

QY 131 ATTATGGGTACTCTGTGGAGAGAACCAACCACTATTATTTGTGTCATCAGATGCTA 190
DB 113 ATTATGGGTACTCTGTGGAGAGAACCAACCACTATTATTTGTGTCATCAGATGCTA 172

QY 191 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGACC 250
DB 173 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 232

QY 251 CCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATA 310
DB 233 CCNACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATA 292

QY 311 ACATGATAGATCAGATGCATAGGATATAATCAGTTTATGGATGAAGCCCTAAAGCCAT 370
DB 293 ACATGATAGATCAGATGCATAGGATATAATCAGTTTATGGATGAAGCCCTAAAGCCAT 352

QY 371 GTGTAATTAACCCACCTCTGTGTACTTTAAATTTGCACTAATTTGATATACCTAAGA 430
DB 353 GTGTAATTAACCCACCTCTGTGTACTTTAAATTTGCACTAATTTGATATACCTAAGA 412

QY 431 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAAAATT 490

DB 413 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATCATGAGAGAAAGGAGAAATAAAAAATT 472
QY 491 GCTCTTTCTATATCACCACAGCATAGAAATAGGTTAAAGAAAGAAATATCCACTTTTAA 550
DB 473 GCTCTTTCTATATCACCACAGCATAGAAATAGGTTAAAGAAAGAAATATGCACCTTTTA 532
QY 551 ATAGACTTGTAGTAGTACCNAATAGAAAATCTAATAATATCTAAGTATATAGGTTAATAAGTT 610
DB 533 ATAGACTTGTAGTAGTACCNAATAGAAAATCTAATAATATCTAAGTATATAGGTTAATAAGTT 592
QY 611 GTAACACCTCAGTCATTACACAGCCCTGTCAAAGGTATCTTTTCAGCCAATATCCCATAC 670
DB 593 GTAACACCTCAGTCATTACACAGCCCTGTCAAAGGTATCTTTTCAGCCAATATCCCATAC 652
QY 671 ATTATTGTCTCCGGCTGGGTTTGGGATGCTTAAAGTGTAAACAATAAGACATTCATGAT 730
DB 653 ATTATTGTCTCCGGCTGGGTTTGGGATGCTTAAAGTGTAAACAATAAGACATTCATGAT 712
QY 731 CAGGACCATGCACAAATGTGACGACAGTACAAATGTACACATGGAATTAGGCCAGTGTGT 790
DB 713 CAGGACCATGCACAAATGTGACGACAGTACAAATGTACACATGGAATTAGGCCAGTGTGT 772
QY 791 CAACTCAACTCTGTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATTTAGATCTGAAA 850
DB 773 CAACTCAACTCTGTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATTTAGATCTGAAA 832
QY 851 ATTTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAATGAATCTCTAGTAAATTAAT 910
DB 833 ATTTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAATGAATCTCTAGTAAATTAAT 892
QY 911 GTACAAGACCCCAACAACAATACAAAGAGAGGTTATCTATAGGACCCAGGAGAGCATTTT 970
DB 893 GTACAAGACCCCAACAACAATACAAAGAGAGGTTATCTATAGGACCCAGGAGAGCATTTT 952
QY 971 ATGCAAGAGAAAAATATATAGAGATATAAGACAGCAATGTATTAACATTTAGTAGAGCAA 1030
DB 953 ATGCAAGAGAAAAATATATAGAGATATAAGACAGCAATTTGTAACATTTAGTAGAGCAA 1012
QY 1031 AATGGATTAACACTTTTACACAGATAGTTATAAATTAAGAGAAAAATTTAGGAAATAAAA 1090
DB 1013 AATGGATTAACACTTTTACACAGATAGTTATAAATTAAGAGAAAAATTTAGGAAATAAAA 1072
QY 1091 CAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTTTAAT 1150
DB 1073 CAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTTTAAT 1132
QY 1151 GTGGAGGGGAATTTTCTTCTACTGTAATACAGCAAACTGTTTAATAGTACTTTGGAAATGTTA 1210
DB 1133 GTGGAGGGGAATTTTCTTCTACTGTAATACAGCAAACTGTTTAATAGTACTTTGGAAATGTTA 1192
QY 1211 CTGGAGGACAAATGGCACTGAAGGAATGACATAATCACACTCCCAATGCAGAAATAAAC 1270
DB 1193 CTGGAGGACAAATGGCACTGAAGGAATGACATAATCACACTCCCAATGCAGAAATAAAC 1252
QY 1271 AAATTTAAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAGGAC 1330
DB 1253 AAATTTAAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAGGAC 1312
QY 1331 AAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTAAACAAGAGATGAGGTAATAGTA 1390
DB 1313 AAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTAAACAAGAGATGAGGTAATAGTA 1372
QY 1391 CTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATAGGACAAATTCGGAGAA 1450
DB 1373 CTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATAGGACAAATTCGGAGAA 1432
QY 1451 GTGAATTTATAAATATAAAGTAGTAAAGATTGAACCAATAGGAGTAGCACCACAGG 1510
DB 1433 GTGAATTTATAAATATAAAGTAGTAAAGATTGAACCAATAGGAGTAGCACCACAGG 1492
QY 1511 CAAAGAGAGAAACAGTGCACAAAGAGAAAAAGAGGGGGAGG 1550
DB 1493 CAAAGAGAGAAACAGTGCACAAAGAGAAAAAGAGCAGTGGG 1532

RESULT 8
AAL56170
ID AAL56170 standard; DNA; 2562 BP.
XX
AC AAL56170;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human immunodeficiency virus envelope glycoprotein 160 coding sequence.
XX
KW HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;
KW gene; db; anti-HIV.
XX
OS Human immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT 1..2559
FT /*tag= a
FT /product= "gp 160"
XX
PN WO2003077838-A2.
XX
PD 25-SEP-2003.
XX
PF 05-MAR-2002; 2002WO-US007144.
XX
PR 05-MAR-2002; 2002WO-US007144.
XX
PA (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.
XX
PI Dimitrov DS, Chow Y, Phogat SK, Broder CC;
XX
DR WPI: 2003-779074/73.
DR P-PSDB; ABU64218.
XX
PT New HIV antigenic composition comprising an HIV envelope glycoprotein 160
PT having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
PT subunit useful for protecting a human from HIV infection.
XX
PS Disclosure; Page 61-62; 65pp; English.
XX
CC The present invention relates to an HIV antigenic composition, comprising
CC an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
CC subunit, where the carboxy-terminal end of gp120 is covalently linked
CC through a peptide linker of at least 5 amino acids, to the amino-terminal
CC end of gp41. The HIV antigenic composition is useful for protecting a
CC human from HIV infection, potentially in the form of a vaccine. The
CC present sequence is the HIV gp160 coding sequence
XX
SQ Sequence 2562 BP; 897 A; 433 C; 604 G; 628 T; 0 U; 0 Other;

Query Match 64.3%; Score 1448; DB 10; Length 2562;
Best Local Similarity 99.1%; Pred. No. 5.3e-295;
Matches 1467; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 74 TGCTCTTGGGATATTGATGATCTGATGCT--ACAGAAAAATTGGGGTCACAGTCT 130
DB |||||||
QY 53 TGCTCTTGGGATATTGATGATCTGATGCTGCAAAAAAGAAAAACGGTGGGTCAAACT 112
DB |||||||
QY 131 ATTATGGGTACTCTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTA 190
DB |||||||
QY 113 ATTATGGGTACTCTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTA 172
DB |||||||
QY 191 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCAAGACC 250
DB |||||||
QY 173 AAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGTGTACCAAGACC 232
DB |||||||
QY 251 CCAACCCACAGAAGTATTGGGAATGTGACAGAAAAATTTTAACTGTGGAAAAATA 310
DB |||||||
QY 233 CCAACCCACAGAAGTATTGGGAATGTGACAGAAAAATTTTAACTGTGGAAAAATA 292
DB |||||||

QY 311 ACATGGTAGATCAGATGATAGGATATAATCAGTTTATGGATGAAGCCTAAAGCCAT 370
DB |||||||
QY 293 ACATGGTAGATCAGATGATAGGATATAATCAGTTTATGGATGAAGCCTAAAGCCAT 352
DB |||||||
QY 371 GTGTAAATTAACCCACCTCTGTGTACTTTTAAATTTGCACTAAATTTTGAATATACCTAAGA 430
DB |||||||
QY 353 GTGTAAATTAACCCACCTCTGTGTACTTTTAAATTTGCACTAAATTTTGAATATACCTAAGA 412
DB |||||||
QY 431 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAATAAAATTT 490
DB |||||||
QY 413 ATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAAATAAAATTT 472
DB |||||||
QY 491 GCTCTTTCTATATCACCAAGCATAAGAAATAAGGTAAGGTAAGAAAGATATGCACTTTTAA 550
DB |||||||
QY 473 GCTCTTTCTATATCACCAAGCATAAGAAATAAGGTAAGGTAAGAAAGATATGCACTTTTAA 532
DB |||||||
QY 551 ATAGACTTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTAAATAGTT 610
DB |||||||
QY 533 ATAGACTTTGATGTAGTACCAATAGAAAAATACTAATAATACTAAGTATAGTTAAATAGTT 592
DB |||||||
QY 611 GTAAACACCTCAGTCAATTACAGGCGCTGTCCAAAGGTATCTTTTCCAGCCAAATTTCCCATAC 670
DB |||||||
QY 593 GTAAACACCTCAGTCAATTACAGGCGCTGTCCAAAGGTATCTTTTCCAGCCAAATTTCCCATAC 652
DB |||||||
QY 671 ATTATTGTGTCCTGGCTGGGTTTGGATGCTAAAGTGTAAACAAATTAAGACATTTCAATGGAT 730
DB |||||||
QY 653 ATTATTGTGTCCTGGCTGGGTTTGGATGCTAAAGTGTAAACAAATTAAGACATTTCAATGGAT 712
DB |||||||
QY 731 CAGGACCATGCACAAATGTCAGCAGTACATGTACATGGAATTTAGGCCAGTGGTCT 790
DB |||||||
QY 713 CAGGACCATGCACAAATGTCAGCAGTACATGTACATGGAATTTAGGCCAGTGGTCT 772
DB |||||||
QY 791 CAACTCAACTGCTGTTAAATGGCAGCTAGCAGAAAGAGACATAGTAATTTAGATCTGAAA 850
DB |||||||
QY 773 CAACTCAACTGCTGTTAAATGGCAGCTAGCAGAAAGAGACATAGTAATTTAGATCTGAAA 832
DB |||||||
QY 851 ATTTTACAGACAAATGCTAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTAATTT 910
DB |||||||
QY 833 ATTTTACAGACAAATGCTAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTAATTT 892
DB |||||||
QY 911 GTACAGACCCCAACCAACAAATCAAGAAAGGTTATCTATAGGACCCAGGAGGACATTTT 970
DB |||||||
QY 893 GTACAGACCCCAACCAACAAATCAAGAAAGGTTATCTATAGGACCCAGGAGGACATTTT 952
DB |||||||
QY 971 ATGCAAGAGAAACAAATAATAGGATATAAGACAAAGACATTTGTAACATTAGTAGAGCAA 1030
DB |||||||
QY 953 ATGCAAGAGAAACAAATAATAGGATATAAGACAAAGACATTTGTAACATTAGTAGAGCAA 1012
DB |||||||
QY 1031 AATGGAATAACACTTTTACACAGATAGTTATAAAATTTAAGAGAAAAATTTAGGAATAAAA 1090
DB |||||||
QY 1013 AATGGAATAACACTTTTACACAGATAGTTATAAAATTTAAGAGAAAAATTTAGGAATAAAA 1072
DB |||||||
QY 1091 CAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGACAGATTTTAATTT 1150
DB |||||||
QY 1073 CAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGACAGATTTTAATTT 1132
DB |||||||
QY 1151 GTGAGGGGGAATTTCTTCTACTGTAATACAGACAACTGTTTAAATAGTACTTGGAAATGTTA 1210
DB |||||||
QY 1133 GTGAGGGGGAATTTTCTTCTGTAATACAGCACTGTTTAAATAGTACTTGGAAATGTTA 1192
DB |||||||
QY 1211 CTGAGGGGACAAATGGCCTGAAGGAAATGACATTAATCACTCAATGTCAGAAATAAAC 1270
DB |||||||
QY 1193 CTGAGGGGACAAATGGCCTGAAGGAAATGACATTAATCACTCAATGTCAGAAATAAAC 1252
DB |||||||
QY 1271 AAATTTAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCAGAGAC 1330
DB |||||||
QY 1253 AAATTTAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCAGAGAC 1312
DB |||||||
QY 1331 AAATTTAGATGTTTCATCAATAATTTACAGGGCTGCTACTACTAAAGAGATGGAGGTAAATAGTA 1390
DB |||||||
QY 1313 AAATTTAGATGTTTCATCAATAATTTACAGGGCTGCTACTACTAAAGAGATGGAGGTAAATAGTA 1372
DB |||||||
QY 1391 CTGAGACTGAGACTGAGATCTTTCAGACTGGAGGAGGAGATATGAGGGACAATTTGGAGAA 1450
DB |||||||

Qy	1312	GCCCTCTCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGCTGCTACTAACA	1371
Db	1361	GCCCTCTCCATCACAGGACAAATTAGATGTTTCATCAAATATTACAGGCTGCTACTAACA	1320
Qy	1372	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTCTTCAGACTCTGGAGGAGGAGAT	1431
Db	1321	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTCTTCAGACTCTGGAGGAGGAGAT	1380
Qy	1432	ATGAGGACCAATTGGAGAAGTGAATTATATAAAATATAAAGTAGTAAAGATTGAACCAATA	1491
Db	1381	ATGAGGACCAATTGGAGAAGTGAATTATATAAAATATAAAGTAGTAAAGATTGAACCAATA	1440
Qy	1492	GGAGTAGCACCACCGGCGCAAGAGAAACAGTGCAAAAGAGAAAAAAGAGGGGAGG	1550
Db	1441	GGAGTAGCACCACCGGCGCAAGAGAAACAGTGCAAAAGAGAAAAAAGAGCAGTGGG	1499
RESULT 10			
ACA63268			
ID	ACA63268 standard; DNA; 2574 BP.		
XX	ACA63268;		
XX	22-APR-2004 (first entry)		
DT	HIV-1 immunogenic sequence #4.		
DE	Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;		
KW	immunogenic; virucide; ds.		
KW	Human immunodeficiency virus type 1.		
XX	WO2004001051-A2.		
PN	31-DEC-2003.		
XX	20-JUN-2003; 2003WO-EP007146.		
PF	20-JUN-2002; 2002EP-00291550.		
PR	(INSP) INST PASTEUR.		
PA	(CNRS) CENT NAT RECH SCI.		
PA	Tangy F, Lorin C, Mollet L, Delebecque F;		
PI	WPI; 2004-082508/08.		
XX	New recombinant mononegavirales measles virus expressing a heterologous		
XX	amino acid, useful for preparing immunogenic or vaccine composition for		
PT	the prophylaxis or treatment of measles.		
PT	Disclosure; Fig 16G; Opp; English.		
XX	The present invention relates to a recombinant mononegavirales measles		
XX	virus expressing a heterologous amino acid, which is capable of eliciting		
CC	a humoral and/or cellular immune response against the heterologous amino		
CC	acid sequence including in individuals having pre-existing measles virus		
CC	immunity. The recombinant virus is useful for preparing immunogenic or		
CC	vaccine composition for the prophylaxis or treatment of measles. The		
CC	present sequence is a HIV immunogenic sequence shown in the		
CC	exemplification of the invention		
XX	Sequence 2574 BP; 864 A; 440 C; 637 G; 633 T; 0 U; 0 Other;		
XX	Query Match 59.4%; Score 1338.6; DB 12; Length 2574;		
XX	Best Local Similarity 94.3%; Pred. No. 5.8e-272;		
XX	Matches 1414; Conservative 0; Mismatches 49; Indels 36; Gaps 1;		
Qy	52	TGGATCTCGGCTCGAGATCTATGCTCTCTGGGATATTGATGATCTGTAGTCTCAGAA	111
Db	37	TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTCTCAGAA	96


```

Db      1601 TTTTATACACAGGAGAAATAATAGGAGATATAAGACAAGCACATTTGTAACCTTTAGTAGA 1660
Qy      1027 GCAAAATGAATAACACTTTTACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAAT 1086
Db      1661 GCABAATGAATGACACTTTAATAAGATAGTTATAAATTAAGAGAACAAATTTGGGAT 1720
Qy      1087 AAAACAATGACCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGACAGATTTT 1146
Db      1721 AAAACAATAGTCTTTAAGCACTCCTCAGAGGGGACCCAGAAATTTGTGACGCACAGTTTT 1780
Qy      1147 AATTGTGGAGGGGAATCTCTTACTGCTAATACAGCACACTCTTTAATAGTACTTTGGAT 1206
Db      1781 AATTGTGGAGGGGAATTTTCTACTGTAATTAACACAACACTGTTAATAGTACTTTGGAT 1840
Qy      1207 GTTACTGAGGAGGACAAATGGCACTGAAAGGAAATGACATAATCACACTCCCAATGCAGAAATA 1266
Db      1841 GTTACTGAGAGCTCAATTAACACTGTAGAAATATACACATCACACTCCCATGCGAGATA 1900
Qy      1267 AAACAAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACA 1326
Db      1901 AAACAAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACA 1960
Qy      1327 GCACAAATAGATGTTTCATCAATATTACAGGCTGCTACTTAACAGAGATGGAGTAAT 1386
Db      1961 GGACAAATTAGATGTTTCATCAATATTACAGGCTGCTATTAAACAGAGATGGTGG---T 2017
Qy      1387 AGTACTGAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGAGATATAGGAGCAATTTGG 1446
Db      2018 CTTGAGGACACAGACCGAGTCTTCAGACCTCGAGGAGGAGATATAGGAGTAATTTGG 2077
Qy      1447 AGAAGTGAATTAATAATATATAAGTAGTAAAGTAGTAAAGTAGTAAAGTAGTAAAGTAGTAA 1506
Db      2078 AGAAGTGAATTAATAATATATAAGTAGTAAAGTAGTAAAGTAGTAAAGTAGTAAAGTAGTAA 2137
Qy      1507 AGGCAAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1550
Db      2138 AAGGCAAGAGAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2181

```

RESULT 12

```

AAT58551
ID      AAT58551 standard; cDNA; 3807 BP.
XX
AC      AAT58551;
XX
DT      17-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      25-MAR-1997 (first entry)
XX
DE      Human Immunodeficiency Virus-1 strain BA-L env gene.
XX
KW      Acquired immune deficiency syndrome; AIDS; envelope protein; env gene;
KW      vaccine; db.
XX
OS      Human immunodeficiency virus 1; (strain BA-L).
XX
FH      Key Location/Qualifiers
CDS     648..3215
FT      /*tag= a
FT      /product= "envelope_protein"
XX
PN      US5576000-A.
XX
PD      19-NOV-1996.
XX
PF      15-FEB-1995; 95US-00388809.
XX
PR      17-OCT-1990; 90US-00599491.
PR      25-FEB-1993; 93US-00022835.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX

```

```

PI      Gallo RC, Franchini G, Lori FC, Popovic M, Reitz MS, Gartner S;
PI      Markham PD;
XX
DR      WPI; 1997-011206/01.
DR      P-PSDB; AAW11581.
XX
PT      New isolated envelope protein of HIV-1 strain BA-L and recombinant
PT      equivalents - useful as immunogens for vaccines and antibody prodn.,
PT      typical of US clinical isolates.
XX
PS      Example; Fig 8; 86pp; English.
XX
CC      A HindIII fragment of unintegrated viral DNA representing the BA-L genome
CC      was cloned into lambda phage Charon 28 DNA from total DNA of peripheral
CC      blood lymphocytes infected with and producing HIV-1(BA-L). A positive
CC      clone was selected by hybridisation using a HIV-1 env probe. This clone,
CC      designated BA-L1, was found to contain the entire gene for the envelope
CC      protein on a 2.8 kb HindIII-XbaI fragment and a 0.4 kb EcoRI-HindIII
CC      fragment. When cloned together these fragments comprise the env gene, as
CC      well as the coding regions for rev and the rev-responsive element of env,
CC      both necessary for efficient expression in eukaryotic cells. The claimed
CC      recombinantly produced envelope protein can be used as an immunogen for
CC      raising antibodies against HIV. (Updated on 25-MAR-2003 to correct PF
CC      field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ      Sequence 3807 BP; 1307 A; 662 C; 937 G; 901 T; 0 U; 0 Other;
Query Match      54.4%; Score 1225.2; DB 2; Length 3807;
Best Local Similarity 90.1%; Pred No. 4.7e-248;
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;
Qy      73 ATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTGCAGTCTAT 132
Db      702 ATGCTCCTTGGGATATTGATGATCTGTAGTGTCTGAGAAAAATTTGGGTGCAGTCTAT 761
Qy      133 TATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCATCAGATGCTAAA 192
Db      762 TATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCATCAGATGCTAAA 821
Qy      193 GCATATGATACAGAGGTACATAATGTTTGGGCGCACACATGCTGTGTACCCACAGACCCC 252
Db      822 GCATATGATACAGAGGTACATAATGTTTGGGCGCACACATGCTGTGTACCCACAGACCCC 881
Qy      253 AACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTATGTGAAAAATAAC 312
Db      882 AACCCACAAGAGTAGAATTGAAAAATGTGACAGAAAAATTTTAACTATGTGAAAAATAAC 941
Qy      313 ATGTTAGATCAGATGATGAGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCATGT 372
Db      942 ATGTTAGAACAAATGTCATGAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCATGT 1001
Qy      373 GTAAATTTAACCCCACTCTGTGTTACTTTTAAATTCACCTAAATTTGA-----ATATCACT 426
Db      1002 GTAAATTTAACCCCACTCTGTGTTACTTTTAAATTCACCTAGTTTGGGATGCTACTAAT 1061
Qy      427 AAGATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAA 486
Db      1062 GGGAAATGACACTAATACCCTAGTAGTAGCAGGGGAATGGTGGGGGAGGAGAAATGAAA 1121
Qy      487 AATGCTCTTCTTATATCACCACAGCATAGAAATAAGGTAAGGTAAGAAAGAAATATGCATT 546
Db      1122 AATGCTCTTCTTCAATATCACCACAAACATAAGAGGTAAGGTAAGGTAAGAAAGAAATATGCATT 1181
Qy      547 TTTAATAGACTTGTAGTAGTACCAATAAGAAATCTAATACTAATAGTATAGGTTAATA 606
Db      1182 TTTAATAAATTTGATATAGCACCAATAGATATAATAGTATAATAGTATAGGTTGATA 1241
Qy      607 AGTTGTAAACACCTCAGTCAATTACACAGGCTGTCCAAAGGATATCTTTTCAGCAATTC 666
Db      1242 AGTTGTAAACACCTCAGTCAATTACACAGGCTGTCCAAAGGATATCTTTTCAGCAATTC 1301
Qy      667 ATACATTAATTTGTCCCGCTGGGTTTCGGATGCTAAAGTGTAAACAAATAGCAATTCAAT 726

```


Db 1302 ATACATTATTGTCGCCGCTGGTTTTGCGATTCTTAAAGTGTAAGAATAAGAAGTTCAAT 1361
Qy 727 GGATCAGGACCATGACAAATGTGACGACAGTACAAATGTACACATGGAATTTAGGCCAGTG 786
Db 1362 GGAAAGGACCATTGTACAAATGTGACGACAGTACAAATGTACACATGGAATTTAGGCCAGTA 1421
Qy 787 GTGTCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAAGAAGACATAGTAATAGATCT 846
Db 1422 GTATCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAAGAAGAGGTAGTAATAGATCC 1481
Qy 847 GAAATTTTCACAGACAATGCTAAAAACCATATAGTACAGCTAAATGAAATCTGTAGTAAT 906
Db 1482 GCCAATTTTCGGGCAATGCTAAAAGTCAATATAGTACAGCTGAATGAATCTGTAGAAAT 1541
Qy 907 AATTGTCAAGACCCCAACAACATACAAAGAGAAGTTATCTATAGGACCCAGGAGACGA 966
Db 1542 AATTGTCAAGACCCCAACAACATACAAAGAAAAGTATACATATAGGACCCAGGAGACGA 1601
Qy 967 TTTTATGCAAGAAGAAACATATAGGAGATATAACACAAGCACATTTGTAACATTTAGTAGA 1026
Db 1602 TTTTATACAAAGGAGAAATATAGGAGATATAACACAAGCACATTTGTAACCTTAGTAGA 1661
Qy 1027 GCATAATGGAATAACACTTTTCAACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAAT 1086
Db 1662 GCATAATGGAATGACACTTTAAATAGATAGTTATAAAATTAAGAGAACAAATTTGGGAAT 1721
Qy 1087 AAAACAATAGCCTTTAAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGACACAGTTT 1146
Db 1722 AAAACAATAGTCTTTAAAGCACTCCTCAGAGGGGACCCAGAAATTTGTACGACACAGTTT 1781
Qy 1147 AATTGTGAGGGGAATCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTTGGAAT 1206
Db 1782 AATTGTGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAAATAGTACTTTGGAAT 1841
Qy 1207 GTTACTGAGGGACAAATGGCACTGAAAGGAATGACATAATCACACTCCCAATGCAGATA 1266
Db 1842 GTTACTGAAGAGTCAAAATAACACTGTAGAAATAACACAATCACACTCCCAATGCAGATA 1901
Qy 1267 AAACAAATTAATAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCAATCACA 1326
Db 1902 AAACAAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCAATCACA 1961
Qy 1327 GGACAAATTAGATGTTTCATAATATTACAGGCTGCTACTAAAGAGATGGAGTAAAT 1386
Db 1962 GGACAAATTAGATGTTTCATAATATTACAGGCTGCTATTAAAGAGATGGTGG---T 2018
Qy 1387 AGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGACAAATTGG 1446
Db 2019 CCTGAGGACAAACAGACCCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGATAATTGG 2078
Qy 1447 AGAAGTGAATTAATAATATAAAGTAGTAAGATTGAACCAATAGGAGTAGCACCACC 1506
Db 2079 AGAAGTGAATTAATAATATAAAGTAGTAAGATTGAACCAATAGGAGTAGCACCACC 2138
Qy 1507 AGGCAAAAGAGAGAGAGTGGTGCAAGAGAAAAAGAGGGGGAGG 1550
Db 2139 AAGGCAAAAGAGAGAGTGGTGCAAGAGAAAAAGAGAGTGGG 2182

RESULT 13
AD052562
ID AD052562 standard; DNA; 9540 BP.
XX
AC AD052562;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human immunodeficiency virus 1 parent JRCSF DNA.
XX
KW Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy;
KW vaccine; ds.
XX
OS Human immunodeficiency virus 1.

XX US2004101823-A1.
PN 27-MAY-2004.
XX 19-DEC-2002; 2002US-00325468.
XX 21-DEC-2001; 2001US-0343524P.
XX (MAXY-) MAXYGEN INC.
XX Soong NW, Pekrun K, Shibata R;
PI WPI; 2004-399670/37.
XX GENBANK; M38429.
DR
XX
PT New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a
composition for treating or preventing infection caused by HIV-1.
XX
PS Disclosure; SEQ ID NO 46; 310pp; English.
XX
CC The present invention relates to human immunodeficiency virus 1 (HIV-1)
viral variants and nucleic acids and polypeptides thereof having improved
replication properties for development of suitable animal models for the
study of HIV-1 pathogenesis. The invention is useful for treating and
preventing HIV-1 infection. The invention is also useful in gene therapy
and in the preparation of vaccines. The present sequence is human
immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the
invention.
XX
SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;
Query Match 54.3%; Score 1222.2; DB 12; Length 9540;
Best Local Similarity 90.1%; Pred. No. 2.4e-247;
Matches 1334; Conservative 0; Mismatches 128; Indels 15; Gaps 2;
Qy 74 TGCTCTTTGGGATATTGATGATCTCTAGTGTCTACAGAAAAATTTGGGTACAGTCTATT 133
Db 6291 TGCTCTTTGGGACATTATGATCTCTAGTGTGTAGAAAAAGTTGGGTACAGTCTATT 6350
Qy 134 ATGGGGTACCTGTGTGGAGAGAGCAACACCACTCTATTTTGTGCATCAGATGCTAAAG 193
Db 6351 ATGGGGTACCTGTGTGGAAAGAAAACACCACTCTATTTTGTGCATCAGATGCTAAAG 6410
Qy 194 CCTATGATACAGAGGTACATAATGTTGGGCCACACATGCTGTACCCACAGACCCCA 253
Db 6411 CATATGATACAGAGGTACATAATGTTGGGCCACACATGCTGTACCCACAGACCCCA 6470
Qy 254 ACCCAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTGTGGAAAAATAACA 313
Db 6471 ACCCAAGAGTAGTATTGGGAAATGTAAACAGAAAGATTTTAACTGTGGAAAAATAACA 6530
Qy 314 TGGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAAAGCCCTAAAGCCATGTG 373
Db 6531 TGGTAGAACAGATGACGAGGAGATGTAATCAATTTATGGGATCAAAAGCTTTAAAGCCATGTG 6590
Qy 374 TAAATTTAAACCCACTCTGTGTCTTTTAAATTTGCACTTAATTTGAATATCACTAAGATA 433
Db 6591 TAAATTTAAACCCACTCTGTGTCTTTTAAATTTGCAAGAGATG-----GAATG 6638
Qy 434 CTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAAAATTTGCT 493
Db 6639 CTACTAATCCCACTAGTAGTAGTGAGGGAATGATGGAGAGAGAGAAATTTAAAGCTGCT 6698
Qy 494 CTTTCTATATACCAAGCATTAAGAAATAAGGTAAAGAAAGAAATATGCACTTTTAAATA 553
Db 6699 CTTTCAATATACCAAAAGCATTAAGAGATAAGGTGCAGAAAGAAATATGCTCTTTTATA 6758
Qy 554 GACTTGTGTAGTACCAATAGAAAACTAATAATTAAGTATAGTTAAATAGTTGTA 613
Db 6759 AACTGTGTAGTACCAATAGATAATAAGAAATAATACCAAAATATAGTTAATAGTTGTA 6818
Qy 614 ACACCTCAGTCAATTACACAGGCTGTGCCAAAGGTATCTTTTCAGCCAAATCCCATACATT 673

Db 6819 ACACCTCAGTCATACAAAGCTGTCAAAGGTATCCTTTGAACCAATTCCTCATACATT 6878
Qy 674 ATTGTGTCCCGCTGGTTGGATGCTAAAGTGTAAACAATAAGACATTCATGATCAG 733
Db 6879 ATTGTGCCCGCTGGTTGGATGCTAAAGTGTAAACAATAAGACATTCATGGAAG 6938
Qy 734 GACCATGCAAAATGTGACGACAGTACCAATGTACATGTAATAGGCAAGTGGTCAA 793
Db 6939 GACAATGTAAAAATGTGACGACAGTACCAATGTACATGTAATAGGCAAGTGGTCAA 6998
Qy 794 CTCACCTGCTGTAATGCGACGTAGCAGAGAGACATAGTAAATAGATCTGAAAT 853
Db 6999 CTCACCTGCTGTAATGCGACGTAGCAGAGAGAGATGTAATAGATCTGCAAT 7058
Qy 854 TCACAGACAATCCTAAACCAATAGTACACCTAAATGAATCTGTAGTAATTAATTGTA 913
Db 7059 TTACGACCAATCTAAACCAATAGTACACCTGAATGAATCTGTAAATTAATTGTA 7118
Qy 914 CAAGACCCAAACAATCAAGAAAGGTTATCTATAGGACGAGGAGAGCATTTATG 973
Db 7119 CAAGGCCAGCAACAATCAAGAAAGGTTATCATATAGGACGAGGAGAGCATTTATA 7178
Qy 974 CAAGAGAAACATATAGGAGATATAGCAGACGACATTTGAACATTTAGTAGACCAAT 1033
Db 7179 CAACAGGAGAAATATAGGAGATATAGCAGACGACATTTGAACATTTAGTAGACCAAT 7238
Qy 1034 GGAATAACACTTTACCAACAGATAGTTATAAAATTAAGAGAAATTTAGGAATAAAACAA 1093
Db 7239 GGAATAACACTTTAAACAGATAGTTGAAATTAAGAGAAATTTAAATAAAACAA 7298
Qy 1094 TAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGAATGACAGTTTAAATTG 1153
Db 7299 TAGCTTTTACTCACTCCTCAGAGGGGATCCAGAAATTTGAATGACAGTTTAAATTG 7358
Qy 1154 GAGGGGAATTTCTTACTGTATACAGCACTGTTTAAATAGTACTTGGAAATGACTG 1213
Db 7359 GAGGGGAATTTTCTTACTGTAAATCAACAACTGTTTAAATAGTACTTGGAAATGACTG 7418
Qy 1214 GAGGACAAATGGCACTGAAGAAATGACATATCACTCAATGCAAGATTAACAA 1273
Db 7419 AAAAGTCAAGTGGCACTGAGGAAATGACACCTCACTCACTCCATGCAAGATTAACAA 7478
Qy 1274 TTATAAATATGCGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCAAGACAA 1333
Db 7479 TTATAAATATGCGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATTAAGACAA 7538
Qy 1334 TTAGATGTTCAATATATCAGGCTGCTACTTAACAAGATGAGGATTAATAGTACTG 1393
Db 7539 TTAGATGTTCAATATATCAGGCTGCTACTTAACAAGATGAGGATTAATAGTACTG 7595
Qy 1394 AGACTGAGACTGAGATCTTCAGACCTGGAGGAGGATATGAGGACAAATTTGGAAGTG 1453
Db 7596 AGAGTGAGATCGAGATCTTCAGACCTGGAGGAGGACATGAGGACAAATTTGGAAGTG 7655
Qy 1454 AATTATATAAATATAAGTAGTAAGATTAACCAATAGGATAGCACCACCCAGGGCAA 1513
Db 7656 AATTATATAAATATAAGTAGTAAGATTAACCAATAGGATAGCACCACCCAGGGCAA 7715
Qy 1514 AGAGAGAAACAGTGAAGAGAGAAAGAGGGGGAGG 1550
Db 7716 AGAGAGAGAGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7752

RESULT 14

ADP20074

ID ADP20074 standard; DNA; 9540 BP.

XX AC

XX ADP20074;

DT 09-SEP-2004 (first entry)

XX DE

Human immunodeficiency virus 1 isolate JRCSF nucleotide sequence.

XX immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSF;
XX gene; ds.
OS Human immunodeficiency virus 1.
XX Key Location/Qualifiers
LTR 1..635
FT /*tag= a
FT /partial
FT 790..2304
FT /*tag= b
FT /product= "gag"
FT 2085..5108
FT /*tag= c
FT /product= "pol"
FT 5053..5631
FT /*tag= d
FT /product= "vif"
FT 5571..5861
FT /*tag= e
FT /product= "vpr"
FT 6073..6318
FT /*tag= f
FT /product= "vpU"
FT 6236..8782
FT /*tag= g
FT /product= "env"
FT 8784..9434
FT /*tag= h
FT /product= "nef"
FT 9103..9540
FT /*tag= i
FT /partial
XX WO2004053100-A2.
XX 24-JUN-2004.
XX 11-DEC-2003; 2003WO-US039534.
XX 11-DEC-2002; 2002US-0432869P.
XX 24-APR-2003; 2003US-0465350P.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Wilson I, Pantophlet R;
XX WPI; 2004-480933/45.
XX P-PSDB; ADP20067, ADP20068, ADP20069, ADP20070, ADP20071, ADP20072,
XX ADP20073.
XX GENBANK; M38429.
XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against
PT the polypeptide, useful preventing or treating human immunodeficiency
PT virus (HIV) infection, especially HIV-1 infection.
XX Disclosure; Page 139-141; 149pp; English.
XX The present invention describes an immunogenic mutant HIV gp120
CC polypeptide that can stimulate a neutralising antibody response against a
CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic
CC mutant HIV-1 gp120 polypeptide (1a) that can stimulate a neutralising
CC antibody response against a panel of HIV-1 comprising HIV-1 primary
CC isolates of at least two different clades, where the mutant gp120 has at
CC least one amino acid mutation in at least one epitope of the HIV-1 gp120
CC polypeptide specifically bound by a neutralising antibody, which reduces
CC binding affinity of the non-neutralising antibody; (2) an immunogenic
CC mutant HIV-1 gp120 polypeptide (1b) having at least one amino acid
CC mutation in at least one epitope of the gp120 polypeptide specifically
CC bound by a non-neutralising antibody; (3) a vaccine (11) comprising one

or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5) an isolated HIV neutralising antibody (IV) fraction obtained by using (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V) obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in a subject, by administering an HIV neutralising antibody produced in response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV-1 infection in a human subject, involves administering HIV-1 neutralising antibodies to the subject, where the HIV-1 neutralising antibodies comprise antibodies stimulated in response to (II); (9) HIV neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV neutralising antibodies (VII) obtained by using (Ib); and (11) isolated HIV-1 neutralising antibodies obtained by harvesting spleen and lymph nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV activities, and can be used in vaccines and in HIV binding agents. (Ia) and (Ib) are useful for inducing antibodies that can neutralise HIV-1 which involves immunising a subject with a (Ia) or (Ib). The antibodies are useful for preventing or ameliorating HIV, especially HIV-1, infection in a subject. The present sequence represents an HIV-1 isolate JRC5F genomic nucleotide sequence, which is given in the exemplification of the present invention.

Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 54.3%; Score 1222.2; DB 12; Length 9540;

Best Local Similarity 90.3%; Pred. No. 2.4e-247; Matches 1334; Conservative 0; Mismatches 128; Indels 15; Gaps 2;

QY	74	TGCTCTTGGGATATGATGATCTGTAGTGTACAGAAAATTTGGGTACAGTCTATT	133
DB	6291	TGCTCTTGGGACATTAATGATCTGTAGTGTAGAAAAGTTGGGTACAGTCTATT	6350
QY	134	ATGGGGTACCTGTGGAGAGNAGCAACCACTCTATTTTGCATCAGATGCTAAG	193
DB	6351	ATGGGGTACCTGTGGAGAGNAGCAACCACTCTATTTTGCATCAGATGCTAAG	6410
QY	194	CCTATGATACAGAGTACATTAATTTTGGGCCACACATGCTGTACCCACAGACCCA	253
DB	6411	CATATGATACAGAGTACATTAATTTTGGGCCACACATGCTGTACCCACAGACCCA	6470
QY	254	ACCCACAAAGAGTAGTATGGGAATGTGACAGAAAATTTTAAATGCGAAAATAACA	313
DB	6471	ACCCACAAAGAGTAGTATGGGAATGTGACAGAAAATTTTAAATGCGAAAATAACA	6530
QY	314	TGGTATGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	373
DB	6531	TGGTATGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	6590
QY	374	TAAATTTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAATATCACTA	433
DB	6591	TAAATTTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAATATCACTA	6638
QY	434	CTACTAATCCCACTAGTAGCAGCTGGGAAATGATGAGAAAGGAGAAATAAATAAT	493
DB	6639	CTACTAATCCCACTAGTAGTAGGGAATGATGAGAAAGGAGAAATAAATAAT	6698
QY	494	CTTTCTATATCCACACAGCATAAGAAATAGGTAAAGAAAGAAATGCACTTTTATA	553
DB	6699	CTTTCTATATCCACACAGCATAAGAAATAGGTAAAGAAAGAAATGCACTTTTATA	6758
QY	554	GACTTGTAGTAGTACCAATAGAAAATCTAATAATCTAAGTATAGGTTAATAAGTTGA	613
DB	6759	AACTGGATGTAGTACCAATAGAAAATCTAATAATCTAAGTATAGGTTAATAAGTTGA	6818
QY	614	ACACCTCAGTCAATACAGGCTGTCCAAAGGTATCTTTTCCAGCAATTTCCCATACAT	673
DB	6819	ACACCTCAGTCAATACAGGCTGTCCAAAGGTATCTTTTCCAGCAATTTCCCATACAT	6878
QY	674	ATTGTGTCCTGGCTGGTGTGGATGCTTAAAGTGTAAAGTGTAAAGTGTAAAGTGT	733
DB	6879	ATTGTGTCCTGGCTGGTGTGGATGCTTAAAGTGTAAAGTGTAAAGTGTAAAGTGT	6938
QY	734	GACCATGCACAAATGTCACAGCAGTACAAATGTACACATGGAATTAGGCCAGTGGTCAA	793

DB	6939	GACAATGTAAAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCAGTAGTATCAA	6998
QY	794	CTCAACTGCTCTTAAATGGCAGTCTAGCAGAAAGAGACATAGTAATTAGACTCTGAAAT	853
DB	6999	CTCAACTGCTCTTAAATGGCAGTCTAGCAGAAAGAGAGGTTGTAAATTAGACTCTGCAAT	7058
QY	854	TCACAGACAAATGCTTAAACCAATAATAGTACAGCTTAAATGAATCTGTAGTAATTAATGTA	913
DB	7059	TTAGGACAAATGCTTAAACCAATAATAGTACAGCTTAAATGAATCTGTAAATTAATGTA	7118
QY	914	CAAGACCCAAACAATAACAAGAGAGGTTATCTATAGGACCGAGGAGAGCATTTTATG	973
DB	7119	CAAGCCCGACCAACAATAACAAGAGAGGTTATCTATAGGACCGAGGAGAGCATTTTATA	7178
QY	974	CAAGAGAAACATTAATAGGACATATAAGCAAGACCATTTGAACATTTAGTAGAGCAAAAT	1033
DB	7179	CAACAGGAGAAATAATAGGAGATATAAGCAAGACCATTTGAACATTTAGTAGAGCAAAAT	7238
QY	1034	GGAATAACACTTTTACAACAGATAGTTATAAAATTTAAGAGAGAAAATTTAGGAATTAACA	1093
DB	7239	GGAATAACACTTTTACAACAGATAGTTATAAAATTTAAGAGAGCAATTTTAATTAACA	7298
QY	1094	TAGCTTTTAATCAATCTCAGAGGGGACCCAGAAAATTTGTAATGACAGTCTTTAATGTTG	1153
DB	7299	TAGCTTTTAATCAATCTCAGAGGGGACCCAGAAAATTTGTAATGACAGTCTTTAATGTTG	7358
QY	1154	GAGGGAAATTTTCTACTGTAAATCAACACAACTGTTTAAATAGTACTTTGGAAATGACTG	1213
DB	7359	GAGGGAAATTTTCTACTGTAAATCAACACAACTGTTTAAATAGTACTTTGGAAATGACTG	7418
QY	1214	GAGGACAAATGCGCATGAAGGAAATGACATAATCACACTCCCAATGCAAGATTAACA	1273
DB	7419	AAAGTCAAGTGGCACTGAAGGAAATGACATCACTACTCCCATGCAAGATTAACA	7478
QY	1274	TTATAAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCTCCCTCCCATCAAGAGCA	1333
DB	7479	TTATAAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCTCCCTCCCATCAAGAGCA	7538
QY	1334	TTAGATGTTCACTCAAAATTTACAGGCTGTACTTAAACAGAGATGAGGTATAGTACTG	1393
DB	7539	TTAGATGTTCACTCAAAATTTACAGGCTGTACTTAAACAGAGATGAGGTATAGTACTG	7595
QY	1394	AGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGACAAATTTGAGAGTG	1453
DB	7596	AGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGACAAATTTGAGAGTG	7655
QY	1454	AATTATATAATATAAGTAGTAAAGATTTGAACCAATAGGAGTAGCACCCACAGGCA	1513
DB	7656	AATTATATAATATAAGTAGTAAAGATTTGAACCAATAGGAGTAGCACCCACAGGCA	7715
QY	1514	AGAGAGAACAGTGCAG	1550
DB	7716	AGAGAGAGAGTGGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7752

RESULT 15

AAQ14753
ID AAQ14753 standard; DNA; 3807 BP.

XX AAQ14753;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 05-FEB-1992 (first entry)

XX HIV-1 BA-L clone.

XX human immunodeficiency virus; United States; MN isolate; AIDS;

KW envelope protein; ss.

XX Human immunodeficiency virus 1.

XX

FH Key Location/Qualifiers
 FT CDS 394..476
 FT /*tag= b
 FT /product= "rev"
 CDS 648..3215
 FT /*tag= a
 FT /product= "env"
 XX
 PN USN7599491-N.
 XX
 PD 15-OCT-1991.
 XX
 PF 17-OCT-1990; 90US-00183830.
 XX
 PR 17-OCT-1990; 90US-00599491.
 XX
 PA (USSH) NAT INST OF HEALTH.
 XX
 PI Reitz M;
 XX
 DR WPI; 1991-346752/47.
 DR P-PSDB; AAR14905.
 XX
 PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in
 PT therapeutics, vaccines and diagnostic tests.
 XX
 PS Example 3; Fig 8; 61pp; English.
 XX
 CC A HindIII fragment of unintegrated viral DNA representing the HIV-1 (BA-
 CC L) genome was cloned by standard techniques into lambda phage Charon 28
 CC DNA from total DNA of peripheral blood macrophages infected with and
 CC producing HIV-1 (BA-L). A positive clone was selected by hybridisation
 CC using a HIV-1 envelope probe. This clone, designated BA-L1, contained the
 CC entire env gene. The insert was subcloned and sequenced. The BA-L plasmid
 CC clone has been deposited as ATCC 40890. The sequence also contains the
 CC coding region for the rev protein which is needed for efficient
 CC expression of the envelope protein in eukaryotic cells. (Note: Revised
 CC entry submitted to correct the patent number format of US Government-
 CC owned NTIS applications to prevent clashes with ongoing US granted patent
 CC numbers. For further information please visit the Derwent web site at
 CC www.derwent.com/dwpi/updates/ntis.us.html.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;
 Query Match 54.1%; Score 1218.8; DB 2; Length 3807;
 Best Local Similarity 89.8%; Pred. No. 1e-246; Mismatches 142; Indels 9; Gaps 2;
 Matches 1333; Conservative 0;
 QY 73 ATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGGTCACTCTAT 132
 DB ATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGGTCACTCTAT 761
 QY 133 TATGGGTACCTGTGTGGAGAGAACCAACACACTCTATTTTGTGCAATCAGATGCTAAA 192
 DB TATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCAATCAGATGCTAAA 821
 QY 193 GCCTATGATACAGAGTACATATGTTGGGCCACACATGCTGTACCCACAGACCCC 252
 DB GCATATGATACAGAGTACATATGTTGGGCCACACATGCTGTACCCACAGACCCC 881
 QY 253 AACCACCAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTTAAATGTGAAAAATAAC 312
 DB AACCACCAAGAGTAGATTTGAAATTTGACAGAAAAATTTTAAATGTGAAAAATAAC 941
 QY 313 ATGTGATGATCAGATGATGAGATATAATCAGTTTATGGATGAAAGCTTAAAGCCATGT 372
 DB ATGTGATGAAATGATGATGAGATATAATCAGTTTATGGATGAAAGCTTAAAGCCATGT 1001
 QY 373 GTAAAAATTAACCCCACTCTGCTTAAATTTGCACTTAATTTGA-----ATATCACT 426
 DB GTAAAAATTAACCCCACTCTGCTTAAATTTGCACTTAATTTGAGGAATGCTACTAAT 1061

QY 427 AAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATAAAA 486
 DB GGGAAATGACACTAATACCACTAGTAGCAGGGAATGTTGGGGGAGGAGAAATGAAA 1121
 QY 487 AATTGCTCTTTCTATATCACCACAGCATATAGAAATAGGTAAGAAAGAAATATGCATT 546
 DB AATTGCTCTTTCAATATCACCACAAATAGAGGTAAAGGTGCGAAAGAAATATGCATT 1181
 QY 547 TTTAATAGACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 DB TTTTATAAATGATATAGCACCATAATATAGTATATATATATATATATAGTATGATA 1241
 QY 607 AGTTGTAACACTCAGTCAATACAGGCTGTGCAAAAGGTATCTCTTTCAGGCAATTC 666
 DB AGTTGTAACACTCAGTCAATACAGGCTGTGCAAAAGGTATCTCTTTCAGGCAATTC 1301
 QY 667 ATACATTATTTGTCCTCCGCTGGGTTTGCATGCTTAAAGTGTAAACAATAAGACATTCAAT 726
 DB ATACATTATTTGTCCTCCGCTGGGTTTGCATGCTTAAAGTGTAAAGTGTAAAGTGTCAAT 1361
 QY 727 GGATCAGGACCATGCAAAATGTCAGCACAGTACATGTCATACATGGAATTTAGGCCAGTG 786
 DB GGAAAAGGACCATGTCACAAATGTCAGCACAGTACATGTCATACATGGAATTTAGGCCAGTA 1421
 QY 787 GTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAAATTAATGATCT 846
 DB GTATCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAAATTAATGATCT 1481
 QY 847 GAAATTTTCAGACAAATGCTTAAACCATATATAGTACAGCTTAAATGAATCTGCTAGTAAAT 906
 DB GCCAAATTTGGGGGACAAATGCTTAAAGTCAATATAGTACAGCTTAAATGAATCTGCTAGAAAT 1541
 QY 907 AATTGTCAAGAACCCCAACAAATCAACAAGAAAGGTTATCTATAGGACCCAGGAGAGCA 966
 DB AATTGTCAAGAACCCCAACAAATCAACAAGAAAGTATACATATAGGACCCAGGAGAGCA 1601
 QY 967 TTTTATGCAAGAAACAAATATAGGAGATATAGCAAGACATGTTAAACATTAATGATGATA 1026
 DB TTTTATCAACAGGAGAAATATAGGAGATATAGCAAGACATGTTAAACATTTACTACTAGA 1661
 QY 1027 GCAAAATCGAATACACCTTTACACAGATAGTTATATAATTAAGAGAGAAAAATTTAGGAAT 1086
 DB GAAAATCGAATGACACTTTTAAATAGATAGTTATATAATTAAGAGAGAAAAATTTGGGAAT 1721
 QY 1087 AAAACAATAGCTTTTAAATCAATCTCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTTT 1146
 DB AAAACAATAGCTTTTAAACACTCTCTCAGGAGGGGACCCAGAAATTTGTGACGACAGTTTT 1781
 QY 1147 AATTGTGAGGGGAATTTCTTCTAGTAAATACAGCAACCTGTTTAAATAGTACTTTGGAAAT 1206
 DB AATTGTGAGGGGAATTTTCTCTGTAATTTCAACACAACTGTTTAAATAGTACTTTGGAAAT 1841
 QY 1207 GTTACTGAGGGACAAATGCGCACTGAAGAAATGACATAATACACTCCATGCAAGATA 1266
 DB GTTACTGAAGAGTCAAAATCACTGTGAAAAATAACCAATCACTCCCATGCAAGATA 1901
 QY 1267 AAACAAATTTATAATATGTGCGAGAAATGAGMAAGCAATGTATGCCCTCCCATCACA 1326
 DB AAACAAATTTATAATATGTGCGAGAAATGAGMAAGCAATGTATGCCCTCCCATCACA 1961
 QY 1327 GGACAAATTTAGATGTTCAATAATTTACAGGGCTGTCTAATAAGAGATGAGAGGTAAT 1386
 DB GGACAAATTTAGATGTTTCAATAATTTACAGGGCTGTCTAATAAGAGATGAGAGGTAAT 2018
 QY 1387 AGTACTGAGACTGAGACTGAGATCTTTCAGCTGGGAGGAGATATGAGGCAATTTGG 1446
 DB CCTGAGGACAAAGACCGAGGTCTTCAGCTGGGAGGAGATATGAGGCAATTTGG 2078
 QY 1447 AGAAGTGAATTTATATAAATATAAAGTAGTAAAGAAATTTGAACCAATAGGAGTAGCACCACC 1506
 DB AGAAGTGAATTTATATAAATATAAAGTAGTAAAGAAATTTGAACCAATAGGAGTAGCACCACC 2138
 QY 1507 AGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAAGAGGGGGAGG 1550

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 131.432 Seconds
(without alignments)
12178.890 Million cell updates/sec

Title: US-09-687-864A-12
Perfect score: 2252
Sequence: 1 aagtttcgcgcgtctgtgta.....ctcagtgataatctagata 2252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A-COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B-COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A-COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225.2	54.4	3807	1	US-08-022-835-5
2	1225.2	54.4	3807	1	US-08-388-809-5
3	1225.2	54.4	3807	2	US-08-647-714-5
4	1173.4	52.1	4527	2	US-08-944-449-8
5	1173.4	52.1	4527	3	US-09-353-362-8
6	1172.6	52.1	3807	2	US-08-417-210A-78
7	1172.6	52.1	3807	4	US-09-136-159A-78
8	1172.4	52.1	2571	1	US-08-254-358-3
9	1172.4	52.1	2571	1	US-08-475-391-3
10	1172.4	52.1	2571	2	US-08-709-609-3
11	1172.4	52.1	2571	4	US-09-552-572-3
12	1172.4	52.1	2571	4	US-09-936-572-3
13	1172.4	52.1	2571	5	PCT-US95-07178-3
14	1172.4	52.1	6474	3	US-08-651-472-66
15	1172.4	52.1	6474	3	US-08-358-928-66
16	1172.4	52.1	6926	3	US-08-651-472-69
17	1172.4	52.1	6926	3	US-08-358-928-69
18	1172.4	52.1	9739	1	US-08-022-835-1
19	1172.4	52.1	9739	1	US-08-388-809-1
20	1172.4	52.1	9739	2	US-08-647-714-1
21	1172.4	52.1	9746	1	US-08-022-835-3
22	1172.4	52.1	9746	1	US-08-388-809-3
23	1172.4	52.1	9746	2	US-08-647-714-3
24	1171.8	52.0	2552	2	US-08-448-603A-27
25	1171.8	52.0	2552	3	US-09-134-075-27
26	1171.8	52.0	2552	3	US-09-492-739-27
27	1171.4	52.0	1539	3	US-07-956-483-21

28	1171.4	52.0	1539	3	US-08-472-240A-13
29	1168.6	51.9	1532	2	US-08-037-816A-15
30	1168.6	51.9	1532	2	US-08-530-146-15
31	1168.6	51.9	2573	2	US-08-448-603A-29
32	1168.6	51.9	2573	3	US-09-134-075-29
33	1168.6	51.9	2573	3	US-09-492-739-29
34	1165.4	51.7	1532	2	US-08-037-816A-27
35	1165.4	51.7	1532	2	US-08-530-146-27
36	1162.2	51.6	9737	2	US-08-944-449-7
37	1162.2	51.6	9737	3	US-09-353-362-7
38	1162	51.6	1932	4	US-09-475-515-31
39	1162	51.6	2457	4	US-09-475-515-32
40	1161	51.6	1419	4	US-09-475-515-30
41	1160.8	51.5	1929	4	US-09-602-864-12
42	1160.4	51.5	2570	2	US-08-448-603A-31
43	1160.4	51.5	2570	3	US-09-134-075-31
44	1160.4	51.5	2570	3	US-09-492-739-31
45	1158.4	51.4	1527	3	US-07-956-483-26

ALIGNMENTS

RESULT 1
US-08-022-835-5
; Sequence 5, Application US/08022835
; Patent No. 5420030
; GENERAL INFORMATION:
; APPLICANT: Reitz Jr., Marvin S.
; APPLICANT: Franchini, Genoveffa
; APPLICANT: Markham, Phillip D.
; APPLICANT: Gallo, Robert C.
; APPLICANT: Lori, Franco C.
; APPLICANT: Popovic, Mikulas
; APPLICANT: Gaunter, Suzanne
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USBS
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,835
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

LOCATION: 648..3215									
US-08-022-835-5									
Query Match 54.4%; Score 1225.2; DB 1; Length 3807;									
Best Local Similarity 90.1%; Pred. No. 1.4e-293;									
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;									
QY	73	ATGCTCCCTTGGGATATTCATGATCTGTAGTGTCTACAGAAAATTCGTGGTCCACAGTCTAT	132						
DB	702	ATGCTCCCTTGGGATATTAATGATCTGTAAATGCTGAAGAAAATTTGGGTCCACAGTCTAT	761						
QY	133	TATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGTCATCGATGCTAAA	192						
DB	762	TATGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGTCATCGATGCTAAA	821						
QY	193	GCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCCC	252						
DB	822	GCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCCC	881						
QY	253	AACCCACAAGAGTAGTATTCGGAATCTGCAGAAAATTTTAACTGTGGAATAAATAC	312						
DB	882	AACCCACAAGAGTAGTATTCGGAATCTGCAGAAAATTTTAACTGTGGAATAAATAC	941						
QY	313	ATGGTAGATCAGATCGATCAGGATATAATCAGTTTTATGGGATGAAGCCTTAAAGCCATGT	372						
DB	942	ATGGTAGAACAAATCATGAGGATATAATCAGTTTTATGGGATCAAAGCCTTAAAGCCATGT	1001						
QY	373	GTAAATTAACCCCACTCTGTGTTACTTTTAAATTCACCTAATTTGA-----ATATCACT	426						
DB	1002	GTAAATTAACCCCACTCTGTGTTACTTTTAAATTCACCTGATTTTGGGAATGCTACTAAT	1061						
QY	427	AAGATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATAAA	486						
DB	1062	GGGAATGACACTAATACCCTAGTAGTAGCAGGGAATGGTGGGGAGAGGAATGAAA	1121						
QY	487	AATTCCTCTTTCTATATCACCACAGCATAAGAAAATAAGGTAAGAAAGAAATATGCACTT	546						
DB	1122	AATTCCTCTTTCAATATCACCACAAACATAAGAGGTAAAGTGCAAGAAAGAAATATGCACTT	1181						
QY	547	TTTAATAGACTGTAGTAGTACCAATAGAAAATCTAATACTAATAGTAGTTAATA	606						
DB	1182	TTTTATAAATTTGATATAGACCAATAGATAATAATAGTAATAATAGTAGTTGATA	1241						
QY	607	AGTTGTAACCTCAGTCATACACAGCCTGTCCAAAGGATCTCTTTTCAGCCAAATCCC	666						
DB	1242	AGTTGTAACCTCAGTCATACACAGCCTGTCCAAAGGATCTCTTTTCAGCCAAATCCC	1301						
QY	667	ATACATTATTGTGTCCTGGCTGGGTTTGGATGCTTAAAGTGTAAACAATAAGACATTTCAAT	726						
DB	1302	ATACATTATTGTGTCCTGGCTGGGTTTGGATGCTTAAAGTGTAAAGAATAAGAAAGTTCAAT	1361						
QY	727	GGATCAGGACACATGACAAAATGTACACAGCAGTACAAATGTACACATGGAAATTAGGCCAGTG	786						
DB	1362	GGAAAGGAGCATTGTACAAATGTACACAGCAGTACAAATGTACACATGGAAATTAGGCCAGTA	1421						
QY	787	GTGTCACCTCAACTGCTGTTAAATGCGAGTCTAGCAGAAAGACATAGTAATAGATCT	846						
DB	1422	GTATCAACTCAACTGCTGTTAAATGCGAGTCTAGCAGAAAGACATAGTAATAGATCT	1481						
QY	847	GAATAATTTTACAGACAATGCTAAAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAAT	906						
DB	1482	GCCAAATTCGCGGACAAATGCTAAAGTCAATAATAGTACAGCTGAATGAATCTGTAGAAAT	1541						
QY	907	AATGTACAGACCAACCAACAAATACAGAGAAGGTTATCTATAGGACCGAGGAGCA	966						
DB	1542	AATGTACAGACCAACCAACAAATACAGAGAAGGTTATCTATAGGACCGAGGAGCA	1601						
QY	967	TTTTATGCAAGAGAAAATAATAGAGATAAAGCAAGCAGCATTTGTAACATTTAGTAGA	1026						
DB	1602	TTTTATACACAGGAGAAAATAATAGAGATAAAGCAAGCAGCATTTGTAACATTTAGTAGA	1661						
QY	1027	GCAAAATGGAATPAACACTTTACACAGATAGTTATAAATTAAGAGAAAAATTTAGGAAT	1086						

RESULT 2

US-08-388-809-5
; Sequence 5, Application US/08388809
; Patent No. 5576000
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & PINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,809
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/022,835
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: LESLIE A. SERUNIAN
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4092US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800

```
;
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3215
;
US-08-388-809-5

Query Match      54.4%; Score 1225.2; DB 1; Length 3807;
Best Local Similarity 90.1%; Pred. No. 1.4e-293;
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 73 ATGCTCCTTGGGATATTCATGATCTGTAGTGTCTACAGAAAATTTGGGGTCAAGTCTAT 132
DB |||||
QY 702 ATGCTCCTTGGGATATTAATGATCTGTAAATGCTGAAGAAAATTTGGGGTCAAGTCTAT 761
DB |||||
QY 133 TATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCAGATCTAAA 192
DB |||||
QY 762 TATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCAGATCTAAA 821
DB |||||
QY 193 GCCTATGATACAGAGGTACATAATGTTTGGGCCACATGCTGTGTACCCACAGACCCC 252
DB |||||
QY 822 GCATATGATACAGAGGTACATAATGTTTGGGCCACATGCTGTGTACCCACAGACCCC 881
DB |||||
QY 253 AACCACCAAGAGTAGTATTGGGAATGTGACAGAAAATTTTAAATGCTGGAATAATAC 312
DB |||||
QY 882 AACCACCAAGAGTAGTATTGGGAATGTGACAGAAAATTTTAAATGCTGGAATAATAC 941
DB |||||
QY 313 ATGTAGATCAGATCAGATGAGGATATAATCAGTTTATGGGATGAAGCCTTAAAGCCATGT 372
DB |||||
QY 942 ATGTAGAACAAATGATGAGGATATAATCAGTTTATGGGATGAAGCCTTAAAGCCATGT 1001
DB |||||
QY 373 GTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTGA-----ATATCACT 426
DB |||||
QY 1002 GTAAATTAACCCCACTCTGTGTTACTTTAAATTCACATAATTGA-----ATATCACT 1061
DB |||||
QY 427 AAGATACACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAGGAGGAATAAAA 486
DB |||||
QY 1062 GGAATGACATTAATACCACTAGTAGTAGCAGGGAATGTTGGGGGAGGAGGAATAAAA 1121
DB |||||
QY 487 AATGCTCTTTCTATATCACCAACAGCATATAAGATAAGGTAAAGAAAAGATAATGCACCT 546
DB |||||
QY 1122 AATGCTCTTTCAATATCACCAACATATAGAGGTAGGTGCAGAAAGATAATGCACCT 1181
DB |||||
QY 547 TTTAATAGACTGTAGTAGTACCAATAGAAAATATAATAATACATAATAGTATAGGTTAATA 606
DB |||||
QY 1182 TTTTATAAATTTGATATAGCAACCAATAGATAATAATAGTATAATAGATATAGGTTGATA 1241
DB |||||
QY 607 AGTTGTAACTCAGTCACTTACACAGCGCTGTCCAAAGGTATCCTTTCAGCCAAATCCC 666
DB |||||
QY 1242 AGTTGTAACTCAGTCACTTACACAGCGCTGTCCAAAGGTATCCTTTCAGCCAAATCCC 1301
DB |||||
QY 667 ATACATTAATGTGTCGCCGCTGGTTCGATGCTTAAAGGTGTAACAATAAGACATTTCAAT 726
DB |||||
QY 1302 ATACATTAATGTGTCGCCGCTGGTTCGATGCTTAAAGGTGTAACAATAAGAGATTTCAAT 1361
DB |||||
QY 727 GGATCAGGACCATGACAAAATGTACAGCACAGTACATGATGATGGAATTTAGGCCAGTG 786
DB |||||
QY 1362 GGAAGAGGACCATGTACAAAATGTACAGCACAGTACATGATGGAATTTAGGCCAGTA 1421
DB |||||
QY 787 GTGTCAACTCAACTCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAAATAGATCT 846
DB |||||
QY 1422 GTATCAACTCAACTCTGTTAAATGGCAGTCTAGCAGAAAGAGAGGTAGTAAATAGATCT 1481
DB |||||
QY 847 GAAATTTTACAGACAAATGCTAAAACCAATAATAGTACAGCTAAATGAATCTGTACTAAT 906
DB |||||
QY 1482 GCCAATTTGGCGGACAAATGCTAAAGTCAATATAGTACAGCTGAATGAATCTGTAGAAAT 1541
DB |||||

RESULT 3
US-08-647-714-5
; Sequence 5, Application US/08647714
; Patent No. 5869313
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C. LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,714
; FILING DATE:
; PRIOR APPLICATION DATA:
;
```

APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4092US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 648..3215
US-08-647-714-5

Query Match 54.4%; Score 1225.2; DB 2; Length 3807;
Best Local Similarity 90.1%; Pred. No. 1.4e-293;
Matches 1337; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 73 ATGCTCCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGTGGGTACAGCTCTAT 132
DB 702 ATGCTCCTGGGATATTGATGATCTGTATGCTGAAGAAAATTGTGGGTACAGCTCTAT 761
QY 133 TATGGGGTACCTGTGTGGAGAAAGCAACACCACCTCTATTTTGTGCATCAGATGCTAAA 192
DB 762 TATGGGGTACCTGTGTGGAGAAAGCAACACCACCTCTATTTTGTGCATCAGATGCTAAA 821
QY 193 GCCTATGATACAGAGTACATAATGTTGGGCCACACATGCTGTGTACCCACAGACCCC 252
DB 822 GCATATGATACAGAGTACATAATGTTGGGCCACACATGCTGTGTACCCACAGACCCC 881
QY 253 AACCCACAAGAGTAGTATTGGGAATGTGACAGAAAAATTTTAAATGTGGAATAATAAC 312
DB 882 AACCCACAAGAGTAGAATTGAAAATGTGACAGAAAATTTTAAATGTGGAATAATAAC 941
QY 313 ATGTGTAGATCAGATGCATGAGATATAATCAGTTTATGGGATGAAAGCCTTAAAGCCATGT 372
DB 942 ATGGGTAGAACAAATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTTAAAGCCATGT 1001
QY 373 GTAAATTAACCCCACTCTGTGTACTTTAAATTCACCTAAATTGA-----ATATCACT 426
DB 1002 GTAAATTAACCCCACTCTGTGTACTTTAAATTCACCTAAATTGAAGGATGCTACTAAT 1061
QY 427 AAGAATCTACTTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATAAAA 486
DB 1062 GGAATGACACTTAATACCACTAGTAGTAGCAGGGGATGGTGGGGGAGGAGAAATGAAA 1121
QY 487 AATTCCTCTTCTATATACCAACAGATAGAAAATAAGGTTAAAGAAAGAAATATGCACTT 546
DB 1122 AATTCCTCTTCTATATACCAACAGATAGAAAATAAGGTTAAAGAAAGAAATATGCACTT 1181
QY 547 TTTAATAGACTGTAGTAGCAATAGAAAATCTAATACTAATCTAAGTTATAGTTAATA 606
DB 1182 TTTTATAACTTGTATAGCAATAGATAATAATAGTAAATAGATATAGTTGTGATA 1241
QY 607 AGTTGTAACACCTCAGTCAATTACAGAGGCTGTCCAAAGGTATCCTTTTTCAGCAATTC 666
DB 1242 AGTTGTAACACCTCAGTCAATTACAGAGGCTGTCCAAAGGTATCCTTTTTCAGCAATTC 1301
QY 667 ATACATTAATGTGTCCCGCTGGGTTTGGGATGCTTAAAGTGTAAACATAAGACATTCAT 726
DB 1302 ATACATTAATGTGTCCCGCTGGGTTTGGGATGCTTAAAGTGTAAAGATAAGAAAGTTCAAT 1361

QY 727 GGATCAGGACCATGCACAAATGTGCAGCACAGTACAATGTACAATGGAATTTAGCCAGTG 786
DB 1362 GGAAGAGGACCATGTACAATGTGCAGCACAGTACAATGTACAATGGAATTTAGCCAGTA 1421
QY 787 GTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTTAGATCT 846
DB 1422 GTATCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGAGTAGTAATTTAGATCC 1481
QY 847 GAAATTTTCAGACAAATGCTAAACCATAATAGTACAGCTAAATGAATCTGTAGTAAT 906
DB 1482 GCCAATTTTCGGGACAATGCTAAAGTCAATATAGTACAGCTGAATGAATCTGTAGAAAT 1541
QY 907 AATTGTCAAGACCCCAACAACAATCAAGAAAAGTATACATATAGGACCGAGCAGCA 966
DB 1542 AATTGTCAAGACCCCAACAACAATCAAGAAAAGTATACATATAGGACCGAGCAGCA 1601
QY 967 TTTTATGCAAGAAACATTAATAGGAGATATAGAACAGCACATTTGAAATTTAGTAGA 1026
DB 1602 TTTTATACACAGGAGAAATTAATAGGAGATATAAGAACAGCACATTTGAACTTTAGTAGA 1661
QY 1027 GCAAAATGGAATAACACTTTTACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAAT 1086
DB 1662 GCAAAATGGAATGACACTTTTAAATGAAGATAGTTATAAAATTAAGAGAAAAATTTAGGAAT 1721
QY 1087 AAAACAATAGCTTTTAAATCAATCCTCAGGAGGGACCCAGAAAATTTGTAAATGCACAGTTTT 1146
DB 1722 AAAACAATAGCTTTTAAAGCACTCTCAGGAGGGACCCAGAAAATTTGTGACGACAGTTTT 1781
QY 1147 AATTGTGAGGGGAATTTCTTCTGTAATACAGCAAACTGTTTAAATAGTACTTTGGAAT 1206
DB 1782 AATTGTGAGGGGAATTTTCTTCTGTAATTAACACAACTGTTTAAATAGTACTTTGGAAT 1841
QY 1207 GTTACTGAGGAGCAAAATGGCAGTGAAGAAATGACATAATCACTCCAATGCAGAAATA 1266
DB 1842 GTTACTGAGGAGTCAAAATCACTGTGAAAATTAACAATCACTCCATGCAGAAATA 1901
QY 1267 AAAACAATTAATAATATGTGCAGAAAAGTAGSAAAAGCAATGTATGCCCTCCCATCA 1326
DB 1902 AAAACAATTAATACTGTGCAGGAAGTGAAGAGAGCAATGTATGCCCTCCCATCA 1961
QY 1327 GGACAAATAGATGTTCAATCAAAATTAATACAGGCTGTACTAAACAGAGATGGAGTAAT 1386
DB 1962 GGACAAATAGATGTTCAATCAAAATTAATACAGGCTGTACTAAACAGAGATGGAGTAAT 2018
QY 1387 AGTACTGAGCTGAGACTGAGATCTTCAGACTCGAGGAGGAGATATCAGGAGCAATTTGG 1446
DB 2018 CCGAGGAGCAACAGACCGAGGTCTTCAGACTCGAGGAGGAGATATCAGGAGTAATTTGG 2078
QY 1447 AGAAGTGAATTAATAATAATAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCACC 1506
DB 2079 AGAAGTGAATTAATAATAATAAGTAGTAAGAATTTGAACCAATAGGAGTAGCACCACC 2138
QY 1507 AGGCAAGAGAGAACAGACAGTGCACAAAGAAAAAGAGGGGGAGG 1550
DB 2139 AAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAAGAGCAGTGGG 2182

RESULT 4
US-08-944-449-8
; Sequence 8, Application US/08944449
; Patent No. 5985613
; GENERAL INFORMATION:
; APPLICANT: KURTH, REINHARD
; APPLICANT: BAIER, MICHAEL
; APPLICANT: METZNER, KARIN
; APPLICANT: WERNER, ALBRECHT
; TITLE OF INVENTION: Use of an "immunodeficiency-virus suppressing
; TITLE OF INVENTION: lymphokine (ISL)" to inhibit the replication of
; TITLE OF INVENTION: viruses, particularly of retroviruses
; FILE REFERENCE: 8341-7065
; CURRENT APPLICATION NUMBER: US/08/944,449
; CURRENT FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: EP 95113013.2


```

; EARLIER FILING DATE: 1995-08-18
; EARLIER APPLICATION NUMBER: DE 195 13 152.5
; EARLIER FILING DATE: 1995-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-08-944-449-8

Query Match      52.1%; Score 1173.4; DB 2; Length 4527;
Best Local Similarity 86.0%; Pred. No. 1e-280;
Matches 1339; Conservative 0; Mismatches 206; Indels 12; Gaps 3;

QY 52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTCTAGTCTGTAGTCTACAGAA 111
DB 515 TGCTTGGAGATGGGGCAGATGCTCTCTGGGATGTTAATGATCTCTAGTCTGTAGTCTACAGAA 574

QY 112 AAATTGGGTACAGCTCTATTATGGGGTACCTGTGTGGAGAGAGCAACACCACTCTA 171
DB 575 AAATTGGGTACAGCTCTATTATGGGGTACCTGTGTGGAGAGATGCAACCACTCTCTA 634

QY 172 TTTTGTGCATCAGTGTAAAGCTATGATACAGAGGTACATATGTTTGGGCCACACAT 231
DB 635 TTTTGTGCATCAGATGCTTAAAGCATATGATACAGAGGTACATATGTTTGGGCCACACAT 694

QY 232 GCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAT 291
DB 695 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAT 754

QY 292 TTTTAACATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
DB 755 TTTTAACATGTGGAAAAATAACATGGTAGACCAAGATGCATGAGGATATAGTCAGTTTATGG 814

QY 352 GATGAAAGCCTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATTGCACT 411
DB 815 GATCAAGCCCTAAGCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATTGCACT 874

QY 412 AATTGTAATATCACTAAGATATCTACTTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG 471
DB 875 GATT-----ATTTGGGAATGCTACTTAATACCAATAGTAGTGGGGGAACGGTGGAG 928

QY 472 AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAAG 531
DB 929 AAAGAGAAATAAAAAATCTCTCTTTCAATATCACCACAGGCATAGAGATAGGTACAG 988

QY 532 AAAGATATGCATTTTTTAATAGACTTTGATGTAGTACCAATA--GAAATATCTATAAT 588
DB 989 AAGGCATATGCATATTTTTTAATTAACCTTTGATGTAGTACCAATAGATGATATACTAAT 1048

QY 589 ACTAAGTATAGGTTAATAAGTTGTAAACCTCAGTCAATTACAGAGGCTCTCCAAAGGTA 648
DB 1049 ACCAGCTATAGGTTGATACATTTGTAATTCCTCAGTCAATTACAGAGCTCTCCAAAGGTA 1108

QY 649 TCCTTTTCAGGCCAATTCCTCATACATTAATGTGTCTCCGGCTGGGTTTGGCATGCTAAAGTGT 708
DB 1109 TCCTTTTCAGGCCAATTCCTCATACATTAATGTGTCTCCGGCTGGTCTTTCGATTTCTAAGTGT 1168

QY 709 AACAAATAAGACATTTCAATGGATCAGGACCAATGCAAAATGTCTAGCAGCAGTACAAATGTACA 768
DB 1169 AATAATAAGAAAGTTTCAGTGGAAAAGGTCAATGTACAAATGTCTAGCAGCAGTACAAATGTACA 1228

QY 769 CATGGAAATTAGGCCAGTGGTGTCACTCACTCTGTTTAATGGCAGTCTAGCAGAGAA 828
DB 1229 CATGGAAATTAGGCCAGTGGTGTCACTCACTCTGTTTAATGGCAGTCTAGCAGAGAA 1288

QY 829 GACATAGTAATTAGATCTGAAAAATTTTCACAGACAAATGCTAAAAACCAATAATAGTACAGCTA 888
DB 1289 GAGGTAGTAATTAGATCTGAAATTTTCACGAAACAAATGCTAAAACCAATAATTAGTACAGCTG 1348

QY 889 AATGAAATCTGTAGTAATTAAATTGTACAAAGACCCCAACAAATAACAAGAAAGGTTATCT 948

```

```

; NAME: KLESNER, Sharon N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P8341-9012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4527 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-353-362-8

Query Match      52.1%; Score 1173.4; DB 3; Length 4527;
Best Local Similarity 86.0%; Pred. No. 1e-280;
Matches 1339; Conservative 0; Mismatches 206; Indels 12; Gaps 3;

QY 52 TGGATCTCGGCTTCAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAA 111
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 515 TGCCTGTGGAGATGGGCGACGATGCTCCTTGGGATGTTAATGATCTGTAGTGTGCGAA 574
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 112 AAATTTGCGGTACACAGTCTATTATGCGGTACCTGTGAGAGAGCAACACCACTCTA 171
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 575 AATTTGTGGGTACACAGTTATTATATGGGTACCTGTGTGGAAGATGCAACCACTACTCTA 634
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 172 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 635 TTTTGTGATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT 694
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 232 GCCTGTGTACACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 695 GCCTGTGTACACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 754
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 292 TTTACATGTGGAATAAATGATGTAGATCAGATGATGAGGATATATCAGTTTATGG 351
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 755 TTTACATGTGGAATAAATGATGTAGATGATGAGGATATATCAGTTTATGG 814
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 352 GATGAAGCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTTAAATGCACT 411
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 815 GATCAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTTAAATGCACT 874
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 412 AATTTGAATATCATAAGAACTACTACTATCCACTAGTAGCAGCTGGGAAATGATGAG 471
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 875 GATT-----ATTGGGGAATCTACTAATACCAATAGTAGTGGGGGACCGTGGAG 928
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 472 AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCAAGCATAAAGAAATAAGGTAAAG 531
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 929 AAAGAAATAAATAAATACTGCTCTTTCAATATCACACAGGATTAAGATTAAGGTACAG 988
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 532 AAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATA- - -GAAAAATACTAATAAT 588
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 989 AAGGCATATGCATATTTTATATAAATCTGTATGTAGTACCAATAGATGATGATAATACTAAT 1048
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 589 ACTAAGTATAGTTAATAAGTTGTAAACCTCAGTCATTTACACAGCCCTGTCCAAGGTA 648
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1049 ACCAGCTAGGTGATACATTTGTAATTCCTCAGTCATTTACACAGACCTGTCCAAGGTA 1108
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 649 TCCTTTTCAGCAATTTCCCATACATTTATGTGTCGGCTGGGTTTGGCGATGCTAAAGTGT 708
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1109 TCCTTTGAGCCAAATTCCTATACATTTATGTGTCGGCTGGGTTTGGCGATGCTAAAGTGT 1168
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 709 AAACAATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGACACAGTACAAATGTACA 768
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1169 AATAATAAGAAAGTTCAAGTGGAAAAAGTCAATGTACAAATGTGACACAGTACAAATGTACA 1228
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 769 CATGAAATTTAGCCAGTGTGTCACTCACTGCTGTTAAATGGCGAGTGTACAGAGNA 828
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1229 CATGAAATTTAAGCCAGTGTGTCACTCACTGCTGTTAAATGGCGAGTGTACAGAGNA 1288
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 829 GACATAGTAATTAGATCTGAAAAATTTTCACAGACAAATGCTTAAAAACCATATATAGTACAGCTA 888
```

RESULT 6

```

US-08-417-210A-78/c
; Sequence 78, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PROLETTI, ENZO
; APPLICANT: PARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1289 GAGGTAGTAATTAGATCTGACAAATTTTCAGAACCAATGCTAAACCATATTAGTACAGCTG 1348
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
889 AATGAATCTGTAGTAATTAATTTGTACAGACCCCAACATACACAGAGAGGTTATCT 948
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1349 AATGTATCTGTAGAAAATTAATTTGTACAGACCCCAACCAATAGAGAGGAGGATAACT 1408
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
949 ATAGGACCCAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATTAAGACAAGCA 1008
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1409 AGTGACCCAGGGAAGTACTTTTATACACAGAGAAATTAATAGGAGATATTAAGAAAAGCA 1468
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1009 CATTGTAACTATTAGTAGCAAAATGGAATTAACACTTTTCAACAGATAGTTATAAAATTA 1068
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1469 TATTGTAACTATTAGTAGCAAAATGGAATTAACACTTTTGAACAGGTAGTACAAAATTA 1528
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1069 AGAGAAAATTTAGGAATAAAACAAATAGCCCTTTTAATCAATCCTCAGGAGGGGACCCAGAA 1128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1529 AGAGAACAAATTTGGGAATAAAACAAATAGTATTTAAACAATCCTCAGGAGGAGACCCAGAA 1588
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1129 ATTGTAAATGCACAGTTTAAATTTGTGGAGGGAATTTCTTCTACTGTGTAATACAGCAACTG 1188
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1589 ATTGTAAATGCACAGTTTAAATTTGTAGAGGGAATTTTCTACTGTGTAATACACAAACTG 1648
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1189 TTTAATAGTACTTGGAAATGTTTACTGGAGGGCAAAATGGCACTGGAAGGAAATGACATAATC 1248
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1649 TTTAATAGTACTTGGAAATGAAAATAGTACTTTGGAATGCTACT- - -GGAATGACACTATC 1705
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1249 ACATCCCAATGCAGAAATAAAACAAATTAATAATATATGTCGAGAAAGTAGGAAAAGCAATG 1308
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1706 ACATCCCAATGCAGAAATAAAACAAATTAATAACATGTGCGAGGAAGTAGGAAAAGCAATG 1765
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1309 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTA 1368
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1766 TATGCCCTCCCATCGAAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTACTA 1825
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1369 ACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGAGGA 1428
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1826 ACAAGAGATGGTGGTGGTGACAAAGAAAGTACCACCGAGATCTTTAGACCTGCAGAGGA 1885
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1429 GATATGAGGACAAATTTGAGAAAGTGAATTAATAATATAAGTAGTAAGATTGAACCA 1488
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1886 AATATGAAGGACAAATTTGAGAAAGTGAATTAATAATATAAGTAGTAAGATTGAACCA 1945
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1489 ATAGAGTAGCACCCACAGGCGCAAGAGAGAAACAGTGCAAGAGAGAAAAAGAGGGGA 1548
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1946 TTAGAGTAGCACCCACAGGCAAGAGAGAGAGTGGTGCAAGAGAGAAAAAGAGCAGTG 2005
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1549 GCGGTTTCAGGAGGTGGAGGTTCTTGAGGTTGGCGGATCGGATCCAGAGAGGTTGGAC 1605
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2006 GGAGTAGTAGGAGCTATGTTCTTGGGTTCTTGGGAGCAGCAGGAGCACTATGGGC 2062
```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-417-210A-78

Query Match          52.1%; Score 1172.6; DB 2; Length 3807;
Best Local Similarity 88.1%; Pred. No. 1.5e-280;
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;

QY 52 TGGATCTCGGCTTCGAGATCTATGCTCTCTGGGATATTGATGATCTGTAGTCTACAGAA 111
DB 1668 TGGGGGTGGAGATGGGGACCATGCTCTCTGGGATGTTGATGATCTGTAGTCTACAGAA 1609

QY 112 AAATTTGGGTGACAGTCTTATTTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171
DB 1608 AAATTTGGGTGACAGTCTTATTTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 1549

QY 172 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
DB 1548 TTTTGTGATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489

QY 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291
DB 1498 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGTAAATGTGACAGAAAT 1429

QY 292 TTTTACATGTGAAAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
DB 1428 TTTTACATGTGAAAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1369

QY 352 GATGAAAGCCTAAAGCCTATGTTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 411
DB 1368 GATCAAGCCTAAAGCCTATGTTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 1309

QY 412 AATTTG-----AATATCAAGAAATATCTAATCCCACTAGTAGTACGAGTGG 459
DB 1308 GATTTGGAGGAATACTAATAATCAATATAGTACTGTCTAATAACAATAGTAAATAGCGAG 1249

QY 460 GGAATGATGGAGAAAGGAGAAATAAATAATGCTCTTTCTATATCACCACAGCATAGA 519
DB 1248 GGAACAATAAAGGGAGGAGAAATGAATAAATCTCTCTTTCAATATCACCACAGCATAGA 1189

QY 520 AATAAGGTAAAGAAAGATATGCACTTTTAAATAGACTTTGATGTAGTACCAATAGAAAT 579
DB 1188 GATAAGATGCAGAAAGATATGCACTTTTAAATAGACTTTGATGTAGTATCAAT---AAT 1132

QY 580 ACTAATAATACCTAAGTATAGGTTAATAGTTGTAAACCTCAGTCAATACACAGGCTGT 639
DB 1131 AATGATAGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCAATACACAGGCTGT 1072

QY 640 CAAAAGGTATCTTTTCAGGCAATTCGCATACATATTGTTGTCCTCCGCTGGGTTTCGATG 699
DB 1071 CAAAAGATATCTTTTCAGGCAATTCGCATACATATTGTTGTCCTCCGCTGGGTTTCGATG 1012

QY 700 CTAAGGTGTAACAATAAGACATTTCAATGATCAGAGCAATGACAAATGTCAGACAGTA 759
DB 1011 CTAAGGTGTAACAATAAGATTTCAATGATGAGAAAGATCATGTAAATAATGTCAGACAGTA 952

QY 760 CAATGTACATGGAATTAGGCCAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTA 819
```

```

DB 951 CAATGTACATGGAATTAGGCCAGTATGATCAACTCACTGCTGTTAAATGGCAGTCTA 892
QY 820 GCAGAAAGAGACATAGTAATTAATGATCTGAAATTTTACAGACAAATGCTTAAACCAATA 879
DB 891 GCAGAAAGAGAGGAGTATGATCTGAGAAATTTCAATGATGATGATGATGATGATGATG 832
QY 880 GTACAGCTAAATGAATCTGTAGTAATTAATGTTACAGACCCCAACCAATTAACAAGA 939
DB 831 GTACATCTGAATGAATCTGTACAAATTAATGTTACAGACCCCACTACAAATAAAGAAA 772
QY 940 AGGTTATCTATAGGACCCAGGAGAGCATTTTATGCAAGAGAAACATATAGAGATATA 999
DB 771 AGGATACATATAGGACCCAGGAGAGCATTTTATACAAACAAATATATATAGGAATATA 712
QY 1000 AGACAAAGCACAATTGTAACATTTAGTAGACCAAAATGGAATTAACACATTTTACAA 1059
DB 711 AGACAAAGCACAATTGTAACATTTAGTAGACCAAAATGGAATGACACTTTTAAGACAG 652
QY 1060 ATAAATTTAAGAGAAAATTTAGGAATAAACAAATAGCCTTTTAAATCAATCTCAGAG 1119
DB 651 AGCAAAATTTAAAGAAACAAATTTAAGAAATAAACAATAGTCTTTTAAATCAATCTC 592
QY 1120 GACCAGAAAATTTGTAATGCAACAGTTTAAATTTGTGGAGGGGAATTTCTTCTACTG 1179
DB 591 GACCAGAAAATTTGTAATGCAACAGTTTAAATTTGTGGAGGGGAATTTCTTCTACTG 532
QY 1180 GCACAACCTGTTTAAATAGTACTTTGGAATGTTACTGTGGAGGACAAATGGCACTGA 1236
DB 531 TCACCACTGTTTAAATAGTACTTTGGAATGTTAAATTAATCTTGGAAATTAATCTAC 472
QY 1237 AATGACATAATCACACTCCCAATGCAAGAAATAAACAATAATTAATATGTTGGAGAA 1296
DB 471 AATAACAATATCACACTTCAATGCAAAATAAACAATAATTAATAAATGTTGGAGAA 412
QY 1297 GGAAGCAATGATGATGCTCCCTCCCAATCAGAGCAAAATTAGTATGTTCAATTAAT 1356
DB 411 GGAAGCAATATATGCTCCCTCCCAATGCAAGCAAAATTAGTATGTTCAATTAATTA 352
QY 1357 GGGCTGCTACTTAAACAAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGAT 1413
DB 351 GGGCTGCTACTTAAACAAGAGATGGTAAAGNACACGACACGACACCGAGATCTTC 292
QY 1414 AGACCTGGAGGAGAGATATAGGAGCAATTTGGAGAGTGAATTAATAATAATATAAGTA 1473
DB 291 AGACCTGGAGGAGAGATATAGGAGCAATTTGGAGAGTGAATTAATAATAATAAGTA 232
QY 1474 GTAGAAATTTGAACCAATAGGATAGCACCACCCAGGCAAGAGAGAAACAGTGCAGAA 1533
DB 231 GTAAACAATTTGAACCAATAGGATAGCACCACCCAGGCAAGAGAGAAAGAGTGGTGC 172
QY 1534 GAAAAAAGA 1542
DB 171 GAAAAAAGA 163
```

RESULT 7
US-09-136-159A-78/c
; Sequence 78, Application US/09136159A
; Patent No. 6596279
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136,159A
; CURRENT FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06

; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-09-136-159A-78

Query Match 52.1%; Score 1172.6; DB 4; Length 3807;
Best Local Similarity 88.1%; Pred. No. 1.5e-280;
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;
QY 52 TGGATCTCGGCTTCAGATCTATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAA 111
DB 1668 TGGGGGTGGAGATGGGGCACCATGCTCTCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609
QY 112 AAATTTGGTGGTCCACAGTCTATTATGGGTGCTCTGTGGAGAGAACCAACCACTCTA 171
DB 1608 AAATTTGGTGGTCCACAGTCTATTATGGGTGCTCTGTGGAGAGAACCAACCACTCTA 1549
QY 172 TTTTGTGCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATTTGTTGGGCCACACAT 231
DB 1548 TTTTGTGCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATTTGTTGGGCCACACAT 1489
QY 232 GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT 291
DB 1488 GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT 1429
QY 292 TTTAATGATGTGAAAAATAACATGTTAGATCAGATGCAATGAGATATATCAATTTATGG 351
DB 1428 TTTAATGATGTGAAAAATAACATGTTAGATCAGATGCAATGAGATATATCAATTTATGG 1369
QY 352 GATGAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTTACTTTAAATTCACAT 411
DB 1368 GATGAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTTACTTTAAATTCACAT 1309
QY 412 AATTTG-----AATATCACTAAGATATCTACTTAATCCCACTAGTAGCAGCTGG 459
DB 1308 GATTTGAGGAATACCTACTAATACCAATATAGTACTGCTTAATCAATAGTAAATAGCGAG 1249
QY 460 GGAATGATGGAGAAAGGAGAAATAAAAAATTCCTCTTCTATATCACCACAGCATAAAGA 519
DB 1248 GGAACAATAAGGGAGGAGAAATGAATAAATCTCTTTCAATATCACCACAGCATAAAGA 1189
QY 520 AATAAGGTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGATACCAATAGAAAAAT 579
DB 1188 GATAAGATGCAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGATACCAATAGAAAAAT 1132
QY 580 ACTAATAATACCTAAGTATAGTTAATAGTTGTAACACCTCAGTCACTTATACACAGCCTGT 639
DB 1131 AATGATAGTACCAGTATAGTTGTAATAGTTGTAATACCTCAGTCACTTATACACAGCCTGT 1072
QY 640 CCAAGAGTATCTTTTCCAGCAATTCCTATACATATTGTTGTCCTCCGCTGGGTTTCGGATG 699
DB 1071 CCAAGAGTATCTTTTCCAGCAATTCCTATACATATTGTTGTCCTCCGCTGGGTTTCGGATG 1012
QY 700 CTAAGTGTAAACAATAAGACATTCATGGATCAGGACCAATGCACAAATGTTCAGCACAGTA 759
DB 1011 CTAAGTGTAAACAATAAGACATTCATGGATCAGGACCAATGCATGTAAAAAATGTTCAGCACAGTA 952

QY 760 CAATGTTACACATGGAAATTTAGGCCAGTGTGTCAACTCACTGCTGTTTAAATGGCAGTCTA 819
DB 951 CAATGTTACACATGGAAATTTAGGCCAGTGTGTCAACTCACTGCTGTTTAAATGGCAGTCTA 892
QY 820 GCAGAAGAAGACATAGTAATTTAGATCTCTGAAATTTTCACAGACAATTCGTCTAAACCAATA 879
DB 891 GCAGAAGAAGAGGTAGTAATTTAGATCTCTGAAATTTTCATGATGATGCTCTAAACCAATCATA 832
QY 880 GTACAGCTAATGATCTGTAGTAAATTTGTTACAGACCCCAACCAACAATACAGAGA 939
DB 831 GTACATCTGAATGATCTGTACAAATTTAAATTTGTTCAAGACCCCACTCAATAAAGAAAA 772
QY 940 AGGTTATCTATAGGACCAAGGAGAGCATTTTATGCAAGAAGAAACATATATAGGAGATATA 999
DB 771 AGGATACATATAGGACCAAGGAGAGCATTTTATACACAAAATAATATATATAGGAACTATA 712
QY 1000 AGACAAGCACATTTGTAACATTTAGTAGAGCAAAAATGGAAATAACATTTTACACAGATGTT 1059
DB 711 AGACAAGCACATTTGTAACATTTAGTAGAGCAAAAATGGAAATAACATTTTAAAGACAGATGTT 652
QY 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAACAATAGCCTTTAATCAATCTCAGAGGG 1119
DB 651 AGCAAAATTTAAAGAAACAATTTAAGAATAAACAATAGTCTTTAATCAATCTCAGAGGG 592
QY 1120 GACCCAGAAAATTTGTAATGTCACAGTTTAAATTTGTTGGGGGAAATCTTCTCTGTAAATACA 1179
DB 591 GACCCAGAAAATTTGTAATGTCACAGTTTAAATTTGTTGGGGGAAATCTTCTCTGTAAATACA 532
QY 1180 GCACAACCTGTTTAAATGTAATGTTGAAATGTTTACTGGAGGGACAAAATGGCACTGAAGG---A 1236
DB 531 TCACCACCTGTTTAAATGTAATGTTGAAATGTTTACTTGGAAATAATACTACAGGGTCA 472
QY 1237 AATGACATAATCACAATGCAATGCAAGATAAACAATAAATAATATATATGTGGCAGAAAGTA 1296
DB 471 AATAACATATCACAATGCAATGCAAGATAAACAATAAATAATATATATGTGGCAGAAAGTA 412
QY 1297 GGAAGAACAATGTTATGCCCTCCCATCACAGACAAAATAGATGTTTCAATCAATATTACA 1356
DB 411 GGAAGAACAATGTTATGCCCTCCCATCACAGACAAAATAGATGTTTCAATCAATATTACA 352
QY 1357 GGGCTGCTACTAACAAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTC 1413
DB 351 GGGCTGCTACTAACAAGAGATGGTGGTAAAGACACGGACACCAACACACACAGATCTTC 292
QY 1414 AGACCTGAGAGGAGGATATCAGGACAAATTTGGAGAGCTGAATATATATAAATATAAGTA 1473
DB 291 AGACCTGAGAGGAGGATATCAGGACAAATTTGGAGAGCTGAATATATATAAATATAAGTA 232
QY 1474 GTAAGAATTTGAACCAATAGGATAGCACCCACAGGCAAGAGAGAAAGACAGTGCAAAAGA 1533
DB 231 GTAACAATTTGAACCAATAGGATAGCACCCACAGGCAAGAGAGAAAGAGTGGTGACAGAGA 172
QY 1534 GAAAAAAGA 1542
DB 171 GAAAAAAGA 163

RESULT 8

US-08-254-358-3
; Sequence 3, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

```

; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,358
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5659785and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-254-358-3

Query Match 52.1%; Score 1172.4; DB 1; Length 2571;
Best Local Similarity 88.2%; Pred. No. 1.4e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4

Qy 58 TCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117
Db 40 TGGGGATGGGGCACGATGCTCCTTGGGTATTAAATGATCTGTAGTGTCTACAGAAAAATTG 99

Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 177
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 159

Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAGCCCTGT 219

Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGAATTGGTAAATGTGACAGAAAAATTTTAAAC 279

Qy 298 ATGTGGAAAAATAACATGGTATAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGGTATAGATGATGAGGATATAATCAGTTTATGGGATCAA 339

Qy 358 AGCCTAAGGCCATGTGTAATAATTAAACCCCACTCTGTGTCTTTTAAATTTGCACATAATTG 417
Db 340 AGCCTAAGGCCATGTGTAATAATTAAACCCCACTCTGTGTCTTTTAAATTTGCACGATTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAAATPAGCGAGGAACA 459

Qy 466 ATGAGAGAAAGGAGAAAAATAAAAAATTGCTCTTTTATATATATATATATATATATATATATAG 525
Db 460 ATAAAGGGAGGAGAAAAATGAAAAAATCTGCTCTTTTCAATATATATATATATATATATATATAG 519

Qy 526 GTAAGAGAAAGAAATATGCACTTTTAAATAGATCTGATGTAGTACCAATATAGAAAAATCTAAT 585
Db 520 ATGAGAGAAAGAAATATGCACTTTTAAATAGATCTGATGTAGTACCAATATAGTATCAATAG ---AATATAT 576

Qy 586 AATACTAAGTATAGTTTAAATAGTTGTAACACCTCAGTCAATTACACAGGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAGTTGTAATACCTCAGTCAATTACACAGCTTTGTCCAAAG 636

Qy 646 GTATCTTTTCAGCAAATCCCATATATTGTTGTCCCGGCTGGGTTTGCATGCTCTAAAG 705

```

;
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578621land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-475-391-3

Query Match 52.1%; Score 1172.4; DB 1; Length 2571;
Best Local Similarity 88.2%; Pred. No. 1.4e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

QY 58 TCGGCTTCGAGATCTATGCTCTCGGATATATTGATGATCTGAGTGTGACAGAAAATTG 117
DB 40 TGGGATGGGCACGATGCTCTCGGTTATTAATGATCTGAGTGTGACAGAAAATTG 99

QY 118 TGGGTACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACACCACTCTATTTTGT 177
DB 100 TGGGTACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACACCACTCTATTTTGT 159

QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 237
DB 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 219

QY 238 GTACCCACAGACCCCAACCCCAAGAGTATGTTGGGAAATGTGACAGAAAATTTAAC 297
DB 220 GTACCCACAGACCCCAACCCCAAGAGTATGTTGGTAAATGTGACAGAAAATTTAAC 279

QY 298 ATGTGGAAAATAACATGCTAGATCAGATGCTAGGATATATATCAGTTTATGGATGAA 357
DB 280 ATGTGGAAAATAACATGCTAGATCAGATGCTAGGATATATATCAGTTTATGGATGAA 339

QY 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAATTG 417
DB 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAATTG 399

QY 418 -----AATATCACTAAGAACTACTAATATCCCACTAGTAGCAGCTGGGGAATG 465
DB 400 AGGAATCTACTAATACCAATAATAGTACTGTCTAATAACAATAGTAATAGCGAGGAAACA 459

QY 466 ATGGGAAGAGGAATAAATAATTTCTCTATATACCAAGCATAGAAATAG 525
DB 460 ATAAAGGGAGGAATAAATAATTTCTCTATATACCAAGCATAGAAATAG 519

QY 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTAGTACCAATAGAAAATCTAAT 585

DB 520 ATGCAGAAAGAAATATGCACCTCTCTTTATAAACTTGATATAGTATCAATAG---ATAATGAT 576
QY 586 AATACTAAGTATAGGTTAATAAGTTTGAACACCTCAGTCATTACACAGCCTGTCCAAAG 645
DB 577 AGTACCAGCTATAGGTTGATTAAGTTTGAATACCTCAGTCATTACACAAGCTTGTCCAAAG 636
QY 646 GTATCCTTTACAGCAAAATCCCATACATTATTGTGTCCCGGCTGGGTTTGCAGATGCTAAAG 705
DB 637 ATATCCTTTGAGCCAAATCCCATACATTATTGTGCCCGGCTGGTTTTGCAGATCTTAAA 696
QY 706 TGTAAACAATAAGACATTCAATGGATCAGGACCATGACAAATGTCAGACAGTACAAATGT 765
DB 697 TGTAAACGATAAAAGTTTCAGTGGAAAAGCATGTAAATAATGTTCAGCACAGTACAAATGT 756
QY 766 ACACATGGAATTAGCCAGTGTGTCACTCAACTCACTGTCTTAAATGGCAGTCTACAGAA 825
DB 757 ACACATGGAATTAGCCAGTGTGTCACTCAACTCACTGTCTTAAATGGCAGTCTACAGAA 816
QY 826 GAAGACATAGTAATTTAGATCTGAAAATTTTCACAGACAAATGCTTAAACCATATAGTACAG 885
DB 817 GAGAGGTAGTAATTTAGATCTGAGNAATTTCTGATATGCTTAAACCATCATAGTACAT 876
QY 886 CTAATGAATCTGTAGTAAATTTAATTGTAACAAGACCCAAACAATAACAAGAAAGGTTA 945
DB 877 CTGAATGAATCTGTACAAATTTAATTGTACAAGACCCAACTACAATAAAGAAAAAGGATA 936
QY 946 TCTATAGCACAGGAGGAGCAATTTATGCAAGAGAAACATAATAGGAGATATAGACAA 1005
DB 937 CATATAGCACAGGAGGAGCAATTTATACAACAAAAATAATAGGAACTATATAAGACAA 996
QY 1006 GCACATTGTAACATTAGTAGAGCAAAATGGAAATAACACTTTTACACAGATAGTTATAAAA 1065
DB 997 GCACATTGTAACATTAGTAGAGCAAAATGGAAATGACACTTTTAAAGACAGATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAATTTAGGAATAAACAATAGCTTTTAAATCAATCTCAGGAGGGAGCCCA 1125
DB 1057 TTAAGAGAAAATTTAGGAATAAACAATAGTCTTTTAAATCAATCTCAGGAGGGAGCCCA 1116
QY 1126 GAAATTTGTAATGCAAGTCTTAAATTTGAGGGGAAATCTTCTACTGTGTAATACACACAA 1185
DB 1117 GAAATTTGTAATGCAAGTCTTAAATTTGAGGGGAAATTTTCTACTGTGTAATACATCACA 1176
QY 1186 CTGTTTAATAGTACTTTGGAATG---TTACTGGAGGACAAAATGGCACTGAAGGAAATGAC 1242
DB 1177 CTGTTTAATAGTACTTTGGAATGTTGTAATTAATCTTGGAAATACTACAGGTCATAATAC 1236
QY 1243 ATAATCACATCCCAATGAGAAATAAACAATAATTAATAATATGTCGACAGAAAGTAGAANA 1302
DB 1237 AATATCACATCTCAATGCAAAATAAACAATAATTAATAATATGTCGACAGAAAGTAGAANA 1296
QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTCAATAATTTACAGGGCTG 1362
DB 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTCAATAATTTACAGGGCTA 1356
QY 1363 CTACTAAACAAGAGATGGAGTAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACT 1419
DB 1357 CTATTAACAAGATGTTGTAAGGACACGACGACACGACACCGAGATCTTCAGACT 1416
QY 1420 GGAGAGGAGATATGAGGACAAATTTGAGAGAGTGAATTTATATAATAATTAAGTAGTAAGA 1479
DB 1417 GGAGAGGAGATATGAGGACAAATTTGAGAGAGTGAATTTATATAATAATTAAGTAGTAAGA 1476
QY 1480 ATTGAACCAATAGGAGTAGCACCACAGGCAAGAGAAAGCAAGTGCAGAGAGAAAAA 1539
DB 1477 ATTGAACCAATAGGAGTAGCACCACAGGCAAGAGAAAGCAAGTGCAGAGAGAAAAA 1536
QY 1540 AGAG 1543
DB 1537 AGAG 1540

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-936-572-3

Query Match 52.1%; Score 1172.4; DB 4; Length 2571;
Best Local Similarity 88.2%; Pred. No. 1.4e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

QY 58 TGGGCTTCGAGATCTATGCTCTCGGATATTGATGCTGCTGAGTCTGACGAGAAATTTG 117
DB 40 TGGGATGGGCGACGATGCTCTCTGGGTTATTAATGATCTGCTGCTGACGAGAAATTTG 99
QY 118 TGGGTCACAGCTATTTATGGGTACTCTGTGGAGAGAGCAACCAACCACTCTATTTTGT 177
DB 100 TGGGTCACAGCTATTTATGGGTACTCTGTGGAGAGAGCAACCAACCACTCTATTTTGT 159
QY 178 GCATCAGATGCTAAAGCCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCCCTGT 237
DB 160 GCATCAGATGCTAAAGCCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCCCTGT 219
QY 238 GTACCCACAGACCCCAACCCCAAGTATGTTGGGAATGTCACAGAAATTTTAAAC 297
DB 220 GTACCCACAGACCCCAACCCCAAGTATGTTGGGAATGTCACAGAAATTTTAAAC 279
QY 298 ATGTGGAATAATAACATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAA 357
DB 280 ATGTGGAATAATAACATGCTAGATGATGAGGATATAATCAGTTTATGGATGAA 339
QY 358 AGCCTAAAGCCATGTTAAATTAACCCCACTCTGTGTTACTTTTAAATTTGCACTAATTTG 417
DB 340 AGCCTAAAGCCATGTTAAATTAACCCCACTCTGTGTTACTTTTAAATTTGCACTAATTTG 399
QY 418 -----AATATCACTAAGATACTACTAATCCCACTAGTACAGCTGGGGAATG 465
DB 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAATAGCGGGAAACA 459
QY 466 ATGGAGAAGGAGAAATAAATAATGCTCTTCTTATATCACCACAGCATAGAATAAG 525
DB 460 ATAAAGGAGGAGAAATGAAATACTGCTCTTCAATATCACCACAGCATAGAATAAG 519
QY 526 GTAAAGAAAGATATGCACTTTTAAATAGACTGTATGATAGTACCAATAGAAAATACTAAT 585
DB 520 ATGCAGAAAGATATGCACTTTTAAATAGTATAGTATCAATAGTATCAATAGTATCAAT 576
QY 586 AATACTAGTATAGTATTAATAGTTGTAACCACTCAGTCATACACAGCCCTGTCCTCAAG 645
DB 577 AGTACCACTATAGGTTGATAGTTGTAATACCTCAGTCATTTACACAAAGCTTGTCCAAAG 636
QY 646 GTATCTTTTCAGCCAAATCCCATACATTTATGTCCTCGGCTGGGTTTGGCATGCTAAAG 705
DB 637 ATATCTTTGAGCCAAATCCCATACATTTATGTCCTCGGCTGGGTTTGGCATGCTAAAG 696
QY 706 TGTAAACAATAAGACATTCATAGGATCAGGACCATGACACAAATGTCAGACAGTACAATGT 765
DB 697 TGTAAACAATAAGATTCAGTGGAAGAGATCATGTAAATAATGTCAGCACAGTACAATGT 756
QY 766 ACACATGAAATAGGCCAGTGTGTCATCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
DB 757 ACACATGAAATAGGCCAGTGTGTCATCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGCATAGTAATTTAGATCTGAAATTTTCAGACAAATGCTTAAACCATATAGTACAG 885
DB 817 GAAGGAGTAAATTTAGATCTGAGAAATTTCTGATAATGCTTAAACCATATAGTACAT 876
QY 886 CTAATGAATCTGTAGTAAATTTGTAAGACCCCAACCAATACAGAGAGAGGTTA 945
DB 877 CTGAATGAATCTGTACAAATTTATTTGACAGAGCCCACTACATAAAGAAAGGATA 936
QY 946 TCTATAGGACCGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAGACAA 1005

DB 937 CATATAGGACCGGAGAGCAATTTTATACAAACAAAATAATATAGGAACCTATAGACAA 996
QY 1006 GCACATTGTAACATTTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAA 1065
DB 997 GCACATTGTAACATTTAGTAGAGCAAAATGGAATAACACTTTTAAAGACAGATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAATTTAGGAATAAAACAATAGCCCTTTAATCAATCTCAGGAGGGAGCCCA 1125
DB 1057 TTAAGAGAAAATTTAGGAATAAAACAATAGCTCTTTAATCAATCTCAGGAGGGAGCCCA 1116
QY 1126 GAAATTTGTAATGACAGTTTAAATTTGCGAGGGGAATTTCTCTACTGTAATACACACAA 1185
DB 1117 GAAATTTGTAATGACAGTTTAAATTTGCGAGGGGAATTTTCTACTGTAATACATACCA 1176
QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAATGGCACTGGAAGGAATGAC 1242
DB 1177 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAAATAATACTACAGGGTCAAATAAC 1236
QY 1243 ATAATCACACTCCAAATGCGAGAAATAAACAATAATTAATAATGTCGACAGAAAGTAGGAAA 1302
DB 1237 AATATCACACTCCAAATGCAAAATAAACAATAATTAATAAATGTCGACAGAAAGTAGGAAA 1296
QY 1303 GCAATGATATGCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAAAATTTACAGGGCTG 1362
DB 1297 GCAATGATATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCATCAAAATTTACAGGGCTA 1356
QY 1363 CTACTAAACAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
DB 1357 CTATTAACAAGAGATGGTGGTAAGGACACGACGACGACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGAGATATGAGGGACAATTTGGAGAAAGTGAATTAATAATAATAAGTAGTAGA 1479
DB 1417 GGAGGAGAGATATGAGGGACAATTTGGAGAAAGTGAATTAATAATAATAAGTAGTAGA 1476
QY 1480 ATTGAACCAATAGGATAGTACCCACGAGGACCAAGAGAGACAGTCCAAAGAGAAAA 1539
DB 1477 ATTGAACCAATAGGATAGTACCCACGAGGACCAAGAGAGAGAGTGGTCAGAGAGAAAA 1536
QY 1540 AGAG 1543
DB 1537 AGAG 1540

RESULT 13
PCT-US95-07178-3
; Sequence 3, Application PC/TUS9507178
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07178
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300

```
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-07178-3

Query Match      52.1%; Score 1172.4; DB 5; Length 2571;
Best Local Similarity 88.2%; Pred No. 1.4e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCTATGCTCTCTGGGATATTTGATGATCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGATGGGCACGATGCTCTCTGGGTTATTAATGATCTGTAGTGTACAGAAAAATTG 99

Qy 118 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCAACCACTCTATTTTGT 177
Db 100 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCAACCACTCTATTTTGT 159

Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGT 219

Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGTAAATGTGACAGAAAAATTTAAAC 279

Qy 298 ATGTGGAAAAATAACATGGTGTAGATCAGATGCAATGAGGATATAATCAGTTTATGGATGAA 357
Db 280 ATGTGGAAAAATAACATGGTGTAGATCAGATGCAATGAGGATATAATCAGTTTATGGATCAA 339

Qy 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTTG 417
Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTTG 399

Qy 418 -----AATPATCACTAAGAAATACTACTAATCCCACTAGTATGAGGAGTGGGGAATG 465
Db 400 AGGAATACTACTAATAACCAATAATAGTAGTCTGCTAATAACAATAGTAAATAGCGAGGGAACA 459

Qy 466 ATGGAGAAGGAGAAATAAAAAATTTGCTTTCTATATACCAACAGCATAGAATAAG 525
Db 460 ATAAAGGGAGGAGAAATGAAAAATCGCTCTTTCAATATATACCAACAGCATAGAATAAG 519

Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTATAGTACCAATAAGMAAATACTAAT 585
Db 520 ATGCAGAAGAAATATGCACCTTTTAAATAGACTTGTATAGTATAGTATCAATAG---ATATAGT 576

Qy 586 AATACTAAGTATAGTAAATAGTTGTAAACCTCAGTCATTATACAGAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTAAATAGTTGTAATACCTCAGTCATTATACAGAGCTTGTCCAAAG 636

Qy 646 GTATCCCTTTACGCCAATTTCCCATACATTTATGTGTCCCGCTGGGTTTCCGATGCTAAAG 705
Db 637 ATATCCCTTTGAGCCAAATTTCCCATACATTTATGTGTCCCGCTGGGTTTCCGATGCTAAAG 696

Qy 706 TGTAACAATAAGACATTCATCGATCAGGACCATCACAAATGTGTCAGACAGTACAAATGT 765
Db 697 TGTAACAATAAGATTCATCGTGGAAAGAGATCATGTAAATAATGTGACACAGTACAAATGT 756

Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTGTACAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGTATCACTCAACTGCTGTTAAATGGCAGTGTACAGAA 816

Qy 826 GAAGACATAGTAATTAGATCTGAAAAATTTACAGACAATGCTTAAACCAATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGATCTGAGAATTTTCACTGTAATGCTTAAACCAATATAGTACAT 876

Qy 886 CTAATTAATCTGTAGTAATTAATTTGTAAGACACCCCAACCAATAACAGAAAGAGGTTA 945
Db 886 CTAATTAATCTGTAGTAATTAATTTGTAAGACACCCCAACCAATAACAGAAAGAGGTTA 945
```

```
Db 877 CTGAATGAATCTGTACAAATTTAAATTTGTACAAGACCCCACTACAATAAAAAAGGATA 936
Qy 946 TCTATAGACACGAGAGCAATTTTATGCAAGAGAAACATAAATAGGAGATATAGACAA 1005
Db 937 CATATAGGACACGAGAGCAATTTTATACAAACAAAAATAAATAGGAACTTATAGACAA 996
Qy 1006 GCACATTGTAACTATTAGTAGAGCAAAATGGAAATAACACTTTTCAACACAGATAGTTATAAAA 1065
Db 997 GCACATTGTAACTATTAGTAGAGCAAAATGGAAATAACACTTTTCAACACAGATAGTTAGCAAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCCTTTTAAATCAATCTCAGAGGGGACCCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCTCTTTTAAATCAATCTCAGAGGGGACCCA 1116
Qy 1126 GAAATTTGTAATGACAGTTTAAATTTGGAGGGGAAATCTTCTACTGTAAATACACGACAA 1185
Db 1117 GAAATTTGTAATGACAGTTTAAATTTGGAGGGGAAATTTTCTACTGTAAATACATCACA 1176
Qy 1186 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGGACAAAATGGCACTTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTTGGAATGTTAAATTAATTAATTAATTAATTAATTAATTAATTAAC 1236
Qy 1243 ATAATCACACTCCCAATGCAGAAATAAAAACAAAATTAATAATATGTGGCAAGAAATAGGAAAA 1302
Db 1237 AATATCACACTCCCAATGCAGAAATAAAAACAAAATTAATAATTAATTAATTAATTAATTAATAA 1296
Qy 1303 GCAATGATGCCCCCTCCCATCACAGGACAAATTTAGTGTTCATCAAAATTTACAGGGCTG 1362
Db 1297 GCAATGATGCCCCCTCCCATTTGAAGGACAAATTTAGTGTTCATCAAAATTTACAGGGCTA 1356
Qy 1363 CTACTTAAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGTGAGACACGACGACGACGACGACGACGACGACGACGACGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATATAAATAGTAAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATATAAATAGTAAAGA 1476
Qy 1480 ATTGAACCAATAGGAGTAGCACCCAGGACCAAGGACCAAGAGAGACAGTGCAGAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGCACCCAGGACCAAGGACCAAGGAGAGAGAGAGAGAGAAAA 1536
Qy 1540 AGAG 1543
Db 1537 AGAG 1540
```

```
RESULT 14
US-08-651-472-66/c
; Sequence 66, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/651,472
FILING DATE: 2004/08/14
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 6474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pselp-gp160MN
US-08-651-472-66

Query Match 52.1%; Score 1172.4; DB 3; Length 6474;
Best Local Similarity 88.2%; Pred. No. 2.1e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;
58 TCGGCTTCAGATCTATGCTCTGGGATATTGATGATCTGTAGTGCTACAGAAAATTG 117
Db 3877 TGGGATGGGACAGATGCTCTGGGTATTATTAATGCTGTAGTGCTACAGAAAATTG 3818
118 TGGGTACAGTCTATTATGGGATCCTGTGTGGAGAGAACCAACCACTCTATTATTGT 177
Db 3817 TGGGTACAGTCTATTATGGGATCCTGTGTGGAGAGAACCAACCACTCTATTATTGT 3758
178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATATGTTTGGGCCACACATCCTGT 237
Db 3757 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATATGTTTGGGCCACACATCCTGT 3698
238 GTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAATTTAAC 297
Db 3697 GTACCCACAGACCCCAACCAAGAGTAGTATTGGTAAATGTGACAGAAAATTTAAC 3638
298 ATGTGGAAAAATAACATGTTAGATCAGATGCATGAGGATATTAATCAGTTTATGGGATGAA 357
Db 3637 ATGTGGAAAAATAACATGTTAGATCAGATGCATGAGGATATTAATCAGTTTATGGGATGAA 3578
358 AGCCTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTAAATGCACTAATTGT 417
Db 3577 AGCCTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTAAATGCACTAATTGT 3518
418 -----AATATCACTAAGATATCTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 3517 AGGAATACTACTAATACCAATTAATAGTCTGCTTAATACATAGTAAGCGAGGGAACA 3458
466 ATGGAGAAGGAGAAATAAAAAATTGCTCTTTTCTATATCACCAAGCATTAAGAAAATAG 525
Db 3457 ATAAAGGAGGAGAAATGAAAAATGCTCTCTTCAATATACCCACCAAGCATTAAGATAAG 3398
526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGATACCAATAGAAAATTAAT 585
Db 3397 ATGCAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGATACCAATAGAAAATTAAT 3341
586 AATACATAGTATAGTTAATAGTTTGAACACCTCAGTCATTACACAGCCCTGTCCAAG 645
Db 3340 AGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAGCTTGTCCAAG 3281

646 GTATCCTTTTCAGCCAAATTTCCCATATCAATATTGTGTCCCGCTGGGTTTCCGATGCTAAAG 705
Db 3280 ATATCCTTTTCAGCCAAATTTCCCATATCACTATTGTGCCCCGGCTGGTTTTCGATTTCTAAA 3221
706 TGTACAATAAGACATTCAAATGGATCAGGACCATCAGCAAAATGTGAGCAAGTACATCT 765
Db 3220 TGTAAAGATAAAAGTTTCAAGTGAAGAGATCATGTAAATAATGTGAGCAAGTACATCT 3161
766 ACACATGGAATTTAGGCCAGTGTGCTCAACTCACTCACTCACTCACTCACTCACTCACT 825
Db 3160 ACACATGGAATTTAGGCCAGTGTGCTCAACTCACTCACTCACTCACTCACTCACTCACT 3101
826 GAAGACATAGTAATTTAGATCTGAAATTTTACAGACAAATGCTTAAACCAATATAGTACAG 885
Db 3100 GAAAGAGTGTAAATTTAGATCTGAGAAATTTCTGTAATGCTTAAACCAATATAGTACAT 3041
886 CTAAATGAATCTGTAGTAATTAATTTGTAAGACCCCAACCAATACAAAGAAAGGTTA 945
Db 3040 CTGAATGAATCTGTACAAATTAATTTGTAAGACCCCACTCAATTAAGAAAGGATA 2981
946 TCTATAGGACAGGAGGAGCATTTTATGCAAGAAAGAAATATAGGAGATATAAGACAA 1005
Db 2980 CATATAGGACAGGAGGAGCATTTTATGCAAGAAAGAAATATAGGAGATATAAGACAA 2921
1006 GCACATTTGTAACATTTAGTAGACAAATGGAATACACATTTTACACAGATAGTTATAAA 1065
Db 2920 GCACATTTGTAACATTTAGTAGACAAATGGAATGACACTTTTAAAGACAGATAGTTACAA 2861
1066 TTAAGAGAAAATTTAGGAATAAACAATAGCTTTTAAATCAATCTCAGGAGGAGACCA 1125
Db 2860 TTAAGAGAAAATTTAGGAATAAACAATAGCTTTTAAATCAATCTCAGGAGGAGACCA 2801
1126 GAAATTTGTAATGCAAGTTTTAAATTTGAGAGGGGAATTTCTTACTGTAATACAGACAA 1185
Db 2800 GAAATTTGTAATGCAAGTTTTAAATTTGAGAGGGGAATTTTCTACTGTAATACATCA 2741
1186 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGGAACAAATGGCACTGAAGGAAATGAC 1242
Db 2740 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGGAACAAATGGCACTGAAGGAAATGAC 2681
1243 ATAATCACATCTCAATGAGAAATAAACAATATATATATATATATATATATATATATATAT 1302
Db 2680 ATAATCACATCTCAATGAGAAATAAACAATATATATATATATATATATATATATATAT 2621
1303 GCAATGATGCTCCCTCCCATCAGGACAAATTTAGATGTTTCAATCAATATTTACAGGCTG 1362
Db 2620 GCAATGATGCTCCCTCCCATCAGGACAAATTTAGATGTTTCAATCAATATTTACAGGCT 2561
1363 CTACTAAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 2560 CTACTAAACAGAGATGGTGGTAAGGACACGACGACGACGACGACGACGACGACGACGAC 2501
1420 GGAGGAGAGATATGAGGAGCAATTTGGAGAGTGAATTTATATAATATAAGTAGTAAAG 1479
Db 2500 GGAGGAGAGATATGAGGAGCAATTTGGAGAGTGAATTTATATAATATAAGTAGTAAAG 2441
1480 ATTGAACCAATAGGATAGCACCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1539
Db 2440 ATTGAACCAATAGGATAGCACCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2381
1540 AGAG 1543
Db 2380 AGAG 2377

RESULT 15
US-08-358-928-66/c
; Sequence 66, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter

APPLICANT: PFLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 6474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pSelp-gp160MN
US-08-358-928-66

Query Match 52.1%; Score 1172.4; DB 3; Length 6474;
Best Local Similarity 88.2%; Pred. No. 2.1e-280;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

QY 58 TCGGCTTCGAGATCTATGCTCCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117
DB 3877 TGGGATGGGCACGATGCTCCTGGGTTATTAATGATCTGTAGTGCTACAGAAAAATTG 3818

QY 118 TGGGTCAGTCTATTATGGGTACTGTGGAGAGCAACACCACTCTATTTTGT 177
DB 3817 TGGGTCAGTCTATTATGGGTACTGTGTGGAAAGCAACCACTCTATTTTGT 3758

QY 178 GCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGT 237
DB 3757 GCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 3698

QY 238 GTACCCACAGCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
DB 3697 GTACCCACAGCCCAACCCACAGAGTAGTATTGGTAAATGTGACAGAAAAATTTAAC 3638

QY 298 ATGTGCAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
DB 3637 ATGTGCAAAATAACATGTTAGATGATGAGGATATAATCAGTTTATGGGATGAA 3578

QY 358 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTGTACTTTAAATGCACTAATTG 417

DB 3577 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTGTACTTTAAATGCACTAATTG 3518
QY 418 -----AATATCAGTAAGATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
DB 3517 AGGAATACTACTAATACCAATAATAGTACTCTCTAATAACAATAGTAATAGCGAGGAACA 3458
QY 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAAGCATAGAATAAG 525
DB 3457 ATAAAGGAGGAGAAATCAAAAACTGCTCTTTCAATATCACCACAAAGCATAGAATAAG 3398
QY 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAAT 585
DB 3397 ATGCAGAAAGAAATATGCACCTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATACTAAT 3341
QY 586 AATACTAAGTATAGTTAATAGTTTAAACACCTCAGTCACTTACACGCGCTGTCCAAG 645
DB 3340 AGTACCAGCTATAGTTGATAGTTGTAATACCTCAGTCACTTACACAGCTTGTCCAAG 3281
QY 646 GTATCCTTTTACGCCAATTCCTCATACATTTATGTGTCCCGGCTGGGTTTGCATGCTAAAG 705
DB 3280 ATATCCTTTGAGCCAAATTCCTCATACATTTTGTGCCCCGGCTGGTTTGCATGCTTAAA 3221
QY 706 TGTAAACAATAAGACATTCOAATGGATCAGGACATGCAACAATGTGAGCAGCAGTACAATGT 765
DB 3220 TGTAAACGATAAAAAAGTTCAAGTGGAAAAAGGATCATGTAAAAATGTGAGCAGCAGTACAATGT 3161
QY 766 ACACATGGAATTAGGCCAGTGGTGTCACTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 825
DB 3160 ACACATGGAATTAGGCCAGTGGTGTCACTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 3101
QY 826 GAAGACATAGTAATTTAGATCTGAAAAATTTTCACAGACATGCTTAAACCATTAATAGTACAG 885
DB 3100 GAAGAGGTAGTAATTTAGATCTGAGAAATTTTCACTGATATGCTTAAACCATCATAGTACAT 3041
QY 886 CTAATGAATCTGTAGTAATTTAATTTGTAACAAGACCCAAACAATACAAAGAAAGGTTA 945
DB 3040 CTGAATGAATCTGTACAAATTTAATTTGTACAAGACCCAACTACAAATAAAAGAAAAAGGATA 2981
QY 946 TCTATAGGACCGAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 1005
DB 2980 CATATAGGACCGAGGAGAGCATTTTATGCAACAAAAATAATATAGGAACTATAAGACAA 2921
QY 1006 GCACATTTGTAACATTAGTAGGCAAAAATGGAATTAACACTTTTCAACAGATAGTTTAAAA 1065
DB 2920 GCACATTTGTAACATTAGTAGGCAAAAATGGAATGACACTTTTAAAGACAGATAGTTAGCAA 2861
QY 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAAATCAATCTCAGGAGGGAGCCCA 1125
DB 2860 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAAATCAATCTCAGGAGGGAGCCCA 2801
QY 1126 GAAATTTGTAATGCAAGTTTAAATTTGTGGAGGGGAATTTCTTCTACTGTAAATACACACAA 1185
DB 2800 GAAATTTGTAATGCAAGTTTAAATTTGTGGAGGGGAATTTTCTCTGTAAATACATACCA 2741
QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTTGGAGGACAAATGGCACTTGAAGGAAATGAC 1242
DB 2740 CTGTTTAAATAGTACTTGGAAATGTTTAAATTTGTAATTAATTAATTAATTAATTAATTA 2681
QY 1243 AATAATCACTCCAAATGAGATAAAAAACAATTAATAATATGTCGAGAGAGTAGAGAAA 1302
DB 2680 AATAATCACTCCAAATGAGATAAAAAACAATTAATAATTAATAATTAATAATTAATAATTA 2621
QY 1303 GCAATGATGCCCTCCCATCAGGACAAATTTAGATGTTTCAATCAAAATTTATACAGGGCTG 1362
DB 2620 GCAATGATGCCCTCCCATCAGGACAAATTTAGATGTTTCAATCAAAATTTATACAGGGCTG 2561
QY 1363 CTATCAACAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
DB 2560 CTATCAACAAGAGATGGTGGTAAAGGACACGGACACGACACCGAGATCTTCAGACCT 2501
QY 1420 GGAGAGGAGATATGAGGACAAATTTGGGAGAGTGAATTTATATAATATAAAGTAGTAGA 1479
DB 2500 GGAGAGGAGATATGAGGACAAATTTGGGAGAGTGAATTTATATAATATAAAGTAGTAGA 2441

Qy 1480 ATTGAACCAATAGGAGTAGCACCACCGGCGAAAGAGAGAACAGTGCACAAAGAGAAAA 1539
Db 2440 ATTGAACCAATAGGAGTAGCACCACCGGCGAAAGAGAGAACAGTGCACAAAGAGAAAA 2381
Qy 1540 AGAG 1543
Db 2380 AGAG 2377

Search completed: November 12, 2004, 12:57:30
Job time : 137.632 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 07:54:46 ; Search time 783.268 Seconds
(without alignments)
15528.563 Million cell updates/sec

Title: US-09-687-864A-12
Perfect score: 2252
Sequence: 1 aagcttgcgcacgtctgta.....ctcgagtataatagata 2252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCT05_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1222.2	54.3	9540	17	US-10-325-468-46
2	1198	53.2	2612	15	US-10-414-692-20
3	1197	53.2	1512	9	US-09-759-841-3
4	1179.8	52.4	1422	18	US-10-728-195-7
5	1172.6	52.1	3807	15	US-10-441-788-78
6	1172.4	52.1	2571	9	US-09-999-183-3
7	1172.4	52.1	2571	13	US-10-077-294-3
8	1172.4	52.1	2571	13	US-10-163-886-3
9	1172.4	52.1	2571	14	US-10-263-127-3
10	1172.4	52.1	2571	15	US-10-375-777-3
11	1172.4	52.1	2571	16	US-10-351-938-3
12	1171.8	52.0	2552	10	US-09-966-931-27

13	1171.8	52.0	2552	17	US-10-459-121-27
14	1168.6	51.9	2573	10	US-09-966-931-29
15	1168.6	51.9	2573	17	US-10-459-121-29
16	1166.6	51.8	9715	17	US-10-325-468-44
17	1165.6	51.8	9706	17	US-10-325-468-45
18	1165.4	51.7	9704	17	US-10-325-468-40
19	1165.4	51.7	9942	17	US-10-325-468-5
20	1165.4	51.7	9942	17	US-10-325-468-54
21	1164.4	51.7	2627	15	US-10-177-390-9
22	1162.2	51.6	9737	10	US-09-827-688-12
23	1162.2	51.6	9942	17	US-10-325-468-1
24	1162.2	51.6	9942	17	US-10-325-468-2
25	1162.2	51.6	9942	17	US-10-325-468-7
26	1162.2	51.6	9942	17	US-10-325-468-50
27	1162.2	51.6	9942	17	US-10-325-468-51
28	1162.2	51.6	9942	17	US-10-325-468-56
29	1162	51.6	1932	15	US-10-387-336-31
30	1162	51.6	2457	15	US-10-387-336-32
31	1161	51.6	1419	15	US-10-387-336-30
32	1160.8	51.5	1929	14	US-10-032-162-12
33	1160.6	51.5	9942	17	US-10-325-468-3
34	1160.6	51.5	9942	17	US-10-325-468-52
35	1160.4	51.5	2570	10	US-09-966-931-31
36	1160.4	51.5	2570	17	US-10-459-121-31
37	1159	51.5	9942	17	US-10-325-468-6
38	1158.9	51.5	9942	17	US-10-325-468-55
39	1158.4	51.4	1530	15	US-10-361-849-13
40	1150.6	51.1	2214	15	US-10-336-566-85
41	1150.6	51.1	9505	15	US-10-336-566-9
42	1150.6	51.1	9506	15	US-10-336-566-8
43	1150.6	51.1	9544	9	US-09-798-675-4
44	1150.6	51.1	9544	15	US-10-336-566-7
45	1150.6	51.1	9545	17	US-10-093-953A-4

ALIGNMENTS

RESULT 1
US-10-325-468-46
; Sequence 46, Application US/10325468
; Publication No. US20040101823A1
; GENERAL INFORMATION:
; APPLICANT: Soong, Nay Wei
; APPLICANT: Pekrun, Katja
; APPLICANT: Shibata, Riri
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; FILE REFERENCE: 0166.210US
; CURRENT APPLICATION NUMBER: US/10/325.468
; CURRENT FILING DATE: 2002-12-19
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 9540
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
; FEATURE:
; OTHER INFORMATION: parent JRCSP DNA (GenBank Accession No. M38429)
US-10-325-468-46

Query Match 54.3%; Score 1222.2; DB 17; Length 9540;
Best Local Similarity 90.3%; Pred. No. 1.3e-275;
Matches 1334; Conservative 0; Mismatches 125; Indels 15; Gaps 2;
Qy 74 TGCTCCCTGGGATATTGATGATCTGTAGTCACAGAAAATTTGGGTACAGTCTATT 133
Db 6291 TGCTCCCTGGGACATTATGATCTGTAGTCGTAGAAAAGTTGGGTACAGTCTATT 6350
Qy 134 ATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGGCATCAGATGCTAAAG 193

Db 6351 ATGGGGTACCTGTGTGGAAAGAAACAAACCACTCTATTTTGTGTCATCAGATGCTAAAG 6410
Qy 194 CCTATGATACAGAGGTACATTAATGTTTGGGCCACACATGCTCTGTGTACCCACAGACCCCA 253
Db 6411 CATATGATACAGAGGTACATTAATGTTTGGGCCACACATGCTCTGTGTACCCACAGACCCCA 6470
Qy 254 ACCACAGAAGTAGTATTGGGAATGACAGAAAATTTTAAACATGTGGAAAATAACA 313
Db 6471 ACCCAAGAAGTAGTATTGGGAATGTAACAGAAGATTTTAAACATGTGGAAAATAACA 6530
Qy 314 TGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATCAAAAGCCTAAAGCCATGTG 373
Db 6531 TGGTAGACAGATGACAGAGGATGTAATCAATTTATGGGATCAAAAGCTTAAAGCCATGTG 6590
Qy 374 TAAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTTGAAATATCACTAAGAATA 433
Db 6591 TAAATTAACCCCACTCTGTGTACTTTAAATTTGCAAGATGT-----GAATG 6638
Qy 434 CTACTTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATAAAATTTGCT 493
Db 6639 CTACTTAATACCACCTAGTAGTAGTGAGGGAATGATGGAGAGAGGAGAAATAAAATTTGCT 6698
Qy 494 CTTTCTATATCACCACAAGCATTAAGAAATAAGGTAAGAAAGAAATATGCACCTTTTAAATA 553
Db 6699 CTTTCAATATCACCAAAAGCATAGAGATAGGTGCAGAAAGATATGCTCTTTTATA 6758
Qy 554 GACTTGATGTAGTACCAATAGAAAATACTAATACTAAGTATAGGTTAATAAGTTGTA 613
Db 6759 AACTGGATGTAGTACCAATAGATAATAAGAAATAATACCATAATATAGGTTAATAAGTTGTA 6818
Qy 614 ACACCTCAGTCATTAACACAGCCTCTCCAAAGGTATCTTTTCAGCCAAATCCCATACATT 673
Db 6819 ACACCTCAGTCATTAACACAGCCTCTCCAAAGGTATCTTTTCAGCCAAATCCCATACATT 6878
Qy 674 ATTGTGTCGGGCTGGGTTTGGATGCTAAAGTGTAACAATAAGACATTTCAATGATCAG 733
Db 6879 ATTGTGCCCCGGCTGGTTTGGATCTTAAAGTGTAATAATAGACATTTCAATGGAAG 6938
Qy 734 GACCATGCACAAATGTCAGCAGCAGTACAAATGTACACATGGAAATTAGGCCAGTGGTGCA 793
Db 6939 GACAATGTAAAAATGTCAGCAGCAGTACAAATGTACACATGGAAATTAGGCCAGTATGATCAA 6998
Qy 794 CTCACCTGCTGTTAAATGGCAGCTAGCAGAGAGACATAGTAATTAGATCTGAAATTT 853
Db 6999 CTCACCTGCTGTTAAATGGCAGCTAGCAGAGAGAAAGGTTGTAATTAGATCTGCAATTT 7059
Qy 854 TCACAGACAAATGCTAAAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTTATGTA 913
Db 7059 TTACGGACAAATGCTAAACCAATAATAGTACAGCTGAATGAATCTGTAAATAATTAATTGTA 7118
Qy 914 CAAGACCCAAACAAATACAGAAGAGGTTATCTATAGGACCGAGGAGAGCATTTTATG 973
Db 7119 CAAGGCCAGCAACAATAACAGAAAAGTATACATATAGGACCGAGGAGAGCATTTTATA 7178
Qy 974 CAAGAGAAACATAATAGGAGATATAAGCAGACATTTGTAACATTTAGTAGACAAAT 1033
Db 7179 CAACAGGAGAAATAATAGGAGATATAAGCAAGCAGCATTTGTAACATTTAGTAGACAAAT 7238
Qy 1034 GGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAATTTTAGGATATAAACAA 1093
Db 7239 GGAATAACACTTTTAAAACAGATAGTTGAAAATTAAGAGAACAAATTTAATAATAAACAA 7298
Qy 1094 TAGCCTTTAATCAATCTCAGAGGGGCCAGAAATTTGTAATGCACAGTTTAAATTGTG 1153
Db 7299 TAGCTTTTACTCACTCCTCAGAGGGGATCCAGAAATTTGTAATGCACAGTTTAAATTGTG 7358
Qy 1154 GAGGGGAATTTCTTACTGTAATACAGCACTGTTTAAATAGTACTTGGGAATTTACTG 1213
Db 7359 GAGGGGAATTTTCTTACTGTAATCAACACAACTGTTTAAATAGTACTTGGGAATTTACTG 7418
Qy 1214 GAGGGACAAATGGCACTGAAGGAATGACATTAATCACACTCCCACTGAGAAATAAACAAA 1273
Db 7419 AAAAGTCAAGTGGCACTGAAGGAATGACACCATCATCTCCCATGAGAAATAAACAAA 7478

Qy 1274 TTATAAATATGTGCGAAGAGTAGGAAAGCAATGTATGCCCTCCCATCACAGACAAA 1333
Db 7479 TTATAAATATGTGCGAAGAGTAGGAAAGCAATGTATGCCCTCCCATTAAGAGACAAA 7538
Qy 1334 TTAGATGTTCAATCAATATTTACAGGGCTGCTACTAAACAAGAGATGGAGGTAAATAGTACTG 1393
Db 7539 TTAGATGTTCAATCAATATTTACAGGGCTGCTATTAAACAAGAGATGGTGGTAA---AAATG 7595
Qy 1394 AGACTGAGACTGAGATCTTCAGACTGAGAGAGAGATATGAGGACAAATTTGGAGAAGTG 1453
Db 7596 AGAGTGAGATCGAGATCTTCAGACTGAGAGAGAGACATGAGGACAAATTTGGAGAAGTG 7655
Qy 1454 AATTATATAAATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCCAGGGCAA 1513
Db 7656 AATTATATAAATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCCAGGGCAA 7715
Qy 1514 AGAGAAGAACAGTGCAAAGAGAAAAAGAGGGGGAGG 1550
Db 7716 AGAGAAGAGTGTGCNAAAGAGAAAAAGAGCAGTGGG 7752

RESULT 2
US-10-414-692-20
; Sequence 20, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-ceptor Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; TITLE OF INVENTION: profile
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2612
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-414-692-20

Query Match 53.2%; Score 1198; DB 15; Length 2612;
Best Local Similarity 90.6%; Pred. No. 3.4e-270;
Matches 1341; Conservative 0; Mismatches 115; Indels 24; Gaps 5;

Qy 74 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAAATTTGGGTTCAGGTCTATT 133
Db 450 TGCTCCTTGGGATATTGATGATCTGTAGTGTCTAGAAAAAGTTGGGTTCAGGTCTATT 509
Qy 134 ATGGGGTACCTGTGTGGAGAGAACACCACTCTATTATTTTGTGCATCAGATGCTAAAG 193
Db 510 ATGGGGTACCTGTGTGGAAAGAACACCACTCTATTATTTTGTGCATCAGATGCTAAAG 569
Qy 194 CCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTATCCACAGACCCCA 253
Db 570 CATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTATCCACAGACCCCA 629
Qy 254 ACCCAAGAAAGTAGTATTGGGAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 313
Db 630 ACCCAAGAAAGTAGTATTGGGAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 689
Qy 314 TGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCATGTG 373
Db 690 TGGTAGAACAGATGACAGGAGGATATAATCAGTTTATGGGATCAAAAGCCCTAAAGCCATGTG 749
Qy 374 TAAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTTGAATATCACTAAGAATA 433
Db 750 TAAATTAACCCCACTCTGTGTACTTTAAATTTGCAAGATGT-----GAATG 797
Qy 434 CTACTTAATCCCACTAGTAGCAGCTGGGAATGATGAGAAAGGAGAAATAAAATTTGCT 493


```
|||||
638 TACATTATGCCCCGCTGGTTTGGCATCTTAAAGTGTAAAGTAAAGTTCATG 697
QY
728 GATCAGGACCATGCAAAATGTACAGCAGTACAAATGTACATGTAAGAAATAGGCCAGTGG 787
Db
698 GAAAGGACCATGTTCAAATGTACAGCAGTACAAATGTACATGTAAGAAATAGGCCAGTGG 757
QY
788 TGTCAACTCAACTGCTGTTAAATGSCAGTCTAGCAGAAAGAGACATAGTAATTAGATCTG 847
Db
758 TATCAACTCAACTGCTGTTAAATGSCAGTCTAGCAGAAAGAGAGTATTAATTAGATCCG 817
QY
848 AAAATTTTCCACAGACAATGCTAAACCAATAATAGTACAGTAAATGAAATCTGTAGTAATTA 907
Db
818 AAAATTTCCGGGCAATGCTAAACCAATAATAGTACAGTAAATGAAATCTGTAGTAATTA 877
QY
908 ATTGTACAAGACCCCAACAATAACAGAAAGAGTTATCTATAGGACCCAGGAGAGCAT 967
Db
878 ATTGTACAAGACCCCAACAATAACAGAAAGAGTTATCATATAGGACCCAGGAGAGCAT 937
QY
968 TTTATGCAAGAAACAATAATAGGAGATATAAGCAAGCAATGTTAAACATTTAGTAGAG 1027
Db
938 TATATACAAGAGGAGAAATAATAGGAGATATAAGCAAGCAATGTTAAACCTTTAGTAGAG 997
QY
1028 CAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAATA 1087
Db
998 CAAAATGGAATGACACTTTTAAATAGATAGTTATTAATAATTAAGAGAAACAATTTGGGAATA 1057
QY
1088 AAACAATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGAATGACAGTTTTTA 1147
Db
1058 AAACAATAGTCTTTAAGCATTCCTCAGAGGGGACCCAGAAATTTGACGACACAGTTTTTA 1117
QY
1148 ATTGTGGAGGGAAATCTTCTACTGTAATACAGCAACACTGTTTAATAGTACTTGGAAATG 1207
Db
1118 ATTGTGGAGGGAAATTTTCTACTGTAATTAACCAACACTGTTTAATAGTACTTGGAAATG 1177
QY
1208 TTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACACTCCCAATGCAGAAATA 1267
Db
1178 TTACTGAAGAGTCAAAATTAACACTGTGAATAATTAACATAATCACTCCCATGCAGAAATA 1237
QY
1268 AACAAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1327
Db
1238 AACAAATTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1297
QY
1328 GACAAATTAGATGTTTCATCAATATATACAGGCTGCTACTAACAGAGATGGAGGTAATA 1387
Db
1298 GACAAATTAGATGTTTCATCAATATATACAGGCTGCTATTAAACAAGAGATGGTGTCCCG 1357
QY
1388 GTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGAGCAATTTGA 1447
Db
1358 AGGCCAACA--AGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGAGCAATTTGA 1414
QY
1448 GAAGTGAATTAATAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCA 1507
Db
1415 GAAGTGAATTAATAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCA 1474
QY
1508 GGGCAAGAGAGACAGTGCACAGAGAAAAAGA 1542
Db
1475 AGGCCAAGAGAGAGTGGTGCAGAGAGAAAAAGA 1509
```

```
RESULT 4
US-10-728-195-7
; Sequence 7, Application US/10728195
; Publication No. US20040191269A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Shan
; APPLICANT: Pal, Ranajit
; APPLICANT: Kalyanaraman, V.S.
; APPLICANT: Whitney, Stephen Charles
; APPLICANT: Keen, Tim
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS
; FILE REFERENCE: 07917-269001
```

```
; CURRENT APPLICATION NUMBER: US/10728,195
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/430, 732
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-728-195-7

Query Match      52.4%; Score 1179.8; DB 18; Length 1422;
Best Local Similarity 90.4%; Pred. No. 4.8e-266;
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

QY 115 TTGTGGGTTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTT 174
Db 1 TTGTGGGTTCACAGTCTATTATGGGTACCTGTGTGGAAAGAAAGCAACCACTCTATTT 60

QY 175 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATATGTTGGGCCACACATGCC 234
Db 61 TGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATATGTTGGGCCACACATGCC 120

QY 235 TGTGTACCCACAGACCCCAACCCCAAGAGTGTATTGGGAAATGTGACAGAAAAATTTT 294
Db 121 TGTGTACCCACAGACCCCAACCCCAAGAGTGTAGNAATTTGGAAATGTGACAGAAAAATTTT 180

QY 295 AACATGTGGAAAAATAACATCGTATGATCAGATGATGAGGATATAATCAGTTTATGGGAT 354
Db 181 AACATGTGGAAAAATAACATCGTATGATCAGATGATGAGGATATAATCAGTTTATGGGAT 240

QY 355 GAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATGCACTAAT 414
Db 241 CAAAGCCTAAAGCCATGTGTAAATTAACCTCACTCTGTGTACTTTTAAATGCACTAAT 300

QY 415 TTGA-----ATATCAGTAAAGTAACTACTAATCCCACTAGTAGCAGCTGGGGAATGATG 468
Db 301 TTGAGGAATGCTACTAATTTGGGAAATGACACTAATACCCTAGTAGTAGCAGGGAATGATG 360

QY 469 GAGAAAGGAGAAATAAAAAATTTGCTTTCTTATATACCAACAAGCATTAAGAAATAAGGTA 528
Db 361 GGGGAGGAGAAATGAAAAATTTGCTTTCTTCAAAATCACCACAAACATTAAGAGGTAAAGTG 420

QY 529 AAGAAGAAATATGACATTTTAAATAGACTTGTAGTACCAATAGAAATAACTAATAAT 588
Db 421 CAGAAGAAATATGACATTTTAAATAGACTTGTATAGTACCAATAGAAATAATAATAGTAAAT 480

QY 589 ACTAAGTATAGTTAAATAAGTTGTAACACCTCAGTCATTATACAGGCTGTCCAAAGGTA 648
Db 481 AATAGATATAGTTGATTAAGTTGTAACACCTCAGTCATTATACAGGCTGTCCAAAGGTA 540

QY 649 TCCTTTGAGCAATTTCCCATACATTTATTTGTTGTCGGCTGGGTTTGGCATGCTAAAGTGT 708
Db 541 TCCTTTGAGCAATTTCCCATACATTTATTTGTCGGCTGGGTTTGGCATGCTAAAGTGT 600

QY 709 AACATAGACATTTCAATGGATCAGGACCATGCAAAATGTGTCAGCACAGTACAATGTACA 768
Db 601 AAAGATAAGAGTTCAATGGAAAGGACCACTGTTCAAATGTGTCAGCACAGTACAATGTACA 660

QY 769 CATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAA 828
Db 661 CATGGATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAA 720

QY 829 GACATAGTAATTTAGATCTGAAAAATTTTCAAGCAATGTCTAAACCATTAATAGTACAGTGA 888
Db 721 GAGGTAGTAATTTAGATCTGAAAAATTTTCCGGGACAAATGTCTAAACCATTAATAGTACAGTGA 780

QY 889 AATGAATCTGTAGTAATTTAATTTGTCACAGACCCCAACCAATACAGAGAGAGGTTATCT 948
Db 781 AATGAATCTGTAGTAATTTAATTTGTCACAGACCCCAACCAATACAGAGAGAGGTTATCT 840

QY 949 ATAGGACCCGAGAGAGCATTTTATGCAAGAGAGAAACATAATAGGAGATATAAGACAAGCA 1008
```

```
Db      841 ATAGCACCAGGAGGAGCATTATATACACAGGAGAAATAATAGGAGATATATAGCAAGCA 900
Qy      1009 CATTGTAACATTAGTAGAGCAAAATGGAAATACACTTTTACAACAGATAGTTATAAAATTA 1068
Db      901 CATTGTAACCTTAGTAGAGCAAAATGGAAATGACACTTTTAAATAGATAGTTATAAAATTA 960
Qy      1069 AGAGAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCTCAGGAGGGAGCCAGAA 1128
Db      961 AGAGAAACAATTTGGGAATAAAACAATAGTCTTTAAGCATTCTCAGGAGGGAGCCAGAA 1020
Qy      1129 ATTGTAATGCCACAGCTTTTAATTTGGAGGGGAATCTTCTACTGTAAATACAGCAAACTG 1188
Db      1021 ATTGTAGCGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAAATCAACACAACTG 1080
Qy      1189 TTTAATAGTACTTGGAAATGTTACTCGAGGGGACAAAATGGCACTGGAAGGAAATGACATAATC 1248
Db      1081 TTTAATAGTACTTGGAAATGTTACTGAGNGTCAATATACACTGTAGAAAATTAACCAATC 1140
Qy      1249 ACATCCCAATGAGAAATAAAACAATTAATATATGTGGCAGAAAAGTAGGAAAAGCAATG 1308
Db      1141 ACATCCCAATGAGAAATAAAACAATTAATATATGTGGCAGAAAAGTAGGAAAAGCAATG 1200
Qy      1309 TATGCCCTCCCATCACAGGACAAATTTAGATGTTTCAATCAATATTACAGGGCTGCTACTA 1368
Db      1201 TATGCCCTCCCATCAGAGGACAAATTTAGATGTTTCAATCAATATTACAGGGCTGCTACTA 1260
Qy      1369 ACAAGAGATGGAGGTAATAGTACTCGAGCTGAGACTGAGACTCTTCAGACCTCGAGGAGGA 1428
Db      1261 ACNAGAGATGGTGGTCCAGAGCAAAACA---AGACCGAGGTCTTCAGACCTCGAGGAGGA 1317
Qy      1429 GATATGAGGGCAATTTGGAGAGTAGTGAATTTATATAAATATAAAGTAGTAGTAAGAAATGAACCA 1488
Db      1318 GATATGAGGGCAATTTGGAGAGTAGTGAATTTATATAAATATAAAGTAGTAGTAAGAAATGAACCA 1377
Qy      1489 ATAGAGTAGCACCCACCGGSCAAAGAGAGAACAGTGCA 1529
Db      1378 TTAGAGTAGCACCCACCGGSCAAAGAGAGAGTAGTGGTGA 1418
```

RESULT 5

```
US-10-441-788-78/c
; Sequence 78, Application US/10441788
; Publication No. US2003023987A1
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paolietti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/10/441,788
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/136,159A
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-10-441-788-78
```

```
Query Match      52.1%; Score 1172.6; DB 15; Length 3807;
Best Local Similarity 88.1%; Pred. No. 3.7e-264;
Matches 1329; Conservative 0; Mismatches 159; Indels 21; Gaps 4;

Qy      52 TGGATCTCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTCTCAGAA 111
Db      1668 TGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTCTCAGAA 1609
Qy      112 AAATTGTGGGTACACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACACCACTCTA 171
Db      1608 AAATTGTGGGTACACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACACCACTCTA 1549
Qy      172 TTTTGTGATCAGATGCTTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db      1548 TTTTGTGATCAGATGCTTAAAGCATAATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489
Qy      232 GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db      1488 GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGTAAATGTGACAGAAAT 1429
Qy      292 TTTTAACTGTGGAAAATAAATGATGATCAGATGATGAGGATATATCAATGTTTATGG 351
Db      1428 TTTTAACTGTGGAAAATAAATGATGATGAGGATATATCAATGTTTATGG 1369
Qy      352 GATGAAAGCCCTAAAGCCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACT 411
Db      1368 GATCAAGCCCTAAAGCCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACT 1309
Qy      412 AATTGT-----AATATCTAAGAAATCTACTAATCTCCACCTAGTAGAGCTGG 459
Db      1308 GATTTGAGGAATACTACTAATCAATTAATAGTACTGCTAATAACAATAGTAAATAGCGAG 1249
Qy      460 GGAATGATGGAGAGGAGAAATAAATAATTTGCTCTTTCTATATCACCACAGCATAGA 519
Db      1248 GGAACAATAAGGGAGGAGAAATGAAAACCTGCTCTTTCAATATATCACCACAGCATAGA 1189
Qy      520 AATAAGGTAAAGAGAAATATGCACCTTTTAAATAGACTTGTATGTAGTAGTACCAATAGAAAT 579
Db      1188 GATAAGATGCAGAGAAATATGCACCTCTTCTTATAAACTTGTATATAGTATCAAT---AAAT 1132
Qy      580 ACTAATAATCTAGTATAGTTAATAGTTTAAAGTTGTAAACACTCAGTCACTTACACAGGCTGT 639
Db      1131 AATGATAGTACGAGCTATAGTTGATAAGTTGTAAATAGTCTCAGTCACTTACACAGGCTGT 1072
Qy      640 CCAAGGTATCTTTTCAGCCCAATTTCCCATACATATTGTTGTCCTCCCGCTGGGTTTCGGATG 699
Db      1071 CCAAGATATCTTTTGAGCCCAATTTCCCATACATATTGTTGTCCTCCCGCTGGGTTTCGGATG 1012
Qy      700 CTAAGTGTAAACAATAAGACATTTCAATGGATCAGGACCATGCAACAATGTCTCAGACAGTA 759
Db      1011 CTAAGTGTACGATATAAAGTTCAAGTGGAAAAGATCATGTAAATAATGTCTCAGACAGTA 952
Qy      760 CAATGTACATGGAATTTAGGCCAGTGTGTCAACTCAACTGCTTTTAAATGGCAGTCTA 819
Db      951 CAATGTACATGGAATTTAGGCCAGTGTGTCAACTCAACTGCTTTTAAATGGCAGTCTA 892
Qy      820 GCAGAGAGACATAGTAATTTAGATCTGAAAATTTTCACAGCAATGCTTAAACCATATA 879
Db      891 GCAGAGAGAGGAGTAGTAATTTAGATCTGAGAAATTTCAATGATTAATGCTTAAACCATATA 832
Qy      880 GTACAGCTTAAATGATCTGTAGTAATTAATTTGTACAAGACCCCAACAATAACAAGAGA 939
Db      831 GTACATCTGAATGAATCTGTCAAAATTAATTTGTACAAGACCCCACTCAATAAAGAGAAA 772
Qy      940 AGGTTATCTATAGGACCGAGGAGAGCATTTTATATGCAAGAGAAACATAATATAGGAGATATA 999
```


QY 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCTCAGGAGGGACCCA 1116
QY 1126 GAAATTGTAATGACAGATTTTAAATGTCGAGGGGAATTTCTCTACTGTAAATACAGCACAA 1185
Db 1117 GAAATTGTAATGACAGATTTTAAATGTCGAGGGGAATTTTCTCTACTGTAAATACATCACA 1176
QY 1186 CTGTTTAATAGTACTTGAATG---TTACTGGAGGACAAAATGGCACTGGAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGAATGTAATAATTAATCTTGAATAATTAATCTACAGGGTCAAATAAC 1236
QY 1243 ATAATCACATCCCAATGACAGATAAAACAATAATTAATATGTCGACAAAGTAGGAAAA 1302
Db 1237 AATATCACATCTCAATGCAAAATAAAACAAATTAATAACATGTGGCAGGAATGAGGAAAA 1296
QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTCAATCAAAATTAATACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAATGTTTCAATCAAAATTAATACAGGGCTA 1356
QY 1363 CTACTAACAGAGATGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACCT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGGACACGACACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGAGATATGAGGACAAATTTGGAGAAAGTGAATTAATATAATATAAGTAGTAAGA 1479
Db 1417 GGAGGAGAGATATGAGGACAAATTTGGAGAAAGTGAATTAATATAATATAAGTAGTAACA 1476
QY 1480 ATTGAACCAATAGGAGTAGTACCCACAGGACAAAGAGAGAAACAGTGCAGGAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGTACCCACAGGACAAAGAGAGAGAGAGTGTGTCAGAGAGAAAA 1536
QY 1540 AGAG 1543
Db 1537 AGAG 1540

RESULT 8

US-10-163-886-3
; Sequence 3, Application US/10163886
; Publication No. US20020187129A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020187129A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-163-886-3

Query Match 52.1%; Score 1172.4; DB 13; Length 2571;
Best Local Similarity 88.2%; Pred. No. 3.4e-264;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;
QY 58 TCGGCTTCGAGATCTATGCTCTCTGGGATATTTGATGATCTGTAGTGTCTACAGAAAAATTTG 117
Db 40 TGGGGATGGGCGAGATGCTCTCTGGGTTATTAATGATCTGTAGTGTCTACAGAAAAATTTG 99
QY 118 TGGGTTCAGTCTATTATGGGCTACCTGTGGGAGAGCAACCCACACCTCTATTTTGT 177
Db 100 TGGGTTCAGTCTATTATGGGCTACCTGTGGGAGAGCAACCCACACCTCTATTTTGT 159
QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 219
QY 238 GTACCCACAGACCCCAACCCCAAGAGTAGAATTTGGTAAATGTGACAGAAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGAATTTGGTAAATGTGACAGAAAAATTTTAAAC 279
QY 298 ATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 339
QY 358 AGCCTAAAGCCATGTGTAAAAATTTAACCCCACTCTGTGTCTTCTTTAAATTTGCACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAAAATTTAACCCCACTCTGTGTCTTCTTTAAATTTGCACTAATTG 399
QY 418 -----AATATCACTAAGATATCTACTAATCCACTAGTAGAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTAGTCTGTATAAACAATAGTAATAGCGAGGAACA 459
QY 466 ATGAGAGAGAGAGAAATAAAAAATTTGCTTTCTATATCACCAAGAGATAGAAATTAAG 525
Db 460 ATAAAGGAGAGAGAAATGAAAAAATGCTCTTTCAATATCACCAAGGATAGAGATAAG 519
QY 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTATGATGATGATGATGATGATGATGAT 585
Db 520 ATGAGAGAGAGAAATATGCACTTTTAAATAGACTTGTATGATGATGATGATGATGATGATGAT 576
QY 586 AATACTAGTATAGTTTAAATAGTTTAAACCTCAGTCACTTATACAGAGCTGTCCCAAG 645
Db 577 AGTACCAGCTATAGTTTAAATAGTTTAAACCTCAGTCACTTATACAGAGCTGTCCCAAG 636
QY 646 GTATCTTTTACGCCAATTTCCCATACATATTGTGTCGCCGCTGGGTTTGCAGTGTAAAG 705
Db 637 ATATCTTTTACGCCAATTTCCCATACATATTGTGTCGCCGCTGGGTTTGCAGTGTCTAAA 696
QY 706 TGTAAACAATAAGACATTCATAGGATCAGGACCATGCAAAATGTGAGCAAGTACATGTT 765
Db 697 TGTAAACAATAAGATTCATAGGATCAGTGGAAAAAGGATCATGTAAAAATGTGAGCAAGTACATGTT 756
QY 766 ACATATGGAATTTAGCCAGTGTGTCAACTCACTGCTTTAAATGGGAGTCTACAGAA 825
Db 757 ACATATGGAATTTAGCCAGTGTGTCAACTCACTGCTTTAAATGGGAGTCTACAGAA 816
QY 826 GAAGACATAGTAAATTTAGATCTGAAAAATTTACAGACAATGCTTAAACCAATATAGTACAG 885
Db 817 GAAGAGGTAGTAAATTTAGATCTGAGAAATTTCACTGATATGCTTAAACCAATATAGTACAT 876
QY 886 CTAAATGAATCTGTAGTAAATTTGTTACAGACCCCAACAATATACAGAGAGAGGTTA 945

```
Db 877 CTGAATGAATCTGTACAAATTAATTGTACAGACCACCTACATAAAGAAAAGGATA 936
Qy 946 TCTATAGGACCGGAGAGCAATTTATGCAAGAGAAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCGGAGAGCAATTTATACAAACAAAATAATATAGGAACATATAAGACAA 996
Qy 1006 GCACATTGTAACATTAGTAGACAAAATGGAATAACACATTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTGTAACATTAGTAGACAAAATGGAATAACACATTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAATTTAGGAATAAACAATAGCTTTAAATCAATCCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGACAATTTAAGATTAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116
Qy 1126 GAAATGTAATGCACAGTTTTTAATGTGGAGGGGAATCTTCTACTGTAATACACACAA 1185
Db 1117 GAAATGTAATGCACAGTTTTTAATGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176
Qy 1186 CTGTTTAATAGTACTTGGATG---TTACTGGAGGACAAATGGCACTGAAGGAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGGATGTAATAATCTTGGAAATAATCTACAGGGTCAATAAAC 1236
Qy 1243 ATAATCACACTCAATGCAGATAAACAATAATATAAATATCTGCGAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCAATGCAGATAAACAATAATATAAATATGCGAGGAAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATAGATGTTCATCAATATTAACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATGAAGGACAAATAGATGTTCATCAATATTAACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACT 1419
Db 1357 CTATTAAACAAGAGATGGTGTAGGACACCGACACGACACCGAGATCTTCAGACT 1416
Qy 1420 GGAGAGAGAGATATGAGGACAAATGGAGAGTGAATATATAAATAAAGTAGTAAGA 1479
Db 1417 GGAGAGAGAGATATGAGGACAAATGGAGAGTGAATATATAAATAAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCCACCGGCAAGAGAGAACAGTGCACAAAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCCACCGGCAAGAGAGAGTGGTGACAGAGAAAA 1536
Qy 1540 AGAG 1543
Db 1537 AGAG 1540
```

RESULT 9

```
US-10-263-127-3
; Sequence 3, Application US/10263127
; Publication No. US20030082145A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods
;
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/263,127
; FILING DATE: 02-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US/10/077,294
FILING DATE: 15-Feb-2002
APPLICATION NUMBER: 09/691,604
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030082145A1and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-263-127-3
Query Match 52.1%; Score 1172.4; DB 14; Length 2571;
Best Local Similarity 88.2%; Pred. No. 3.4e-264;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;
Qy 58 TGGGCTTCGAGATCTATGCTCTCTGGGATATTTGATGATCTGTGAGTCTAGTCTACAGAAAAATTG 117
Db 40 TGGGATGGGCACGATGCTCTCTGGGTTATTTAATGATCTGTAGTGTACAGAAAAATTG 99
Qy 118 TGGGTACAGATCTATTTATGGGTACTCTGTGGAGAGAGAGAACACCACTCTATTTTGT 177
Db 100 TGGGTACAGATCTATTTATGGGTACTCTGTGGAGAGAGAGAACACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTTAAAGCCTATGATACAGAGGTACATAATGTTTGGCCACACATGCTCT 237
Db 160 GCATCAGATGCTTAAAGCCTATGATACAGAGGTACATAATGTTTGGCCACACAGCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGAATTTGGTAAATGTGACAGAAAAATTAAAC 279
Qy 298 ATGTGGAAAAATACATGCTAGATCAGATGATGAGGATATATATCAGTTTATGGGATGA 357
Db 280 ATGTGGAAAAATACATGCTAGATCAGATGATGAGGATATATATCAGTTTATGGGATCA 339
Qy 358 AGCTTAAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTG 417
Db 340 AGCTTAAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTG 399
Qy 418 -----AATATCACTAAGAAATACTACTATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTATACCAATAATAGTACTGCTAATAACAATAGTAAATAGCGAGGAAACA 459
Qy 466 ATGGAGAAAGAGAAATAAAAAATTGCTCTTTCTATATACCAAGCATATAAGAAATAAG 525
Db 460 ATAAAGGGAGAGAAATGAAAAACTGCTCTTTCAATATACCAAGCATATAAGAGATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTATGATGATGATGATGATGATGATGAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTTAAATAGACTTGTATGATGATGATGATGATGATGATGAT 576
Qy 586 AATACTAAGTATAGGTTAATAAGTTTAAACACCTCAGTCATTATACAGAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTATACAGAGCTTGTCCAAAG 636
Qy 646 GTATCCTTTTACGCAATTTCCCATACATTTATGTGTGCCGGCTGGGTTTGCAGATGCTAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACATTTATGTGTGCCGGCTGGGTTTGCAGATTTCAAA 696
Qy 706 TGTAAACAATAGACATTTCAATGGATCAGGACCAATGACAAATGTGACGACAGTACAAATGT 765
Db 697 TGTAAACAATAGACATTTCAATGGATCAGGACCAATGATCAATGATGATGATGATGATGATGAT 756
```


766 ACACATGGAATTAGCCAGTGTGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
757 ACACATGGAATTAGCCAGTGTGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
826 GAAGACATAGTAATTAGATCTGAAATTTTCACAGACAATGCTAAACCATATAGTACAG 885
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
817 GAAGAGGTAGTAATTAGATCTGAGAAATTTCTGATATGCTTAAACCATCATAGTACAT 876
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
886 CTAATAGTAATCTGTAGTATTAATTGTTACAGACCCCAACAATATCAAGAGAGGTTA 945
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
877 CTGAATGAATCTGTACAAATTAATTGTACAGACCCCACTCAATATAAAGAGAGGATA 936
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
946 TCTATAGACACAGGAGAGCAATTTATGCAAGAGAACATAATAGGAGATATAGACAA 1005
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
937 CATATAGACACAGGAGAGCAATTTATATACAAACAAAATATAATAGGAACTATAGACAA 996
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1006 GCACATTTGAATAGTAGAGCAAAATGGAATAACACTTTACACAGATAGTTATAAAA 1065
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
997 GCACATTTGAATAGTAGAGCAAAATGGAATGACACTTTAAGACAGATAGTTAGCAA 1056
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCTCAGGAGGGACCCA 1125
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGTCTTTAATCAATCTCAGGAGGGACCCA 1116
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1126 GAAATTTGAATGACAGACTTTTAATTTGAGAGGGAAATCTTCTACTGTAATACAGCACA 1185
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1117 GAAATTTGAATGACAGACTTTTAATTTGAGAGGGAAATTTTCTACTGTAATACATCACA 1176
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1186 CTGTTTAATAGTACTTTGGAATG---TTACTGGAGGGACAAATGGCACTGAAGGAAATGAC 1242
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1177 CTGTTTAATAGTACTTTGGAATGTTAATTAATCTTGGAAATNATACAGGGTCAATAAC 1236
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1243 ATAATCACACTCAATGACAGATAAAACAAATTAATAATATGTCGCAAGAAAGTAGGAAA 1302
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1237 AATATCACACTCAATGACAGATAAAACAAATTAATAATATGTCGCAAGAAAGTAGGAAA 1296
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1303 GCAATGTATGCCCTCCCATCACAGACAAATAGATGTTCAATCAATTAATACAGGGCTG 1362
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1297 GCAATGTATGCCCTCCCATGGAAGGACAAATTAGATGTTCAATCAATTAATACAGGGCTA 1356
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1363 CTACTAAACAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACT 1419
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1357 CTAATTAACAGAGATGGTGTAAAGACACGGACACGACGACCGAGATCTTCAGACT 1416
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAACTGAATTAATAATAAAGTAGTAAGA 1479
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAACTGAATTAATAATAAAGTAGTAAGA 1476
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1480 ATTGAACCAATAGGATAGCACCCACCGGCAAGAGAGAACAGTGCAGAGAGAGAAA 1539
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1477 ATTGAACCAATAGGATAGCACCCACCGGCAAGAGAGAGAGTGGTGCAGAGAGAGAAA 1536
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1540 AGAG 1543
Db |||||
1537 AGAG 1540

RESULT 10

US-10-375-777-3

; Sequence 3, Application US/10375777

; Publication No. US20030147912A1

; GENERAL INFORMATION:

; APPLICANT: Johnson, Philip R.

; TITLE OF INVENTION: Adeno-Associated Virus Materials and

; Methods

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 S. Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/375,777

; FILING DATE: 26-Feb-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/10/163,886

; FILING DATE: 04-Jun-2002

; APPLICATION NUMBER: 09/292,703

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: No. US20030147912A1and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31975

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2571 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-375-777-3

Query Match 52.1%; Score 1172.4; DB 15; Length 2571;

Best Local Similarity 88.2%; Pred. No. 3.4e-264;

Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCTATCTCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117

Db 40 TGGGATGGGCGACGATGCTCTTGGGTATTATGATCTGTAGTGTCTACAGAAAAATTG 99

Qy 118 TGGGTACAGTCTATTATTTGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 177

Db 100 TGGGTACAGTCTATTATTTGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 159

Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCTGT 237

Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCTGT 219

Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAA 297

Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAA 279

Qy 298 ATGTGGAATAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 357

Db 280 ATGTGGAATAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 339

Qy 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACTAATTG 417

Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACTAATTG 399

Qy 418 -----AATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGGAATG 465

Db 400 AGGAATACTACTAATACCNAATTAATAGTACTGCTAATACAAATAGTAGCGGGGAACA 459

Qy 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCATATAGAAATAAG 525

Db 460 ATAAAGGGAGGAGAAATGAAAACTGCTCTTTCAATATCACCACAGCATATAGAGATAAG 519

Qy 526 GTAAAGAAAGATATGCACTTTTAAATAGACTGTAGTAGTACCAATACAGAAATACATAAT 585

Db 520 ATGCAGAAAGAAATATGCACCTCTCTTTATAAATTTGATATAGTATCAATAG---ATAATGAT 576


```
QY 586 AATACTAAGTATAGGTTAATAGTTGTAACACCTCAGTCATTACACAGCGCTGTCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTACACAGCTTGTCAAAG 636
QY 646 GTATCCTTTTCAGCCCAATCCCATACATATTGTGTCCCGCTGGGTTTCGGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAATCCCATACATATTGTGTCCCGCTGGGTTTCGGATGCTAAAG 696
QY 706 TGTAAACAATAGACATTCATATGATCAGGACCATGCACAAATGTCTACGACAGTACAAATGT 765
Db 697 TGTAAACGATAAAGATTCAGTGGAAAGGATCATGTAAATAATGTCTACGACAGTACAAATGT 756
QY 766 ACACATGGAATAGGCACTGTGTCAACTCACTCTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATAGGCACTGTGTCAACTCACTCTTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATAGTAATAGATCTGAAATTTTACAGACAATGCTTAAACCAATATAGTACAG 885
Db 817 GAAGAGGTAGTAATAGATCTGAGAAATTTCTGTATGCTTAAACCAATCATAGTACAT 876
QY 886 CTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATAACAAGAAAGAGTTA 945
Db 877 CTGAATGAATCTGTACAATTAATTTGTACAAGACCCCAACTACAATAAAGAAAGGATA 936
QY 946 TCTATAGGACCGGAGAGCATTTTATGCAAGAGAAACATATATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCGGAGAGCATTTTATACAACAAAATAATATATAGGAATCTATAGACAA 996
QY 1006 GCACATTTGTAACATAGTAGAGCAAAATGGAATTAACATTTTACAACAGATAGTTATAAA 1065
Db 997 GCACATTTGTAACATAGTAGAGCAAAATGGAATTAACATTTTACAACAGATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAAACAATPAGCTTTTAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAAAATTTAAGAAATAAAACAATPAGCTTTTAATCAATCTCAGGAGGGACCCA 1116
QY 1126 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTGTATATACAGACAA 1185
Db 1117 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTATATACATCACA 1176
QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGGAATTAATATCTTGGAAATPACTACAGGGTCAAAATAC 1236
QY 1243 AFAATCACACTCCAATGCAGATAAAACAATAATATAAATATATGTGGCAAGATAGGAAAA 1302
Db 1237 AATATCACACTTCAATGCAAAATAAAACAATAATATAAATATGTGGCAAGATAGGAAAA 1296
QY 1303 GCAATGTATGCCCTCCCATCAGACAAATTAGATGTTTCAATTAATATTAACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATGGAAGCAAAATTAGATGTTTCAATTAATTAACAGGGCTA 1356
QY 1363 CTACTAAACAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGGACACGGGACACGAAGACACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGAGATATAGGAGCAATTTGGAGAACTGAATTAATAAATAAATAGTACTAAGA 1479
Db 1417 GGAGGAGAGATATAGGAGCAATTTGGAGAACTGAATTAATAAATAAATAGTACTAAGA 1476
QY 1480 ATTGAACCAATAGGAGTAGACCCACCGGGCAAGAGAGAAACAGTGCAGAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGACCCACCGGGCAAGAGAGAGAGTGGTGAGAGAGAAAA 1536
QY 1540 AGAG 1543
Db 1537 AGAG 1540
```

RESULT 11

US-10-351-938-3

; Sequence 3, Application US/10351938

; Publication No. US20040009603A1

```
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/10/351,938
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US/09/552,950
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
; US-10-351-938-3
```

```
Query Match 52.1%; Score 1172.4; DB 16; Length 2571;
Best Local Similarity 88.2%; Pred. No. 3.4e-264;
Matches 1327; Conservative 0; Mismatches 156; Indels 21; Gaps 4;

QY 58 TCGGCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117
Db 40 TGGGGATGGGCGACGATGCTCCTTGGGTTATTAAATGATCTGTAGTGTCTACAGAAAAATTG 99
QY 118 TGGGTACAGTCTATTATGGGTACTCTGTGTGGAGAGAGCAACACCACTCTATTTTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACTCTGTGTGGAGAGAGCAACACCACTCTATTTTGT 159
QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTCT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTCT 219
QY 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGAATTTGGTAAATGTGACAGAAAAATTTAAC 279
QY 238 ATGTGGAAAAATAACATGGTGTAGATCAGATGCATGAGGATATATAATCAGTTTATGGGATGA 357
Db 280 ATGTGGAAAAATAACATGGTGTAGACAGATGCATGAGGATATATAATCAGTTTATGGGATCAA 339
QY 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAATTTG 417
Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAATTTG 399
QY 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTATAGCGAGGAAACA 459
QY 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTTTCTATATACCAAGCAATAAGAAATAAG 525
Db 460 ATAAAGGGAGGAGAAATGAAAAAATGCTCTTTTCAATATACCAAGCAATAAGAGATAAG 519
QY 526 GTAAGAAGAAATATGCACTTTTAAATAGACTTGTATAGCTGTATACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCACTCTTTTATAAATCTTGATATAGTATCAATAG---ATAATGAT 576
QY 586 AATACTAAGTATAGGTTAATAGTTGTAACACCTCAGTCATTACACAGSCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAGTGTATACCTCAGTCATTACACAGCTTGTCCAAAG 636
QY 646 GTATCCTTTACGCCAATTTCCCATACATATTATGTGTCCCGCTGGGTTTCGGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAATTTCCCATACACTATTGTGTGCCCGCTGGTTTTTCGGATTTCTAAAA 696
QY 706 TGTAAACAATAGACATTTCAATGGATCAGGACCATGCACAAATGTCTACGACAGTACAAATGT 765
Db 697 TGTAAACGATAAAGATTCAGTGGAAAGGATCATGTAAATAATGTCTACGACAGTACAAATGT 756
QY 766 ACACATGGAATTAGGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATAGTAATTAGATCTGAAATTTTACAGACAATGCTTAAACCAATATAGTACAG 885
```

```
Db 817 GAAGAGTAGTAATTAGATCTGAGAAATTTCTGTAATGCTAAACCATCATAGTACAT 876
Qy 886 CTAATGAATCTGTAGTAAATTAATTTGTACAGACCCAAACAATACACAGAGAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAGACCCAACTCAATATAAAGAGGATA 936
Qy 946 TCTATAGACAGGAGAGCAATTTATGCAAGAGAAACATAATAGGAGATATAGACAA 1005
Db 937 CATATAGACAGGAGAGCAATTTATACAAACAAAAATATAATAGGAACATATAGACAA 996
Qy 1006 GCACATTTCAATATTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTATATAAA 1065
Db 997 GCACATTTCAATATTAGTAGAGCAAAATGGAATGACACTTTTAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCTCAGAGGGGACCCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGTCTTTAATCAATCTCAGAGGGGACCCA 1116
Qy 1126 GAAATTTGAATGCACAGTTTAAATTTGTGGAGGGGAATTTCTTACTAGTGAATACACACAA 1185
Db 1117 GAAATTTGAATGCACAGTTTAAATTTGTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176
Qy 1186 CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGACAAAATGGCACTGGAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGGAAATGTAATTAATCTTGGAAATAACTACAGGGTCAATAAC 1236
Qy 1243 ATAATCACATCCCAATGCAGATAAAACAAATTAATAATATGTGGCAGAAAGTAGGAAAA 1302
Db 1237 AATATCACATCTCAATGCAAAATAAAACAATTAATAAACAATGTGGCAGAAAGTAGGAAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATCAAAATTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTCAATCAAAATTTACAGGGCTA 1356
Qy 1363 CTACTAAACAAGATGGAGGTAATAGTACTGA---GACTGGAGCTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGAAGACACGGACAGCAGCAGGACCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGA 1476
Qy 1480 ATTGAACCAATAGGAGTAGCACCCACGAGGCAAGAGAGAGACAGTGCBAAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGCACCCACGAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAA 1536
Qy 1540 AGAG 1543
Db 1537 AGAG 1540
```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: 2000-01-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Hallday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (Genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2552
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
;
; US-09-966-931-27
;
; Query Match 52.0%; Score 1171.8; DB 10; Length 2552;
; Best Local Similarity 89.0%; Pred. No. 4.7e-264;
; Matches 1334; Conservative 0; Mismatches 132; Indels 33; Gaps 5;
;
Qy 64 TCGAGATCTATGCTCTTGGGATATTTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTC 123
Db 46 TGGGGCACCATGCTCTCTTGGGATGTTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTC 105
Qy 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACACCACTCTTATTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACACCACTCTTATTTGTGCATCA 165
Qy 184 GATGCTAAAGCCTATGATACAGAGTACATTAATGTTTGGGCCACACATGCTGTGTACCC 243
Db 166 GATGCTAAAGCATATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTACCC 225
Qy 244 ACAGACCCCAACCCCAAGAGTACTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303
Db 226 ACAGACCCCAACCCCAAGAGTACTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 285
Qy 304 AAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGCCTTA 363
Db 286 AAAAATAACATGTTAGAGACAGATGATGAGGATATAATCAGTTTATGGGATCAAAGCTTA 345
Qy 364 AAGCCATGTGTAAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAATATC 423
Db 346 AAGCCATGTGTAAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTG----- 399
Qy 424 ACTAGAGATACCTACTAATCCCACTAGTACGCTGGGAAATGATGAGAGAGAGAGAAATA 483
Db 400 ---AAAAATGCTACTAATACCACTAGTAGCAGCTGGGAAAGATGGAGAGAGAGAAATA 456
Qy 484 AAAAAATGCTCTTTCTATATACCAACAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCA 543
Db 457 AAAAACTGCTCTTTCAATGTCAACCAAGTATAAGAGATAAGATGAAGAATGAATATGCA 516
Qy 544 CTTTTTAATAGACTTGTAGTAGTACCAATAGAGAAATACATAATAACTAAGTATAGTTA 603
Db 517 CTTTTTATAAACTTGTAGTAGTACCAATAG---ATAATGATAATACTAGCTATAGTTTG 573
Qy 604 ATAAGTTGTAAACACCTCAGTCAATACAGAGGCTGTCCAAAGGTATCCTTTTCAGGCAATT 663
Db 574 ATAAGTTGTAAACACCTCAGTCAATACAGAGGCTGTCCAAAGGTATCCTTTTCAGGCAATT 633
Qy 664 CCCATACATTTATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACATTC 723
```

Db 634 CCATACATATTTGTGCCCCGCTGTTTGGGATTTCTAAAGTAGAGATAAAAAGTTC 693
Qy 724 AATGATCAGGACCAATGTCACAAATGTCAGCACAGTACATGATGACATGGAATTAGGCCA 783
Db 694 AACGAAACAGGACCAATGTCACAAATGTCAGCACAGTACATGATGACATGGAATTAGGCCA 753
Qy 784 GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGACATAGTAATAGA 843
Db 754 GTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGAGTGTAAATAGA 813
Qy 844 TCTGAATTTTCACAGACATGCTAAACCAATTAATAGTACACCTAAATGAATCTGTAGTA 903
Db 814 TCTGCCAATTTCTCGACCAATCTAAACCAATTAATAGTACACCTAAATGAATCTGTAGAA 873
Qy 904 ATTAATTTGACAGACCCCAACCAATTAACAGAAAGGTTATCTATAGGACCAAGGAGA 963
Db 874 ATTAATTTGACAGACCCCAACCAATTAACAGAAAGGTTATCTATAGGACCAAGGAGA 933
Qy 964 GCATTTTATGCAAGAAACCAATTAATAGGAGATATAAGACAGCACTGTGTAACATTAGT 1023
Db 934 GCATTTTATGCAAGAAATTAATAGGAGATATAAGACAGCACTGTGTAACCTTAGT 993
Qy 1024 AGACAAAATGGAATAACTTTTAAACACAGATAGTTACAAAATTAAGAGAAATTTAGG 1083
Db 994 AGCAGAAAATGGAATAACTTTTAAACACAGATAGTTACAAAATTAAGAGAAATTTAGG 1050
Qy 1084 AATAAAACAAATAGCTTTTAAATCAATCTCAGGAGGGGCCAGAAATTTGTAATGCACAGT 1143
Db 1051 AATAAAACAAATAGCTTTTAAATCAATCTCAGGAGGGGCCAGAAATTTGTAATGCACAGT 1110
Qy 1144 TTTAATTTGAGGGGGAATTTCTTACTGTATATACAGCACTGTTTAAATAGTACTTGG 1203
Db 1111 TTTAATTTGAGGGGGAATTTCTTACTGTATATACAGCACTGTTTAAATAGTACTTGG 1170
Qy 1204 AATGTTACTGAGGAGCAATGGCAATGCTGAGGAATGA-----CATATACCA 1251
Db 1171 AATGTTACTGAGGAGCAATGGCAATGCTGAGGAATGCACTGGAAGAAATATACCA 1230
Qy 1252 CTCCAATGAGAAATAAACAATTTAATATGTCGAGAAAGTAGGAAAGCAATGTAT 1311
Db 1231 CTCCAATGAGAAATAAACAATTTAATATGTCGAGAAAGTAGGAAAGCAATGTAT 1290
Qy 1312 GCCCTCCCATCAGGACAAATTAGATGTTTCAATCAATATTTACAGGCTGCTACTAACA 1371
Db 1291 GCCCTCCCATCAGGACAAATTTAGATGCTCATCAATATTTACAGGCTGCTACTAACA 1350
Qy 1372 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGAT 1431
Db 1351 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGAT 1404
Qy 1432 ATGAGGACAAATGGAGAGTGAATTTATATAATATAAGTAGTAAGAAATGGAACCAATA 1491
Db 1405 ATGAGGACAAATGGAGAGTGAATTTATATAATATAAGTAGTAAGAAATGGAACCAATA 1464
Qy 1492 GGAGTAGCACCCACAGGCAAGAGAGAAACAGTGCAGAGAGAGAGAGAGAGAGAGAG 1550
Db 1465 GGAGTAGCACCCACAGGCAAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1523

RESULT 13
US-10-459-121-27
; Sequence 27, Application US/10459121
; Publication No. US20040121317A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/459,121
FILING DATE: 10-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/134,075
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/448,603
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Halliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 2552 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2552
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-459-121-27
Query Match 52.0%; Score 1171.8; DB 17; Length 2552;
Best Local Similarity 89.0%; Pred. No. 4.7e-264;
Matches 1334; Conservative 0; Mismatches 132; Indels 33; Gaps 5;
Qy 64 TCGAGATCTATGCTCCTTGGGATATTTGATGATCTGTAGTGTACAGAAAAATTTGGGTG 123
Db 46 TGGGCGACCATGCTCCTTGGGATTTGATGATCTGTAGTGTGCGAGAAAAATTTGGGTG 105
Qy 124 ACAGTCTATTATGGGTACCTGTGGAGAGAGCAACCAACCTCTATTTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGGAGAGAGCAACCAACCTCTATTTTGTGCATCA 165
Qy 184 GATGCTAAAGCTATGATACAGAGGTACATATTTTGGGCCACACATGCTGTGTACCC 243
Db 166 GATGCTAAAGCATATGATACAGAGGTACATATTTTGGGCCACACATGCTGTGTACCC 225
Qy 244 ACAGACCCCAACCCCAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTTAAACATGG 303
Db 226 ACAGACCCCAACCCCAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTTAAACATGG 285
Qy 304 AAAAATACATGTTAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
Db 286 AAAAATACATGTTAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345
Qy 364 AAGCATGTGTAAATTAACCCCACTCTGTGTTTACTTTTAAATTTGACATTAATTTGAATATC 423
Db 346 AAGCATGTGTAAATTAACCCCACTCTGTGTTTACTTTTAAATTTGACATTAATTTGATTTG 399
Qy 424 ACTAAGAAATCTACTTAATCCCACTAGTAGCAGCTGGGAAATGTAGGAGAAAGGAGAAATA 483
Db 400 ---AAAAATGCTACTAATACCACCTAGTAGCAGCTGGGAAAGAGATGGAGAGAGGAGAAATA 456
Qy 484 AAAAATGCTCTTTCTATATCACCACAGCATAGAGAAATAGAGTAAGAGAGAAATATGCA 543
Db 457 AAAAATGCTCTTTCTATATCACCACAGCATAGAGAAATAGAGTAAGAGTAAGAGTAAGATGCA 516

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:05:05 ; Search time 4943.98 Seconds
(without alignments)
16598.440 Million cell updates/sec

Title: US-09-687-864A-12
Perfect score: 2252
Sequence: 1 aagcttgccgcacgtctgta.....ctcagtgataatctagata 2252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_ges1: *
9: gb_ges2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641.2	28.5	786	9	AY416061 Homo sapi
2	641.2	28.5	786	9	AY416062 Pan trogl
3	570	25.3	767	6	CD638712 AGENCOURT
4	505	22.4	806	6	CD521613 AGENCOURT
5	450.8	20.0	783	9	AY416063 Mus muscu
6	399.4	17.7	702	6	CD640741 AGENCOURT
7	395.2	17.5	690	6	CD642064 AGENCOURT
8	389	17.3	796	6	CD520208 AGENCOURT
9	286.4	12.7	571	7	CK794193 AGENCOURT
10	246.4	10.9	740	7	CK834247 AGENCOURT
11	244.4	10.9	492	2	BF599437 AGENCOURT
12	240	10.7	628	7	CK786611 AGENCOURT
13	174.8	7.5	527	8	BH886550 AGENCOURT
14	169	7.5	398	2	AW486605 AGENCOURT
15	138.2	6.1	636	7	CO702364 AGENCOURT
16	108.4	4.8	847	7	CK777858 AGENCOURT
17	85.8	3.8	1306	9	CL078566 AGENCOURT
18	84	3.7	1562	9	CL078533 AGENCOURT
19	82.4	3.7	1843	9	AG435185 AGENCOURT
20	81.4	3.6	1522	9	CL075364 AGENCOURT
21	80.4	3.6	1496	9	CL073855 AGENCOURT
22	80.2	3.6	1533	9	CL040854 AGENCOURT
23	80	3.6	1531	9	CG748014 AGENCOURT
24	79.6	3.5	997	9	CNS005TE Drosophil

25	79.6	3.5	1626	6	CF238805
26	79.4	3.5	1274	9	CL082663
27	78.8	3.5	1373	9	CG750869
28	78.8	3.5	1608	9	CL118721
29	78.6	3.5	727	5	BU294618
30	78.6	3.5	731	5	BU373331
31	78.2	3.5	1811	9	CG753732
32	77.8	3.5	1491	9	CG753221
33	77.4	3.4	1453	9	AJ591978
34	77	3.4	1459	9	CL040025
35	76.8	3.4	1288	9	CL082001
36	76.8	3.4	1292	9	AG278550
37	76.8	3.4	1757	9	CL078645
38	76.8	3.4	2030	9	CL078583
39	76.6	3.4	1104	6	CF264382
40	76.6	3.4	1506	9	CL071996
41	76.6	3.4	1654	9	CL118709
42	76.2	3.4	1154	9	AG341495
43	76.2	3.4	1280	9	AG337879
44	76.2	3.4	1528	9	CG753854
45	76	3.4	1482	9	AG332292

ALIGNMENTS

RESULT 1
AY416061
LOCUS
DEFINITION Homo sapiens TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, 786 bp DNA linear GSS 17-DEC-2003
ACCESSION
VERSION AY416061.1 GI:39772021
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
ORIGIN
Query Match
Best Local Similarity
Matches
Indels
Gaps
Qy

AY416061
Homo sapiens TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, 786 bp DNA linear GSS 17-DEC-2003
Genomic survey sequence.
AY416061.1 GI:39772021
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
(bases 1 to 786)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1..786
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>786
/gene="TNFSF5"
/locus_tag="HCM5765"

28.5%; Score 641.2; DB 9; Length 786;
99.5%; Pred. No. 1.4e-148;
0; Mismatches 3; Indels 0; Gaps 0;
TCCAAGAGGTGACAGATAGAGTAGAAGAGATCTTCATGAAGATTTCATCAT 1649
|||||

```
Db 138 TCATAGAAGGCTGGCAAGATAGATGCAAGGAATCTTCATGAAGATTTTGTATTTCAT 197
QY 1650 GAAACGATACAGAGATCCACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 1709
Db 198 GAAACGATACAGAGATCCACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 257
QY 1710 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1769
Db 258 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317
QY 1770 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 1829
Db 318 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 377
QY 1830 CATAGTCAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 1889
Db 378 CATAGTCAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 437
QY 1890 CACCATGAGCAACAACTTGGTAACTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 1949
Db 438 CACCATGAGCAACAACTTGGTAACTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 497
QY 1950 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 2009
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
QY 2010 AGCTCCATTTATAGCCAGCCTCGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 2069
Db 558 AGCTCCATTTATAGCCAGCCTCGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 617
QY 2070 CAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAACTTCACTTGGG 2129
Db 618 CAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAACTTCACTTGGG 677
QY 2130 AGGAGTATTGAATTGCAACACAGTGTTCGGTGTTCATATGACTGATCCTCAAGCCA 2189
Db 678 AGGAGTATTGAATTGCAACACAGTGTTCGGTGTTCATATGACTGATCCTCAAGCCA 737
QY 2190 AGTGAGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAACTC 2235
Db 738 AGTGAGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAACTC 783
```

```
RESULT 2
AY416062
LOCUS AY416062 786 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416062
VERSION AY416062.1 GI:39772022
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 786)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 786)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
```

```
them based on alignment.
FEATURES
source Location/Qualifiers
1..786
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>786
/gene="TNFSF5"
/locus_tag="HCM5765"
ORIGIN
Query Match 28.5%; Score 641.2; DB 9; Length 786;
Best Local Similarity 99.5%; Pred. No. 1.4e-148;
Matches 643; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1590 TCCAAGAGGTTGCAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1649
Db 138 TCATAGAAGGTTGGACAAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197
QY 1650 GAAACGATACAGAGATCCACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 1709
Db 198 GAAACGATACAGAGATCCACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 257
QY 1710 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1769
Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317
QY 1770 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 1829
Db 318 GAAAGAAAACAGCTTTGAAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 377
QY 1830 CATAGTCAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 1889
Db 378 CATAGTCAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 437
QY 1890 CACCATGAGCAACAACTTGGTAACTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 1949
Db 438 CACCATGAGCAACAACTTGGTAACTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 497
QY 1950 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 2009
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
QY 2010 AGCTCCATTTATAGCCAGCCTCGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 2069
Db 558 AGCTCCATTTATAGCCAGCCTCGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 617
QY 2070 CAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAACTTCACTTGGG 2129
Db 618 CAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAACTTCACTTGGG 677
QY 2130 AGGAGTATTGAATTGCAACACAGTGTTCGGTGTTCATATGACTGATCCTCAAGCCA 2189
Db 678 AGGAGTATTGAATTGCAACACAGTGTTCGGTGTTCATATGACTGATCCTCAAGCCA 737
QY 2190 AGTGAGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAACTC 2235
Db 738 AGTGAGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAACTC 783
RESULT 3
CD638712
LOCUS CD638712 767 bp mRNA linear EST 17-JUN-2003
DEFINITION AGENCOURT_14532410 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30416146 5', mRNA sequence.
ACCESSION CD638712
VERSION CD638712.1 GI:31804800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
```


AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 National Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM215 row: h column: 11
 High quality sequence stop: 564.
 Location/Qualifiers

FEATURES

1..767
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30416146"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctctggcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.3%; Score 570; DB 6; Length 767;
 Best Local Similarity 97.8%; Pred. No. 7.8e-131;
 Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1590 TCCAAAGAGTTGGACAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1649
 DB 27 TCATGAAGTTGGACAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 86
 QY 1650 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTCTTACTGAACGTGTGAGGA 1709
 DB 87 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTCTTACTGAACGTGTGAGGA 146
 QY 1710 GATTAAGCCAGTTTGAAGCGTTTGTGAAGATATATGTAAACAAGAGGAGACGAA 1769
 DB 147 GATTAAGCCAGTTTGAAGCGTTTGTGAAGATATATGTAAACAAGAGGAGACGAA 206
 QY 1770 GAACAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCTCAATTCGGGCACATGT 1829
 DB 207 GAAGAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCTCAATTCGGGCACATGT 266
 QY 1830 CATAAGTGGCCAGCAGTAAACAACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 1889
 DB 267 CATAAGTGGCCAGCAGTAAACAACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 326
 QY 1890 CACCATGAGCAACAATTGGTAAACCTGGAAAATCGGAAACAGCTGACCGTTAAAAGACA 1949
 DB 327 CACCATGAGCAACAATTGGTAAACCTGGAAAATCGGAAACAGCTGACCGTTAAAAGACA 386
 QY 1950 AGGACTCTATTATCTATGCGCAGTACCTTCTGTTCATCGGAAGCTTCGAGTCA 2009
 DB 387 AGGACTCTATTATCTATGCGCAGTACCTTCTGTTCATCGGAAGCTTCGAGTCA 446

QY 2010 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTTACT 2069
 DB 447 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAACTTACT 506
 QY 2070 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGGCAACAATCCATTCACTTGGG 2129
 DB 507 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGGCAACAATCCATTCACTTGGG 566
 QY 2130 AGGAGTATTGAATTCGAACACAGGTGCTTCGGTGTGTTCATGTGACTGATCCAAGCCA 2189
 DB 567 AGGAGTATTGAATTCGAACACAGGTGCTTCGGTGTGTTCATGTGACTGATCCAAGCCA 625

RESULT 4

CD521613 806 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT_14356206 NIH_MGC_191 Homo sapiens cDNA clone
 IMAGE:30413128 5', mRNA sequence.

ACCESSION CD521613
 VERSION CD521613.1 GI:31453331
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 806)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM207 row: j column: 17
 High quality sequence stop: 466.
 Location/Qualifiers

FEATURES

1..806
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30413128"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctctggcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCCATTTATGCCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 22.4%; Score 505; DB 6; Length 806;
 Best Local Similarity 96.7%; Pred. No. 1.3e-114;
 Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
 QY 1590 TCCAAAGAGTTGGACAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1649

Db 232 TCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTGTTGATTTCAT 291

QY 1650 GAAACAGTACAGAGATCAACACAGGAGAAGATCCTTATCTTCTTACTGAACCTGTGAGGA 1709

Db 292 GAAACAGTACAGAGATCAACACAGGAGAAGATCCTTATCTTCTTACTGAACCTGTGAGGA 351

QY 1710 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 1769

Db 352 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 411

QY 1770 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 1829

Db 412 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 471

QY 1830 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 1889

Db 472 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 531

QY 1890 CACCATGAGCAACACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTTAAAGACA 1949

Db 532 CACCATGAGCAACACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTTAAAGACA 591

QY 1950 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 2009

Db 592 AAGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 651

QY 2010 AGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGCGGTAGATTTCGAGAGAAATCTTACT 2069

Db 652 AGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGCGGTAGATTTCGAGAGAAATCTTACT 711

QY 2070 CAGAGTCGAAATACCCAGTTCGCGCAAAACCTT-GCGGGCAACAATCCATTCACTGG 2128

Db 712 CAGAGTCGAAATACCCAGTTCGCGCAAAACCTTGGCGGGCAACAATCCCTTTCCCTTG 771

QY 2129 GAG 2131

Db 772 GGG 774

RESULT 5
AY416063
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AY416063
Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY416063
AY416063.1 GI:39772023
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 783)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 783)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..783
/organism="Mus musculus"

gene
ORIGIN
Query Match 20.0%; Score 450.8; DB 9; Length 783;
Best Local Similarity 82.2%; Pred. No. 4.1e-101;
Matches 531; Conservative 0; Mismatches 112; Indels 3; Gaps 1;
QY 1590 TCCAAGAGGTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTGTTGATTTCAT 1649

Db 138 TCATAGAGATTGATAGGTGCGAAGAGGAAGTAAACCTTCATGAAGATTGTTGATTTCAT 197

QY 1650 GAAACAGTACAGAGATCAACACAGGAGAAGATCCTTATCTTCTTACTGAACCTGTGAGGA 1709

Db 198 AAAAAGGCTAAAGAGATGCAACAAAGGAGAAGGATCTTTATCTTCTTGGTGAACCTGTGAGGA 257

QY 1710 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 1769

Db 258 GATGAGAGGCAATTTGAAGACCTTGTCAAGATATAACGTTTAAACAAGAGA---GAA 314

QY 1770 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAATTCGCGCACATGT 1829

Db 315 ABAAGAAACAGCTTTGAAATGCAAAAAGGTGATGAGGATCCTCAAATTCGAGCACAGT 374

QY 1830 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 1889

Db 375 TGTAAGCCGAAGCCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCAAGAAAGGATATTA 434

QY 1890 CACCATGAGCAACACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTTAAAGACA 1949

Db 435 TACCATGAAAGCAACTTGGTAAATGCTTGAANAATGGGAAACAGCTGACCGTTTAAAGAGA 494

QY 1950 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 2009

Db 495 AGGACTCTATTATATCTATGCTACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCA 554

QY 2010 AGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGCGGTAGATTTCGAGAGAAATCTTACT 2069

Db 555 ACGCCATTCTATCTGTCGGCCTCTGCTGAAGCCACAGCAGTGGATCTGAGAGAAATCTTACT 614

QY 2070 CAGAGTCGAAATACCCAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACTGGG 2129

Db 615 CAAGCGGCAATACCCAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGG 674

QY 2130 AGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCGATGTTTCAATGTGACTGATCCAGGCA 2189

Db 675 CGGAGTGTTCGAATTTACAAGCTGGTGTCTGTTGTCTCAACGCTGACTGAAGCAAGCCA 734

QY 2190 AGTGAGCCATGGCAGTGGCTTCACGCTCTTGGGCTTACTCAAACTC 2235

Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780

CD640741 702 bp mRNA linear EST 17-JUN-2003
AGENCOURT 14542170 NIH MGC 191 Homo sapiens cDNA clone
IMAGE:30414715 5', mRNA sequence.
CD640741
CD640741.1 GI:31808911
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM211 row: 1 column: 20
High quality sequence stop: 571.
Location/Qualifiers

FEATURES

1. .702
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30414715"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PMc - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTAGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.7%; Score 399.4; DB 6; Length 702;
Best Local Similarity 95.9%; Pred. No. 2.7e-88;
Matches 421; Conservative 0; Mismatches 16; Indels 2; Gaps 1;
QY 1590 TCCAGAGGTTGGACAGATGAGATGAAGAGGATCTTCATGAGATTTTGTATTCAT 1649
DB 208 TCATAGAGGTTGGACAGATGAGATGAAGAGGATCTTCATGAGATTTTGTATTCAT 267
QY 1650 GAAACGATACAGATGACACACAGGAGAGATCTTATCTTACTGAACGTGAGGA 1709
DB 268 GAAACGATACAGATGACACACAGGAGAGATCTTATCTTACTGAACGTGAGGA 327
QY 1710 GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGACGAA 1769
DB 328 GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGACGAA 387
QY 1770 GAAAGAAACAGCTTTGAAGTGAAGGATGATCAGATCTCAATTCGGGACATGT 1829
DB 388 GAAAGAAACAGCTTTGAAGTGAAGGATGATCAGATCTCAATTCGGGACATGT 447
QY 1830 CATAGTGAAGGACAGGATGAAACACATCTGTGTGTACAGTGGGCTGAAAGAGGATCTA 1889
DB 448 CATAGTGAAGGACAGGATGAAACACATCTGTGTGTACAGTGGGCTGAAAGAGGATCTA 507
QY 1890 CACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAGCTGACCGTTTAAAGACA 1949
DB 508 CACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAGCTGACCGTTTAAAGACA 567
QY 1950 AGGACTCTATTATCTATGCGCAAGTCACTTCTGTTCCATCGGAGGCTTCGAGTCA 2009
DB 568 AGGACTCTATTATCTATGCGCAAGTCACTTCTGTTCCATCGGAGGCTTCGAGTCA 627
QY 2010 AGCTCCATTATAGCCAGC 2028
DB 628 --GCTCATTTATAGCCAGC 644

RESULT 7
LOCUS

CD642064 690 bp mRNA linear EST 17-JUN-2003
AGENCOURT 14538852 NIH_MGC 191 Homo sapiens cDNA clone
IMAGE:30418744 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CD642064
EST.
CD642064.1 GI:31811566
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 690)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health.. Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM222 row: d column: 17
High quality sequence stop: 536.
Location/Qualifiers

FEATURES
source

1. .690
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30418744"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PMc - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTAGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.5%; Score 395.2; DB 6; Length 690;
Best Local Similarity 99.0%; Pred. No. 2.9e-87;
Matches 397; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1590 TCCAGAGGTTGGACAGATGAGATGAAGGATCTTCATGAGATTTTGTATTCAT 1649
DB 213 TCATAGAGGTTGGACAGATGAGATGAAGGATCTTCATGAGATTTTGTATTCAT 272
QY 1650 GAAACGATACAGATGACACACAGGAGAGATCTTATCTTACTGAACGTGAGGA 1709
DB 273 GAAACGATACAGATGACACACAGGAGAGATCTTATCTTACTGAACGTGAGGA 332
QY 1710 GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGACGAA 1769
DB 333 GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGACGAA 392
QY 1770 GAAAGAAACAGCTTTGAAGTGAAGGATGATCAGATCTCAATTCGGGACATGT 1829

Db 393 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTTGGCGCACATGT 452
 QY 1830 CATAGTCAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 1889
 Db 453 CATAGTCAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 512
 QY 1890 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAAGACA 1949
 Db 513 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAAGACA 572
 QY 1950 AGGACTCTATTATATCTATGCGCCAAAGTCACCTTCTGTTCCA 1990
 Db 573 AGGACTCTATTATATCTATGCGCCAAAGTCACCTTCTGTTCCA 613

RESULT 8
 CD520208 796 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT 14355767 NIH_MGC 191 Homo sapiens cDNA clone
 DEFINITION IMAGE:30412573 5', mRNA sequence.

ACCESSION CD520208
 VERSION CD520208.1 GI:31451926
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.
 COMMENT Office of Cancer Genomics

National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDCM206 row: c column: 14
 High quality sequence stop: 541.

FEATURES
 source

1..796
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30412573"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC 191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgcctggcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.3%; Score 389; DB 6; Length 796;
 Best Local Similarity 98.3%; Pred. No. 1.1e-85;
 Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1590 TCCAAAGAGTTGGCAAGATAGAAGATCTTCATGAAGATTTTGTATTCTAT 1649
 Db 205 TCATAGAAGTTGGCAAGATAGAAGATCTTCATGAAGATTTTGTATTCTAT 264
 QY 1650 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCTCTTACTTGAAGTGTGAGA 1709
 Db 265 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCTCTTACTTGAAGTGTGAGA 324
 QY 1710 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAGAGGAGACGAA 1769
 Db 325 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAGAGGAGACGAA 384
 QY 1770 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTTGGGCAATGT 1829
 Db 385 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTTGGGCAATGT 444
 QY 1830 CATAGTCAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 1889
 Db 445 CATAGTCAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 504
 QY 1890 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAAGACA 1949
 Db 505 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAAGACA 564
 QY 1950 AGGACTCTATTATATCTATGCGCCAAAGTCACCTTCTGTTCCAATCGGAA 1998
 Db 565 AGGACTCTATTATATCTATGCGCCAAAGTCACCTTCTGTTCCAATTCGGGA 614

RESULT 9
 CN794193

LOCUS CN794193 571 bp mRNA linear EST 26-MAY-2004
 DEFINITION 4129335 BARC 8BOV Bos taurus cDNA clone 8BOV_50H03 5', mRNA
 sequence.

ACCESSION CN794193
 VERSION CN794193.1 GI:47690173

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 571)
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
 Matukumalli,L.K.

TITLE Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Richard G. Baumann

Bovine Functional Genomics Lab

ANRI

BLDG 162; BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt '-trim_fasta. Vector identified
 by cross_match using options -minmatch 12 -minscore 18

Plate: 50 row: H column: 03

Seq primer: CCTATTAGGTGACACTATAGAAC

High quality sequence stop: 571.

FEATURES

source

1..571

Location/Qualifiers

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clone="8BOV_50H03"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stages="Lactating, Neonatal"

/lab_host="DH10B Tona"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
Noti; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN	
Query Match	12.7%; Score 286.4; DB 7; Length 571;
Best Local Similarity	89.5%; Pred. No. 3.8e-60;
Matches	308; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY	1892 CCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACAAAG 1951
DB	1 CCTTAAGCAACAACTTGGTAACCTCGGAAACAGCTGCGCGTGAAGACAAAG 60
QY	1952 GACTCTATTATATCTATCCCAAGTCACCTCTCTGTTCCCAATCGGAAAGCTTCGAGTCAAG 2011
DB	61 GATTCTATCATCATCTACACCCCAAGTCACCTCTCTGTTCCCAATCGGAAAGCTTTGAGTCAAG 120
QY	2012 CTCCATTATAGCAGCTCTCGCTTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 2071
DB	121 CTCATTATAGCAGCTCTCGCTTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 180
QY	2072 GAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCAACATCCATTCATCTGGAG 2131
DB	181 GAGCTGCAAAACACCCACAGTTCGCGCAACCTTGGCGGCAACATCCATTCATCTGGAG 240
QY	2132 GAGTATTGTAATGCAACAGTGTCTGGTGTCTGTTCAATGTAGTATCCAGCCCAAG 2191
DB	241 GAGCTTTGTAATGCAATCGGTGTCTGGTGTCTGTTCAATGTAGTATCCAGTCAAG 300
QY	2192 TGAGCATGCGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTC 2235
DB	301 TGAGCAGCGGACGGCTTCACATCATTTGGCTTACTCAAACTC 344

RESULT 10	
LOCUS	CK834247
DEFINITION	4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA
ACCESSION	CK834247
VERSION	CK834247.1 GI:45064536
KEYWORDS	EST.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
AUTHORS	Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL	Unpublished (2004)
COMMENT	Contact: Richard G. Baumann Bovine Functional Genomics Lab ANRI BLDG 162; BARC-EAST, Beltsville, MD 20705, USA Tel: 3015048604 Fax: 3015048744 Email: rbaumann@anri.barc.usda.gov Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '- -trim_fast. Vector identified by cross_match using options -minmatch 12 -minscore 12 Plate: 2 row: M column: 16 Seq primer: CCTATTAGGTGACACTATAGAAC High quality sequence stop: 740. Location/Qualifiers 1..740 /organism="Bos taurus"

/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clones="8BOV 2M16"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stages="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
Noti; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN	
Query Match	10.9%; Score 246.4; DB 7; Length 740;
Best Local Similarity	86.9%; Pred. No. 3.8e-50;
Matches	271; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY	1590 TCCAAGAAAGTTGGACAAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 1649
DB	429 TCACAGAAGATTGGACAAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 488
QY	1650 GAAACACGATCAGAGATGCAACACAGGAGAAAGATCTTATCTTACTGAACTGTGAGGA 1709
DB	489 GAAACACGATCAGAGATGCAATAAAGGAGAGGGTCTTATCTTACTGAACTGTGAGGA 548
QY	1710 GATTAAGACCGATTTGAAGCTTTGTGAAGATATATATGTTAAACAAGAGGACAGAA 1769
DB	549 AATTAGAACCGGTTTGAAGACTTTGGTCAAGGATATATATGCAAAACAAGAGTAAAGAA 608
QY	1770 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAATTTGGGACATGT 1829
DB	609 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAGGCTCAGATAGCGGCACATGT 668
QY	1830 CATAGTGAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGACTATA 1889
DB	669 CATAGTGAGCGCCAGTAAACAAACATCTGTGTTCCTCAGTGGGCCCCCAAGGACTATA 728
QY	1890 CACCATGAGCAA 1901
DB	729 CACCATGAGCAA 740

RESULT 11	
LOCUS	BF599437
DEFINITION	263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	BF599437
VERSION	BF599437.1 GI:11695919
KEYWORDS	EST.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
PUBMED	11282978
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCAGGAG

Plate: 33 row: N column: 5

Seq primer: ATTATGGTGACACTATAG.

Location/Qualifiers

FEATURES

source

1. 492

Location/Qualifiers

/organism="Bos taurus"

/mol_type="rRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 3BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

ORIGIN

Query Match 10.9%; Score 244.4; DB 2; Length 492;

Best Local Similarity 86.8%; Pred. No. 1.1e-49; Mismatches 41; Indels 0; Gaps 0;

Matches 269; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1590 TCCAGAAGGTTGGACAAGATAGAGATCAAGGAATCTTCATGAAGATTGTTGTTATTCAT 1649

DB 133 TCACAGAGATTGGACAAGATAGAGACGAAGGAATCTTCATGAAGATTGTTGTTATTCAT 242

QY 1650 GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGTGAGGA 1709

DB 243 GAAACGATACAGATGCAATAAAGGAGAGGGTCTTATCTTACTGAACGTGTGAGGA 302

QY 1710 GATTAAAGCCAGTTTGAAGGTTTGAAGGATATATGTTAAACAAGAGGAGACGAA 1769

DB 303 AATTAGAAGCCGTTTGAAGACTTGGTCAAGGATATATGTTAAACAAGAGGATTAAGAA 362

QY 1770 GAAAGAAACACGTTTGAATGCAAAAAGGTGATCAGAAATCCTCAAAATGGCGGCACATGT 1829

DB 363 GAAAGAAACACGTTTGAATGCAACAAGGTGATCAGAGGCTCAGATAGCGGCACATGT 422

QY 1830 CATAGTGAGGCGCAGAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 1889

DB 423 CATAGTGAGGCGCAGAGTAAACAACCTCTGTTCTCCAGTGGGCCCCCAAGGATACTA 482

QY 1890 CACCATGAGC 1899

DB 483 CACCCCTAAGC 492

RESULT 12

CN786611

LOCUS

DEFINITION

sequence.

ACCESSION

CN786611

VERSION

CN786611.1

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

REFERENCE

1 (bases 1 to 628)

AUTHORS

Baumann, R.G.; Baldwin, R.L.; Sonstegard, T.S.; Van Tassell, C.P. and

Matukumalli, L.K.

TITLE

Construction and Analysis of a cDNA Library Generated From

Intestinal Muscle and Epithelial Tissues of Holstein Cattle

Unpublished (2004)

JOURNAL

COMMENT

Contact: Richard G. Baumann

Bovine Functional Genomics Lab

ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 18

Plate: 29 row: K column: 22

Seq primer: CCTATTAGGTGACACTATAGAC

High quality sequence stop: 628.

FEATURES

source

1. 628

Location/Qualifiers

/organism="Bos taurus"

/mol_type="rRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clones="8BOV_29K22"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stage="Lactating, Neonatal"

/lab_host="DH10B Tona"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:

NotI; Site 2: EcoRI; Normalized cow cDNA intestinal

library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources, 4 lactating intestinal, 1

neonatal intestinal 4/5 Lactating, Proximal Duodenum,

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal

Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 10.7%; Score 240; DB 7; Length 628;

Best Local Similarity 89.7%; Pred. No. 1.5e-48;

Matches 280; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

QY 1924 GGGAAACAGCTGACCGTTAAAGACAGGAGCTTATTATATCTATGCCCCAGTTCACCTTC 1983

DB 11 GGGAAACAGCTGCGCGTGAAGAC-AGGATCTATTACATCTACCCCAAGTTCACCTTC 69

QY 1984 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCC 2043

DB 70 TGTTC-ATCGGGAACCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCC 128

QY 2044 CCGGTGATTCGAGAGAATCTTACTCAGAGTGCATAATCCACAGTTCGCCCAACCT 2103

DB 129 CCAAGTGGATCAGAGAGAATCTTACTGAGAGCTGCACACCCACAGTTCTTCCAAACCA 188

QY 2104 TCGGGCAACAATCCATTCACCTTGGGAGGAGTATTGAATTGCAACCAAGGTCTTCGGTG 2163

DB 189 TCGGGCAGCAATCCATTCACCTTGGGAGGAGTATTGAATTGCAATCGGTTGCTTCGGTG 248

QY 2164 TTTGTCAATGTGACTGATCCAAAGCCAGTGAGCCATGGCACTGGCTTCACTGCTTTCG 2223

DB 249 TTTGTCAATGTGACTGATCCAAAGTCAAGTGCAGCGGAGCTTTCATCATCATTTGGC 308

QY 2224 TTACTCAAACTC 2235

DB 309 TTACTCAAACTC 320

RESULT 13

BH86550/c

LOCUS

DEFINITION

major genomic clone LB00861a, genomic survey sequence.

ACCESSION

BH86550

VERSION

BH86550.1

KEYWORDS

GSS.

SOURCE

Leishmania major

ORGANISM

Leishmania major

BH86550 527 bp DNA linear GSS 07-AUG-2002

LB00861a.d SP6.1 Leishmania major Friedlin BAC Library Leishmania

major genomic clone LB00861a, genomic survey sequence.

ACCESSION BH86550

VERSION BH86550.1

KEYWORDS GSS.

SOURCE Leishmania major

ORGANISM Leishmania major

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 6345.94 Seconds
(without alignments)
16453.933 Million cell updates/sec

Title: US-09-687-864A-13
Perfect score: 2208
Sequence: 1 aagtttgcgcgcgtctgtg.....aactcgagtgataatctaga 2208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_to.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1471.4	66.6	10000	14 AF038398	AF038398 Simian-Hu
2	1453.8	65.8	2046	6 CO753919	CO753919 Sequence
3	1453.8	65.8	2610	6 CO753921	CO753921 Sequence
4	1453.8	65.8	9860	14 AP217181	AP217181 Simian-Hu
5	1453.8	65.8	9860	14 SIU89134	SIU89134 Simian-Hu
6	1453.8	65.8	10501	6 BD161892	BD161892 Nonhuman
7	1448	65.6	9713	14 HIVU39362	U39362 Human immun
8	1339.8	60.7	2010	6 CO753923	CO753923 Sequence
9	1339.8	60.7	2574	6 CO753925	CO753925 Sequence
10	1263.2	57.2	2553	14 AV247221	AV247221 HIV-1 iso
11	1242.6	56.3	2568	14 AV426111	AV426111 HIV-1 clo
12	1241	56.2	2568	14 AV426112	AV426112 HIV-1 clo
13	1239.4	56.1	2568	14 AV426118	AV426118 HIV-1 clo
14	1237.8	56.1	2568	14 AV426110	AV426110 HIV-1 clo
15	1237.8	56.1	2568	14 AV426113	AV426113 HIV-1 clo
16	1237.8	56.1	2568	14 AV426115	AV426115 HIV-1 clo
17	1237.8	56.1	2568	14 AV426117	AV426117 HIV-1 clo
18	1236.2	56.0	2568	14 AV426114	AV426114 HIV-1 clo
19	1236.2	56.0	2568	14 AV426116	AV426116 HIV-1 clo

20	1227.4	55.6	3061	14 HIVENBAlA	M63929 Human immun
21	1225.8	55.5	3807	6 AR034235	AR034235 Sequence
22	1225.8	55.5	3807	6 I12144	I12144 Sequence 5
23	1225.8	55.5	3807	6 I28919	I28919 Sequence 5
24	1225.8	55.5	3808	14 HIVBALIA	M68893 Human immun
25	1224.6	55.5	2559	14 AY669732	AY669732 HIV-1 iso
26	1223.8	55.4	2547	14 AY426125	AY426125 HIV-1 iso
27	1223.8	55.4	2547	14 AY426127	AY426127 HIV-1 clo
28	1222.2	55.4	2544	14 AY669726	AY669726 HIV-1 iso
29	1222.2	55.4	2547	14 AY426126	AY426126 HIV-1 clo
30	1222.2	55.4	9540	14 HIVJRCFS	M38429 Human immun
31	1221.2	55.3	2568	14 AY247225	AY247225 HIV-1 iso
32	1219	55.2	3211	14 HIVU45960	U45960 Human immun
33	1209.4	54.8	2552	6 I05789	I05789 Sequence 8
34	1208.6	54.7	2559	14 AF025750	AF025750 HIV-1 iso
35	1206.8	54.7	2577	14 AF025763	AF025763 HIV-1 iso
36	1201.2	54.4	3600	14 HIVBRVA	M21098 Human immun
37	1199.2	54.3	8896	14 HIVU63632	U63632 HIV-1 isoLa
38	1197	54.2	1512	6 AX153805	AX153805 Sequence
39	1197	54.2	1512	6 BD017695	BD017695 Assay met
40	1196	54.2	2565	14 AF025754	AF025754 HIV-1 iso
41	1195.6	54.1	2559	14 HIVU36877	U36877 Human immun
42	1195.4	54.1	2553	14 HIVMB314	Y13719 Human immun
43	1195.4	54.1	2571	14 HIVENVVB	L08656 Human immun
44	1195.4	54.1	9074	14 HIVU43096	U43096 Human immun
45	1195	54.1	2559	14 AY247220	AY247220 HIV-1 iso

ALIGNMENTS

RESULT 1	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome.	10000 bp	DNA	linear	VRL 02-FEB-1998
LOCUS	AF038398					
DEFINITION	AF038398.1	GI:2828036				
ACCESSION	AF038398					
VERSION	AF038398.1					
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						

		/note="3' long terminal repeat"							
misc_feature		9307..9823							
repeat_region		/note="U3 region"							
		9824..10000							
		/note="R region"							
ORIGIN									
Query Match 66.6%; Score 1471.4; DB 14; Length 10000;									
Best Local Similarity 98.6%; Pred. No. 5.7e-301;									
Matches 1484; Conservative 0; Mismatches 21; Indels 0; Gaps 0;									
QY	52	TGGATCTCGGCTTCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTCTACAGAA	111						
Db	6375	TGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTCTACAGAA	6434						
QY	112	AAATTGTGGGTTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACACACACACTCTA	171						
Db	6435	AAATTGTGGGTTCACAGTCTATTATGGGTACCTGTGTGGAGAGAACACACACACTCTA	6494						
QY	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231						
Db	6495	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554						
QY	232	GCCTGTGTACCCACAGACCCCAACCCACAGAGTATGTTGGGAATGTGCACAGAAAT	291						
Db	6555	GCCTGTGTACCCACAGACCCCAACCCACAGAGTATGTTGGGAATGTGCACAGAAAT	6614						
QY	292	TTTAAACATGTGAAAAAATAACATGTGTAGATCAGATGCATGAGGATATTAATCAGTTTATGG	351						
Db	6615	TTTAAACATGTGAAAAAATAACATGTGTAGATCAGATGCATGAGGATATTAATCAGTTTATGG	6674						
QY	352	GATGAAGCCTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTAAATTTGCAC	411						
Db	6675	GATGAAGCCTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTAAATTTGCAC	6734						
QY	412	AAATTGAATATCACTAAGAAATCTACTTAATCCCACTAGTACAGCTGGGGAATGATGGAG	471						
Db	6735	AAATTGAATATCACTAAGAAATCTACTTAATCCCACTAGTACAGCTGGGGAATGATGGAG	6794						
QY	472	AAAGGAGAAATAAAAAATTTGCTTTCTTATATCACCAAGCATAAAGAAATTAAGGTAAAG	531						
Db	6795	AAAGGAGAAATAAAAAATTTGCTTTCTTATATCACCAAGCATAAAGAAATTAAGGTAAAG	6854						
QY	532	AAAGAATATGCATTTTAAATAGACTTTGATGTAGTACCAATAGAAAACTAATAATACT	591						
Db	6855	AAAGAATATGCATTTTAAATAGACTTTGATGTAGTACCAATAGAAAACTAATAATACT	6914						
QY	592	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCC	651						
Db	6915	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCC	6974						
QY	652	TTTCAGCCAAATCCCATACATTTATTTGTGCCGGCTGGTTTGGATGCTAAAGTGTAAAC	711						
Db	6975	TTTCAGCCAAATCCCATACATTTATTTGTGCCGGCTGGTTTGGATGCTAAAGTGTAAAC	7034						
QY	712	AATAAGACATTCATGATCAGGACCATGCACAAATGTGCACACAGTACAAATGTACACAT	771						
Db	7035	AATAAGACATTCATGATCAGGACCATGCACAAATGTGCACACAGTACAAATGTACACAT	7094						
QY	772	GGAATATAGGCCAGTGGTGTCAACTCACTGCTTTAAATGCGAGTGTAGCAGAGAGAGAC	831						
Db	7095	GGAATATAGGCCAGTGGTGTCAACTCACTGCTTTAAATGCGAGTGTAGCAGAGAGAGAC	7154						
QY	832	ATAGTAAATTAGATCTGAAAATTTTCACAGCAATGCTAAACCAATAATGATACGCTAAAT	891						
Db	7155	ATAGTAAATTAGATCTGAAAATTTTCACAGCAATGCTAAACCAATAATGATACGCTAAAT	7214						
QY	892	GAATCTGTAGTAAATTAATTTGACAGACCCCAACCAATACAGAGAGAGGTTTATCTATA	951						
Db	7215	GAATCTGTAGTAAATTAATTTGACAGACCCCAACCAATACAGAGAGAGGTTTATCTATA	7274						
QY	952	GGACCAAGGAGAGCAATTTTATGCAAGAGAAACATAATATAGAGATATTAAGCAAGCAAT	1011						

Db	7275	GGACACGGGAGAGCAATTTTATGCAAGAGAAACAATAATAGGAGATATAAGACAAGCACAT	7334		
Qy	1012	TGTAACATTAGTAGACGCAAAATGGAATAACACATTTTCAACACAGATAGTTTATAAATTAAGA	1071		
Db	7335	TGTAACATTAGTAGACGCAAAATGGAATAACACATTTTCAACACAGATAGTTTATAAATTAAGA	7394		
Qy	1072	GAAAAATTTAGGAATAAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGAGCCGAGAAAT	1131		
Db	7395	GAAAAATTTAGGAATAAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGAGCCGAGAAAT	7454		
Qy	1132	GTAATGACACAGTTTAAATTTGAGGGGGAATTTCTTCTACTGTCTAATACAGCACTGTTT	1191		
Db	7455	GTAATGACACAGTTTAAATTTGAGGGGGAATTTCTTCTACTGTCTAATACAGCACTGTTT	7514		
Qy	1192	AATAGTACTTTGGAAATGTTTACTTGGAGGGCAAAATGGCACTGAAGGAAATGACATTAATCA	1251		
Db	7515	AATAGTACTTTGGAAATGTTTACTTGGAGGGCAAAATGGCACTGAAGGAAATGACATTAATCA	7574		
Qy	1252	CTCAATGCGAGATAAAACAAAATTAATAATGTGGCAGAGAAAGTAGGAAAAGCAATGTAT	1311		
Db	7575	CTCAATGCGAGATAAAACAAAATTAATAATGTGGCAGAGAAAGTAGGAAAAGCAATGTAT	7634		
Qy	1312	GCCCTCCCATCAAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTCTCTACTACA	1371		
Db	7635	GCCCTCCCATCAAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTCTCTACTACA	7694		
Qy	1372	AGAGATGGAGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAGAT	1431		
Db	7695	AGAGATGGAGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAGAT	7754		
Qy	1432	ATGAGGACAAATTTGGAGAGTGAATTAATAATAATAATAATAATAATAATAATAATAATA	1491		
Db	7755	ATGAGGACAAATTTGGAGAGTGAATTAATAATAATAATAATAATAATAATAATAATAATA	7814		
Qy	1492	GGAGTACACCCACCGGCAAGAGAGAACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAG	1551		
Db	7815	GGAGTACACCCACCGGCAAGAGAGAACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAG	7874		
Qy	1552	AGAAG 1556			
Db	7875	ATAGG 7879			
RESULT 2					
LOCUS CQ753919 2046 bp DNA linear PAT 01-MAR-2004					
DEFINITION Sequence 24 from Patent WO2004001051.					
ACCESSION CQ753919					
VERSION CQ753919.1 GI:44845220					
KEYWORDS Human immunodeficiency virus 1 (HIV-1)					
SOURCE Human immunodeficiency virus 1					
ORGANISM Human immunodeficiency virus 1					
REFERENCE 1					
Tangy, F., Lorin, C., Mollet, L. and Delebecque, F.					
Recombinant measles viruses expressing epitopes of antigens of rna					
viruses - use for the preparation of vaccine compositions					
JOURNAL Patent: WO 2004001051-A 24 31-DEC-2003;					
INSTITUT PASTEUR (FR)					
FEATURES					
source Location/Qualifiers					
1..2046					
/organism="Human immunodeficiency virus 1"					
/mol_type="unassigned DNA"					
/db_xref="taxon:11676"					
ORIGIN					
Query Match 65.8%; Score 1453.8; DB 6; Length 2046;					
Best Local Similarity 97.9%; Pred. No. 3.6e-297;					
Matches 1473; Conservative 0; Mismatches 32; Indels 0; Gaps 0;					
Qy	52	TGGATCTCGGCTTCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTCTACAGAA	111		

```
Db 37 TGGGGTGGAGATGGGGCCCATGCTCTTGGGATGTTGATGATCTGTAGTGTCTACAGAA 96
Qy 112 AAATTTGGGTTCACAGTCTATTATTTGGGTGCTCTGTGGAGAGCAACACACACTCTA 171
Db 97 AAATTTGGGTTCACAGTCTATTATTTGGGTGCTCTGTGGAGAGCAACACACACTCTA 156
Qy 172 TTTTGTGTCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 157 TTTTGTGTCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCACAAGAACTAGTATTTGGGAAATGTGACAGAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCACAAGAACTAGTATTTGGGAAATGTGACAGAAAT 276
Qy 292 TTTTAAACATGTGGAAATTAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG 351
Db 277 TTTTAAACATGTGGAAATTAACATGGTAGATCAGATGATGAGGATATAAATCAGTTTATGG 336
Qy 352 GATGAAAGCCCTAAAGCCATGTGTAATAACCCCACTCTGTGTACTTTTAAATTTGCACAT 411
Db 337 GATGAAAGCCCTAAAGCCATGTGTAATAACCCCACTCTGTGTACTTTTAAATTTGCACAT 396
Qy 412 AATTGTGAATFACATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAG 471
Db 397 AATTGTGAATFACATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAG 456
Qy 472 AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCAACAGCATAAGAAATAGGTAAAG 531
Db 457 GAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCAACAGCATAAGAAATAGGTAAAG 516
Qy 532 AAAGAATATGACATTTTAAATAGACTTGATGATGATGATGATGATGATGATGATGATGATGAT 591
Db 517 AAAGAATATGACATTTTAAATAGACTTGATGATGATGATGATGATGATGATGATGATGATGAT 576
Qy 592 AAGTATAGTTTAAATAGTTTGAACACCTCAGTCAATATACAGAGGCTGTGCAAGAGGTATCC 651
Db 577 AAGTATAGTTTAAATAGTTTGAACACCTCAGTCAATATACAGAGGCTGTGCAAGAGGTATCC 636
Qy 652 TTTTCAGCAATTTCCCATACATATTGTGTCGCCGCTGGTTTGGATGCTTAAAGTGAAC 711
Db 637 TTTTCAGCAATTTCCCATACATATTGTGTCGCCGCTGGTTTGGATGCTTAAAGTGAAC 696
Qy 712 AATAAGACATTTCAATGATCAGGACCATGACAAATGTGACACAGTACATGATGATGATGATGAT 771
Db 697 AATAAGACATTTCAATGATCAGGACCATGACAAATGTGACACAGTACATGATGATGATGATGAT 756
Qy 772 GGAATTAGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGAC 831
Db 757 GGAATTAGCCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGAC 816
Qy 832 ATAGTAATTAGATCTGAAATTTTCCACAGACATGCTTAAACCAATAATAGTACAGCTAAAT 891
Db 817 ATAGTAATTAGATCTGAAATTTTCCACAGACATGCTTAAACCAATAATAGTACAGCTAAAT 876
Qy 892 GAATCTGTAGTAATTAATTTGACAGAGCCCAACCAATACAAAGAAAGGTTTATCTATA 951
Db 877 GAATCTGTAGTAATTAATTTGACAGAGCCCAACCAATACAAAGAAAGGTTTATCTATA 936
Qy 952 GGACAGGGAGAGCATTTTATGCAAGAGAAACAATAATAGAGATATATAGACAAGACAT 1011
Db 937 GGACAGGGAGAGCATTTTATGCAAGAGAAACAATAATAGAGATATATAGACAAGACAT 996
Qy 1012 TGTAAACATTAGTAGGCAAAATGGAATTAACCTTTTACACAGATAGTTTATATAATTAAGA 1071
Db 997 TGTAAACATTAGTAGGCAAAATGGAATTAACCTTTTACACAGATAGTTTATATAATTAAGA 1056
Qy 1072 GAAAAATTTAGGAATAAAACATAGCCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT 1131
Db 1057 GAAAAATTTAGGAATAAAACATAGCCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT 1116
Qy 1132 GTAATGCAAGTTTTAAATTTGGAGGGGAATTTCTTCTACTGTAAATACAGCAAACTGTTTT 1191
Db 1117 GTAATGCAAGTTTTAAATTTGGAGGGGAATTTTCTACTGTAAATACAGCAAACTGTTTT 1176
```

```
Qy 1192 AATAGTACTTTGGAATGTTACTGGAGGACAAATGGCACTGAAGGAAATGCATATATCACA 1251
Db 1177 AATAGTACTTTGGAATGTTCTGGAGGACAAATGGCACTGAAGGAAATGCATATATCACA 1236
Qy 1252 CTCAATGCAAGATAAAACAAATTTATAATATATGTCGAGAAAAGTAGGAAAAGCAATGTAT 1311
Db 1237 CTCAATGCAAGATAAAACAAATTTATAATATATGTCGAGAAAAGTAGGAAAAGCAATGTAT 1296
Qy 1312 GCCCTCCCATCAGACAGCAAAATTTAGATGTTTCATCAATATTTACAGGCTCTACTACACA 1371
Db 1297 GCCCTCCCATCAGACAGCAAAATTTAGATGTTTCATCAATATTTACAGGCTCTACTACACA 1356
Qy 1372 AGAGATGGAGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAGAT 1431
Db 1357 AGAGATGGAGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGGAGAT 1416
Qy 1432 ATGAGGACAAATTTGGAGAAAGTGAATTTATATAATAATATAAAGTAGTAAGAAATTTGAACCAATA 1491
Db 1417 ATGAGGACAAATTTGGAGAAAGTGAATTTATATAATAATATAAAGTAGTAAGAAATTTGAACCAATA 1476
Qy 1492 GGAGTAGACCCACAGGCAAGAGAGAACACAGTGCARAGAGAAAAGACCGGATCCA 1551
Db 1477 GGAGTAGACCCACAGGCAAGAGAGAACACAGTGCARAGAGAAAAGACCGGATGGGA 1536
Qy 1552 AGAAG 1556
Db 1537 ATAGG 1541
```

```
RESULT 3
CO753921          CO753921          2610 bp      DNA      linear      PAT 01-MAR-2004
LOCUS             Sequence 26 from Patent WO2004001051.
DEFINITION        CO753921
ACCESSION         CO753921
VERSION           CO753921.1  GI:44845221
KEYWORDS           Human immunodeficiency virus 1 (HIV-1)
SOURCE            Human immunodeficiency virus 1
ORGANISM          Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                  lentivirus group.
REFERENCE          Tangy, F., Lorin, C., Mollet, L. and Delebecque, F.
AUTHORS            Recombinant measles viruses expressing epitopes of antigens of rna
TITLE              viruses - use for the preparation of vaccine compositions
JOURNAL            Patent: WO 2004001051-A 26 31-DEC-2003;
KEYWORDS           INSTITUT PASTEUR (FR)
FEATURES           Location/Qualifiers
                   1..2610
                   /organism="Human immunodeficiency virus 1"
                   /mol_type="unassigned DNA"
                   /db_xref="taxon:11676"
```

```
ORIGIN
Query Match      65.8%; Score 1453.8; DB 6; Length 2610;
Best Local Similarity 97.9%; Pred. No. 3.5e-297;
Matches 1473; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
Qy 52 TGGATCTCGGTTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAA 111
Db 37 TGGGGTGGAGATGGGCAACCATGCTCTTGGGATGTTGATGATCTGTAGTGTCTACAGAA 96
Qy 112 AAATTTGGGTTCACAGTCTATTATTTGGGTGCTCTGTGGAGAGAAAGCAACCACTCTA 171
Db 97 AAATTTGGGTTCACAGTCTATTATTTGGGTGCTCTGTGGAGAGAAAGCAACCACTCTA 156
Qy 172 TTTTGTGCATCAGATGCTTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 157 TTTTGTGCATCAGATGCTTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCACAAGAACTAGTATTTGGGAAATGTGACAGAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCACAAGAACTAGTATTTGGGAAATGTGACAGAAAT 276
```



```
gene
<1711..4893
/gene="pol"
CDS
<1711..4893
/gene="pol"
/codon_start=1
/product="pol protein"
/protein_id="AAL55639.1"
/db_xref="GI:18026828"
/translation="VILMERGTLCAMQSPKTKTLMEMKNGPCYQMPCQTGCFPR
PWSMGKAPQPHGSSASGDTNCPGSPSCSAGELHAGQAERKAERKQREALQSG
GDRGAFAQSWLERPVVTAHIEGQPVLELDTGADDSIVTGIELGHPYTPKIVGGIG
GFINTKYEKNVEIWLKRIKGTITGTDTPINIFGRNLLTALGMSLFPYFAKVEPVKV
ALKPKGQPKLCKMPLKREICERKMDQLEEAAPTNPYNTPTFAIKPKDK
NKWRMLIDFRELNVQDFTFVQLGIPHPAGLAKRKRIITVLIDGDAVFSIPLDEPRQ
YTATLPSVNNAERKGIYIKVLPQGHKGSAPAIQYIMRHVLEPFRKANPDVTLVQYM
DDILASDREHDRVVLQKLELNSIGFSTPEEKFKOPFPQWMGTELPWTKRLQ
KIELPQRTWTVDNIQKLVGNLWAAQIYFGIKTKHLICRLIRGQWLTTEEPQWTEMAE
AYEENKIIISQEGEGYQEGKPLEATVKSQDNQMSYKIHQEDKILKVGKFAKINI
THINGVRLAHVIOIKIEKAIVIGQVPKHLPEVKDQWQWMDYQWVTWIPWDFI
STPLVRLVNLVQDPTGEBETYTDGSCNKGKAGYITDRGDKVKVLEOTTNQ
QAELEAFMLATSDGPRANIIVDSQYMGILTGCTPTESESLVNLQIIEEMLKSEIYV
AWFPAHKGIGNQSIDHLVSGQIRQVLFLERIEPAQBEHDKYHSNVKELVFKGLPRI
VARQIVTDCDKHQCHGSEAHQANDLGTWQMDCTHLEGKIIIVAVHVASGFIAEVI
PQETGRQTFALFLKLAGRWPTIHLTDNGANFASQBYKMAWMAWAGIEHTFGVFNPOS
QGVVEAMNHLKNQIDIRIQANSVETIIVLMAVHCNPKRGGIGDMTPAERLINMIT
TEQEIQFOQSKNSKFNFRVYRREGRDQLWKGPCCELLWKGBGAVILKVGTDIKVPRR
KAKTIIDYGGGKEVDSSSHMEDTGEAREVA"
4823..5467
/gene="vif"
CDS
4823..5467
/gene="vif"
/codon_start=1
/product="vif protein"
/protein_id="AAL55640.1"
/db_xref="GI:18026829"
/translation="MEBEKRWIAVPTWRIPELRERWHSILKYLKYKTKDLQKVCYVP
H
KVGAWMTCSRVPFPLQEGSHLEVQVWHLTPKGLWLTAVAVRITWYSKNFTDVT
PYADILLHSTVFPCFTAGEVRAIRGQLLSCCRPRAHKYQVPSLOYLAKVYSDVR
SQENPFTWKQRDRNRRLMAKQNSRGDKRGKPTKGNFPLGLAKVLGILA"
5295..5633
/gene="vpx"
CDS
5295..5633
/gene="vpx"
/codon_start=1
/product="vpx protein"
/protein_id="AAL55641.1"
/db_xref="GI:18026830"
/translation="MSDPREIRIPFGNSGEETIGFAFWLNRVTVEINREAVNHLPREL
IFQVWQRSWEYWHDEQMSPSYKYRYLCLIQALFMHCKKGCRCLGEGHGAGWRPG
PPPPPPGLA"
5634..5939
/gene="vpr"
CDS
5634..5939
/gene="vpr"
/codon_start=1
/product="vpr protein"
/protein_id="AAL55642.1"
/db_xref="GI:18026831"
/translation="MEERPPNEQFPQRPDEWVWVVEELKEALKHFDPRLRLTALG
NHIYNRIGDTEGAGELIRILQRALFMHFRGCGTHSRGPGGPNPLSAIPPSRML"
5939..8775
/feature="derived from HIV-1"
5948..8580
/gene="tat"
CDS
join(5948..6162,8487..8580)
/gene="tat"
/codon_start=1
/product="tat protein"
/protein_id="AAL55643.1"
/db_xref="GI:18026832"
/translation="MEPVDPRLEPWKHPGSKPKTACTNICYCKKCCFHCQVCFTTKALG
ISYKRRKRRRAHONSQTHQASLSKQSPSSQPRGDPGPKEQKVERETETDPVHQ
```

```
gene
6087..8761
/gene="rev"
CDS
join(6087..6162,8487..8761)
/gene="rev"
/codon_start=1
/product="rev protein"
/protein_id="AAL55644.1"
/db_xref="GI:18026833"
/translation="MAGRSGDSDBELIRTVRLIKLLYQSNPPSPSECTGROARRRRR
WRQRQIRISIRILGTYLGRSAEPVLQPLPRLTILDCNDCGTSGTGQVGSPOI
LVSPPTVLESGTKE"
6179..6424
/gene="vpu"
CDS
6179..6424
/gene="vpu"
/codon_start=1
/product="vpu protein"
/protein_id="AAL55645.1"
/db_xref="GI:18026834"
/translation="MOPQIAIIVALVVAIIIAIVMSIIVIEYRKILRQKIDRLIDR
LIBRAEDSGNESEGEISALVEMGVMGHAPVDVDDL"
6339..8948
/gene="env"
CDS
6339..8948
/gene="env"
/codon_start=1
/product="env polyprotein"
/protein_id="AAL55646.1"
/db_xref="GI:18026835"
/translation="MRVKEYQHLWRGWGTMLLGMLMICSATEKLWTVTVYGVV
WREATTTLFCASDAKAYDETVHVNWATHACVPTDPNPQEVVLGNVTNFMKNMVD
QMEHDIISLWDESLKPCVLTPLCVTLNLTNLTNTLTSSMACMEEGEIKNGS
FYITTSIRNKVKKEYALFNLDVVPKNTNTKYRLISCTSVITQACPKVSPQIPI
HYCVAPGAILKCNKTFNGSGCTNVSTQCTHGIRPVYSTOLLNLSAEEDIVIR
SEDTNVNKTIIIVOLNESVINCTRNNTNRERLSIGPRAFTARRNLIGDIRAHCN
ISRAKNMTQQIIVIKLREKFNKTIAFNOSGGDEIIVHSPFCGGEFFYCNTAQLP
LSTNVAGTNGTEGNDITLQCRIKQIINWQKVGKAMYAPPTIGQIRCSNITGLL
NRDGGNSTETETIIFRPGGDMRDNRSELKYKVRIBPIGVAPTRAKRTVOREK
RANGIGAVFTGLGAGSTWGAASVTLTVOARLLSGIVQONNLLRAIRAOQNMLRL
TVWGIQOLARVALERYLDQOLMGIWGSGLKICTTSVPNVVSWNSKSVDDIWNRM
TWMEKEIDNYTDIYDLEKSTQOEKNEKELLELDKWSLWNNFEDITNMLWYIRL
FIMVGGILGLIRIVAVLSIVNRVQGYSPLSFTQLLPASGRPDPRGEBEGGERD
DRSGPSVNGSLIWLADRLSLCLFSYHRLRDLIIIVTRTVELLGRRGEALKYWNLL
QYWSOELKNSAVSLLOQWGSYFHEAVQAVRSATETTLAGAWGDVWETLRRGRWILAI
PRRIQGLLEITLL"
8776..9860
/feature="derived from SIVmac239"
8782..9573
/gene="nef"
CDS
8782..9573
/gene="nef"
/codon_start=1
/product="nef protein"
/protein_id="AAL55647.1"
/db_xref="GI:18026836"
/translation="MGAISMRSRPSCDLRQLLRARGETYGRLLGEVEDGYSSQPG
GLDKLSLSCEGQYQNGOYMTWPNPAEREKLAIRKQNMDDIDDEDDDLVGSV
RPKVPYKTMYSYKLAIDMSHFILKEKGLGYVSARHRIIDIVLEKEGLIPMQDYT
SGGIRYPTKFTGMLWKLVPVNVSDAEQDEDEHLMHPASQSDDDPGEVLAWKFDPT
LATYEAIRYPTPEFGSKSLSEEEVRRRLTARGLLNADKKETR"
9167..9860
/feature="U3 region"
9167..9683
/feature="R6 region"
9684..9860
/feature="R6 region"
ORIGIN
Query Match 65.8%; Score 1453.8; DB 14; Length 9860;
Best Local Similarity 97.9%; Pred. No. 3e-297;
Matches 1473; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 52 TGGATCTCGGCTTCGAGATCAATGCTCCTTGGGATATTGATCTGTAGTGTACAGAA 111
```

D	b		6375	TGGGGGTGCGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTGCTACAGAA	6438
Q	y		112	AAATTGTGGGTGCACAGTCTATTATTGGGTACTCTGTGTGGAGAGAAGCAACCACCACCTCTA	171
D	b		6435	AAATTGTGGGTGCACAGTCTATTATTGGGTACTCTGTGTGGAGAGAAGCAACCACCACCTCTA	6494
Q	y		172	TTTTTGTGCATCAGATGCTTAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
D	b		6495	TTTTTGTGCATCAGATGCTTAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554
Q	y		232	GCCTGTGTACCCACAGACCCCACCCACAAGAAGTAGTATTGGGAATATGTGACAGAAAAT	291
D	b		6555	GCCTGTGTACCCACAGACCCCACCCACAAGAAGTAGTATTGGGAATATGTGACAGAAAAT	6614
Q	y		292	TTTAAACATGTGAAAAATAAACATGCTAGATCAGATGCAATGAGGATATAATTCAGTTTATGG	351
D	b		6615	TTTAAACATGTGAAAAATAAACATGCTAGATCAGATGCAATGAGGATATAATTCAGTTTATGG	6674
Q	y		352	GATGAAAGCCTTAAAGCCATGTGTAAAAATTAAACCCACACTCTGTGTACTTTAAATTTGCAC	411
D	b		6675	GATGAAAGCCTTAAAGCCATGTGTAAAAATTAAACCCACACTCTGTGTACTTTAAATTTGCAC	6734
Q	y		412	AATTTGAAATATCACTAAGAAATPACTACTTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	471
D	b		6735	AATTTGAAATATCACTAAGAAATPACTACTTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	6794
Q	y		472	AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATTAAGAAATAGGTTAAG	531
D	b		6795	AAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATTAAGAAATAGGTTAAG	6854
Q	y		532	AAAGAAATATGCACCTTTTTTAATAGACTTTGATGTAGTACCAATAGAAAAATACCTAATAATAC	591
D	b		6855	AAAGAAATATGCACCTTTTTTAATAGACTTTGATGTAGTACCAATAGAAAAATACCTAATAATAC	6914
Q	y		592	AAGTATAGGTTAATAAGTTGTAAACCTCTAGTCAATTAACAGGCCTGTCCAAAGGTTATCC	651
D	b		6915	AAGTATAGGTTAATAAGTTGTAAACCTCTAGTCAATTAACAGGCCTGTCCAAAGGTTATCC	6974
Q	y		652	TTTTCAGCCAATTTCCCATACATATTGTGTCCCGCTGGTTTGGATGCTATAAGTGTAAAC	711
D	b		6975	TTTTCAGCCAATTTCCCATACATATTGTGTCCCGCTGGTTTGGATGCTATAAGTGTAAAC	7034
Q	y		712	AATAAGACATTCATTTGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT	771
D	b		7035	AATAAGACATTCATTTGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACAT	7094
Q	y		772	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	831
D	b		7095	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	7154
Q	y		832	ATAGTNATTAGATCTGAAAATTTTACAGACAAATCTTAAACCATAATAGTACAGCTAAAT	891
D	b		7155	ATAGTNATTAGATCTGAAAATTTTACAGACAAATCTTAAACCATAATAGTACAGCTAAAT	7214
Q	y		892	GAAATCTGTAGTAAATTAAATTGTACAAGACCCCAAACAATAACAAGAGAAGAGTTATCTATA	951
D	b		7215	GAAATCTGTAGTAAATTAAATTGTACAAGACCCCAAACAATAACAAGAGAAGAGTTATCTATA	7274
Q	y		952	GGACCAGGGAGACATTTTATGCAAGAGAACAATAATAGGAGATATAAGACAAGCACAT	1011
D	b		7275	GGACCAGGGAGACATTTTATGCAAGAGAACAATAATAGGAGATATAAGACAAGCACAT	7334
Q	y		1012	TGTAACATATTAGTAGACMAAATGGAATAACCTTTTACAACAGATAGTTATAAAATTAGA	1071
D	b		7335	TGTAACATATTAGTAGACMAAATGGAATAACCTTTTACAACAGATAGTTATAAAATTAGA	7394
Q	y		1072	GAAAAATTTAGGAATAAAAAATAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT	1131
D	b		7395	GAAAAATTTAGGAATAAAAAATAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAT	7454
Q	y		1132	GTAATGCAACAGTTTTTTAATTGAGAGGGGAATTTCTTCTACTGTAAATACAGACAACTGTTT	1191

Db	7455	GTAAATGCACAGTTTTAAATTTGTGGAGGGGAAATTTTTTCTACTGTATAACAGACCAACTGTTT	7514
Qy	1192	AATAGTACTTTGGAAATGTTTACTTGGAGGGACAAAATGGCACTGAAGGAAATGCATAATCACA	1251
Db	7515	AATAGTACTTTGGAAATGTTTGTGGAGGGACAAAATGGCACTGAAGGAAATGCATAATCACA	7574
Qy	1252	CTCCAAATGCAGAAATAAAAACAAATTTATAATATATGTGGCAGAAAGTAGGAAAGCAATGTAT	1311
Db	7575	CTCCAAATGCAGAAATAAAAACAAATTTATAATATATGTGGCAGAAAGTAGGAAAGCAATGTAT	7634
Qy	1312	GCCCTCCCATCACAGACAAATTTAGATGTTTCATCAATATTACAGGGCTGCTACTTAACA	1371
Db	7635	GCCCTCCCATCACAGACAAATTTAGATGTTTCATCAATATTACAGGGCTGCTACTTAACA	7694
Qy	1372	AGAGATGGAGGTAAATAGTACTTGAGACTTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGAT	1431
Db	7695	AGAGATGGAGGTAAATAGTACTTGAGACTTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGAT	7754
Qy	1432	ATGAGGACCAATTTGGAGAAGTGAATTATATAAATATATAAAGTAGTAAAGATTGAACCAATA	1491
Db	7755	ATGAGGACCAATTTGGAGAAGTGAATTATATAAATATATAAAGTAGTAAAGATTGAACCAATA	7814
Qy	1492	GGAGTACACCCACCAGGCGCAAGAGAGAACACAGTGCAGAGAGAAAAAGACCGGATCCA	1551
Db	7815	GGAGTACACCCACCAGGCGCAAGAGAGAACACAGTGCAGAGAGAAAAAGACCGGATCCA	7874
Qy	1552	AGAAG 1556	
Db	7875	ATAGG 7879	
RESULT 5			
SIU89134			
LOCUS	SIU89134	9860 bp. DNA linear	VRL 21-MAY-1997
DEFINITION	Simian-Human immunodeficiency virus strain SHIV-89.6P, complete genome.		
ACCESSION	U89134		
VERSION	U89134.1	GI:2108163	
KEYWORDS			
SOURCE	Simian-Human immunodeficiency virus		
ORGANISM	Simian-Human immunodeficiency virus		
REFERENCE	1 (bases 1 to 9860)		
AUTHORS	Karlsson,G.B., Halloran,M., Li,J., Park,I.W., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.		
TITLE	Characterization of molecularly cloned simian-human immunodeficiency viruses causing rapid CD4+ lymphocyte depletion in rhesus monkeys		
JOURNAL	J. Virol. 71 (6), 4218-4225 (1997)		
MEDLINE	97296224		
PUBMED	9151808		
REFERENCE	2 (bases 1 to 9860)		
AUTHORS	Reimann,G.B., Halloran,M., Li,J., Park,I., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-FEB-1997) Human Retrovirology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA		
FEATURES	Location/Qualifiers		
source	1. .9860		
	/organism="Simian-Human immunodeficiency virus"		
	/proviral		
	/mol_type="genomic DNA"		
	/strain="SHIV-89.6P"		
	/db_xref="taxon:57667"		
	/clone="SHIV-89.6KB9"		
source	1. .5946		
	/organism="Simian-Human immunodeficiency virus"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:57667"		
	/note="derived from SIIV"		
source	5947. .8778		
	/organism="Simian-Human immunodeficiency virus"		

source	/mol_type="genomic DNA"	
	/db_xref="taxon:57667"	
LTR	8779..5986	
	/organism="Simian-Human immunodeficiency virus"	
misc_feature	/mol_type="genomic DNA"	
	/db_xref="taxon:57667"	
misc_feature	1..301	
	/note="5' LTR"	
gene	1..177	
	/note="R region"	
CDS	178..301	
	/note="U5 region"	
CDS	536..2068	
	/gene="gag"	
CDS	536..2068	
	/gene="gag"	
CDS	/product="gag polyprotein"	
	/protein_id="AAC57419.1"	
CDS	/db_xref="GI:2108164"	
	/translation="MGVRNSVLGSKKADELEKIRLPNGKKKMYMLKHVWMAANELDRF	
CDS	GLAELLENKEQCILSVLAPLPTGSENLSLYNTVCVWICHAEEKVKHTEAAKQ	
	IVORHLVETGTTETMTKTSRPTAPDSGRGNYPVQIIGNVYHLPLSPRTLNAAVKL	
CDS	IEKEFGAEVPGFALSEGCTPYDINMLNCVGDHQAAMQIIRDIINEEAADWLQVR	
	POPAAQQQLRPSPGSDIAGTSSVDEQIQWYRQONPVPNGIYRRHLQGLQKVR	
CDS	MYNPTNLDVKGKPEPQSYVDFYKLSRAEQTDAAVKNMTQTILLIQANPDCKL	
	LKLGVNPTLEMLTACOGVGGQKRLMAELKAPLAPVIPFAAQQORPFRPIK	
CDS	CWNCGKEGSRACPRRQCKGCKMDHVNKCPDRQAQFLGLGPMGKKPRNPMA	
	OVHQGLMPTAPPEDPADVLLKNYMLQKGQREKQRESKPKYKEYVTEDLLHLSLFGG	
CDS	DQ"	
	<1711..4893	
CDS	/gene="pol"	
	<1714..4893	
CDS	/gene="pol"	
	/codon_start=1	
CDS	/product="pol polyprotein"	
	/protein_id="AAC57420.1"	
CDS	/db_xref="GI:2108165"	
	/translation="LELWERTGLCKAMQSPKKTGMLMMWNGPCYQMPRQTGGFRRP	
CDS	WSMGKEAPQPHGSSAGADANSPRPGSCSAKELHAGVQAAERKAERKQREALQGG	
	DRGFAAPQVRRPVVTAHIEGQPVVELLDTGADDSIVTIGELGPHYTPKIVGGIGG	
CDS	FINTKEYKNVEVLGKRIKGTIMTGDTPINIFGRNLLTALGMSLNFPIAKVEPVKVA	
	LXPGDGPKLQWPLSKKEKIVALREICEKWEKDGQLEAPPTNPYNTPTPTFAIKKDKDN	
CDS	KWRMLDFRNLNRTVDFTFVQLGIPHAGLAKRRAITVLDIGDAYFSIPLDEEFQY	
	TAFTLPFSNVASPGKRIYKVLFPQGWKGSIPAIFYTMRHVLEFPFRKANPDVTLVQMD	
CDS	DILLASDRDLDHDRVLLQSKLLNSIGFTPEEFKQDPDPQWGMGYELMPTKWLQK	
	IELPQRETWTVNDIQKLVGLNAAQIYPGIKTKLCRLIRGKMTLITEEVOWTEMAEA	
CDS	EYBENKIILSQEGQCYQEGKPLEATVIKSDONOWSYKIHQEDKILKYGFEAKIKNT	
	HNGVRLLAHVTKTIGKEAIVTMGVQPKFHLVPEKDVQWQWTDYQWTVIPEWDFIS	
CDS	TPPLVRLNVDPIDPEGEBTYTDSGNCKQKEGKAGYITDRGDKVKVLQQTNNQ	
	ADELAPFALMTDSGKANIIIVDSQYVMGIITGPTSESRLVNQIIEEMIKKESEIYA	
CDS	WYPAHKGICGNQEIIDLHVQGRQVLFLEKIIPAQBEHDKYHNVKELVFKFGLPRIV	
	ARQIVTDCKHQKEAIGHQANSDLGTWQMDCTHLEGKIIIVAVHVASGFEAEVIP	
CDS	QETGRTALFLKLAGRWPIHLHTDNGANFASQEVKMVAWAGIEHTFGVPYNQSQ	
	GVVEAMNHLKNQIDIREQANSVETIVLMVHCWMPKRGGIGDMTPAERLINMITT	
CDS	EQEIQQSKSKFKNFVYTYREGDRLQWKGPELLWKGEGAVILKVGDTIDIKVVPRK	
	AKIHKYGGGKEVDSSSHMEDTGEAREVA"	
CDS	4823..5467	
	/gene="vif"	
CDS	4823..5467	
	/gene="vif"	
CDS	/codon_start=1	
	/product="vif protein"	
CDS	/protein_id="AAC57421.1"	
	/db_xref="GI:2108166"	
CDS	/translation="MEEKRWIAVPTWRIPELRLERHSLIKYLKYTKDKLQKVCYVPH	
	FKYGMWAWTCSRVIPLQSGSHLEVQGYHMLTPEKGLSTYAVRIWTYSKNFTWDTVP	
CDS	NADILLHSTYFPCTAGEVRRRAIRGEQLLSCCRFFRAHKYQPSLOYLALKYVSDVR	
	SQENPTWKQWRDRNRRLRMKQNSRGDKQKQKPPKGANFPGLAKVLGILA"	
CDS	5295..5633	
	/gene="vpx"	
CDS	/codon_start=1	
	/product="vpx protein"	
CDS	/protein_id="AAC57422.1"	
	/db_xref="GI:2108167"	
CDS	/translation="MSDPRRIPPGNSGEETIGEAFWLNRTVIEINREAVNHLPREL	
	IFQVQWRSWEYWHDEQGMSPSYVKRYLCLIQKALFMHCCKKGCRCLGEGHAGWRPG	
CDS	PPPPPPGLA"	
	5634..5939	
CDS	/gene="vpr"	
	5634..5939	
CDS	/gene="vpr"	
	/codon_start=1	
CDS	/product="vpr protein"	
	/protein_id="AAC57423.1"	
CDS	/db_xref="GI:2108168"	
	/translation="MEERPPNENQGRBPDEWVVEVEELKEEALKHDFDPRLLLTALG	
CDS	NHIYNRHGDTLEGAGELIRILQRALFMHFRGCTIHSRIGQPGGPNLSAIPPSRML"	
	5948..8580	
CDS	/gene="tat"	
	join(5948..6162,8487..8580)	
CDS	/gene="cat"	
	/codon_start=1	
CDS	/product="tat protein"	
	/protein_id="AAC57424.1"	
CDS	/db_xref="GI:2108169"	
	/translation="MEPYDPRLEPMWKHPGSKPKTACTNICYCKKCFHCOVCFTTKALG	
CDS	ISYKKRQRRAHQNSQTHQASLSKQSSQPRGDPGTGPREKQKKVERETETDPVHQ	
	"	
CDS	6087..8761	
	/gene="rev"	
CDS	join(6087..6162,8487..8761)	
	/gene="rev"	
CDS	/codon_start=1	
	/product="rev protein"	
CDS	/protein_id="AAC57425.1"	
	/db_xref="GI:2108170"	
CDS	/translation="WAGRSGDSDELIKTVRLIKLLYQSNPPSPSLEGTRQARRNRRR	
	WRERQQRISERILGTYLGRSAEPVQLPLPLRLTLUDCNEDCGTSGTQGVSPQI	
CDS	LVESFTVLESQKE"	
	6179..6424	
CDS	/gene="vpu"	
	6179..6424	
CDS	/gene="vpu"	
	/codon_start=1	
CDS	/product="vpu protein"	
	/protein_id="AAC57426.1"	
CDS	/db_xref="GI:2108171"	
	/translation="MQPIQAIVALVVAIIIAIVVMSIVIIIEYRKILRQKIDRLDIR	
CDS	LIERAEDSGNESEGISALVENGVEMGHAPWDVDDL"	
	6339..8948	
CDS	/gene="env"	
	6339..8948	
CDS	/gene="env"	
	/codon_start=1	
CDS	/product="env polyprotein"	
	/protein_id="AAC57427.1"	
CDS	/db_xref="GI:2108172"	
	/translation="MRVREKYQHLRWGRWRTMLGLMLMISATEKLVTVTVYGVVP	
CDS	WREATTTLFCASDAKAYDTEVNVWATHACVPTDPNPQVPLNTEFNMMKNMND	
	QMHEDIISLWDESLKPCVKLTPLCVTLNCTNLTNTKNTNLTSSSWGMEEGEIKNCS	
CDS	FYITTSIRNKVKYALFNRLDVNPVNTSKYRIISCTSVITQACPKVSPQIPPI	
	HYCVPAGFAILKNNKTFNGSGCTNVSTQCTHGRPVVSTQLLNGSLAEBDIVIR	
CDS	SDDFTDNVTIIVQLNSENKTRNTRRELISIGPGAFYARENIIGDIRQACHN	
	ISIRAKWNTLQQIVIKLRVFNKRTAFNQSGGDEFEIWHSCNCGEFPFCYNTAQLF	
CDS	NSTNVAGTNTTEGNDIITLCRIKQIINMMQKVGKMTAPITTCQIRCSNITGLL	
	LTRDGNSTETETEFPRPGGDMRNRSELYKYKVVRIEPIGVAPTRAKRRTVQREK	
CDS	RAGVIGALVFLPGLGAAGSTMGAAVTLTVQARLLSGIIVQQNNLRAIEAQNNMLRL	
	TWGIGKQARVLALERYLQDQLMGICWCSGKLICTTSVPWNVSNKSDVDDIWNMM	
CDS	TWMEWERIDNTDITYDLLESQTOQEKNEKELLELDKWSIWNMFDTIMLWYIRL	
	FMIVGGLIGLRIVAFVADLSIVNRVQGYSPFLSFQTLIPASRGDPREGTEEGEGERD	
CDS	DRSGSPVNGSLALIWDDLRSCLFSYHRLRDLULLIVTRIVELLGRKGWEALKWMNLL	
	"	

gene	QYWSBELKNSAVSLLOQWSYFHEAVQVWRSATETLAGMGDLWETLRRGRMILAI									
	PRRIQGLELTL"									
	8782..9573									
	/gene="nef"									
CDS	8782..9573									
	/gene="nef"									
	/codon_start=1									
	/product="nef protein"									
/protein_id="AAC57428.1"										
/db_xref="GI:2108173"										
/translation="MGGAI SMRRSPSGDLRQLRLRARGETYGRLLGVEEDVGSQSPG										
GLDKGLSLSCGQKYNQGYMTPWNPABEREKLA VRKONMDDIDEDDDLVGVSV										
RPKPLRPMYSKLAIDMSHPFKEKGLGCIYTSARRHLIDILEKEEGIIIPDQDYT										
SGPGIRYPTKTFGWMLKLPVNVNSDEAQEBEHLMPAQTQSQWDDPWGEVLAWKFPDT										
Query Match										
Best Local Similarity 97.9%; Score 1453.8; DB 14; Length 9860;										
Matches 1473; Conservative 0; Mismatches 32; Indels 0; Gaps 0;										
Qy	52	TGGATCTCGGCTTCGAGATCCATGCTCCTCTGGGATATTGATGATCTCTAGTGCTACAGAA	111							
Db	6375	TGGGGGTGGAGATGGGGCACCATGCTCCTCTGGGATGTTGATGATCTCTAGTGCTACAGAA	6434							
Qy	112	AAATTTGGGTCACAGTCTATTATGGGGTACCTCTGTGGAGAGCAACCACTCTA	171							
Db	6435	AAATTTGGGTCACAGTCTATTATGGGGTACCTGTGGAGAGCAACCACTCTA	6494							
Qy	172	TTTTTGTGCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231							
Db	6495	TTTTTGTGCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554							
Qy	232	GCCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAT	291							
Db	6555	GCCTGTGTACCCACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAT	6614							
Qy	292	TTTAAACATGTGGAAAAATAACATGATGATGATGATGATGATGATGATGATGATGATGATG	351							
Db	6615	TTTAAACATGTGGAAAAATAACATGATGATGATGATGATGATGATGATGATGATGATGATG	6674							
Qy	352	GATGAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCAC	411							
Db	6675	GATGAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCAC	6734							
Qy	412	AATTTGAATATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	471							
Db	6735	AATTTGAATATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	6794							
Qy	472	AAAGGAGAAATAAAAAATTTGCTTTCTATATCACCAAGACATAGAAATAAGGTTAAAG	531							
Db	6795	AAAGGAGAAATAAAAAATTTGCTTTCTATATCACCAAGACATAGAAATAAGGTTAAAG	6854							
Qy	532	AAAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCATAAGAAAATCTAATAATACT	591							
Db	6855	AAAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCATAAGAAAATCTAATAATACT	6914							
Qy	592	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCC	651							
Db	6915	AAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCC	6974							
Qy	652	TTTCAGCCCAATTCCTCATACATATTGTGTCGGGCTGGGTTTGGGATGCTTAAAGTGTAAAC	711							
Db	6975	TTTCAGCCCAATTCCTCATACATATTGTGTCGGGCTGGGTTTGGGATGCTTAAAGTGTAAAC	7034							
Qy	712	AATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGACACAGTACAATGTACACAT	771							
Db	7035	AATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGACACAGTACAATGTACACAT	7094							
Qy	772	GGAATTAGGCCAGTGCTGCTCAACTCAACTGCTTTTAAATGGCAGTCTTAGCAGAGAAGAC	831							
Db	7095	GGAATTAGGCCAGTGCTGCTCAACTCAACTGCTTTTAAATGGCAGTCTTAGCAGAGAAGAC	7154							
Qy	832	ATAGTAATTAGATCTGAAAAATTTTCACAGACAATGCTTAAACCATTAATAGTACAGCTAAAT	891							

Db	7155	ATAGTAATTAGATCTGAAGATTTCACAGACAATGTTAAAAACCATTAATAGTACAGCTAAAT 7214
Qy	892	GAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAAGAAGAGGTTATCTATA 951
Db	7215	GAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAAGAAGAGGTTATCTATA 7274
Qy	952	GGACCAGGGAGAGCATTTTATGCAAGAAAGAAACATAATATAGGAGATATTAAGACAAGCAT 1011
Db	7275	GGACCAGGGAGAGCATTTTATGCAAGAAAGAAACATAATATAGGAGATATTAAGACAAGCAT 7334
Qy	1012	TGTAACATTACTAGACGAAAAATGAATAACACTTTTACAACAAGATAGTTATATAAATTAAGA 1071
Db	7335	TGTAACATTACTAGACGAAAAATGAATAACACTTTTACAACAAGATAGTTATATAAATTAAGA 7394
Qy	1072	GAATAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 1131
Db	7395	GAATAATTTAGGAATAAAACAATAGCCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 7454
Qy	1132	GTAATGCACAGTTTTAATTTGTGGAGGGGAATTTCTTCTACTGTATAATACAGCACAACTGTTT 1191
Db	7455	GTAATGCACAGTTTTAATTTGTGGAGGGGAATTTTCTACTGTATAATACAGCACAACTGTTT 7514
Qy	1192	AATAGTACTTGGAAATGTTTACTGGAGGGACAATGSCACTGGAAGGAAATGACATAATCACA 1251
Db	7515	AATAGTACTTGGAAATGTTTACTGGAGGGACAATGSCACTGGAAGGAAATGACATAATCACA 7574
Qy	1252	CTCCAATGCAGATAAAACAAATTAATAATATGTCGCAAGAAAGTAGGAAAAAGCAATGTAT 1311
Db	7575	CTCCAATGCAGATAAAACAAATTAATAATATGTCGCAAGAAAGTAGGAAAAAGCAATGTAT 7634
Qy	1312	CCCCCTCCATCAGAGACAAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACA 1371
Db	7635	CCCCCTCCATCAGAGACAAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACA 7694
Qy	1372	AGAGATGAGAGTAAATAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGAGGAGAT 1431
Db	7695	AGAGATGAGAGTAAATAGTACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGAGGAGAT 7754
Qy	1432	ATGAGGACAAATTTGGAGAAAGTAAATTAATAATATAAAGTAGTAAGAAATTTGAACCAATA 1491
Db	7755	ATGAGGACAAATTTGGAGAAAGTAAATTAATAATATAAAGTAGTAAGAAATTTGAACCAATA 7814
Qy	1492	GGATAGCACCACCCAGGGCAAAGAGAAAGACAGTGCACAAAGAGAAAAAGACCGATCCA 1551
Db	7815	GGATAGCACCACCCAGGGCAAAGAGAAAGACAGTGCACAAAGAGAAAAAGACCGATCCA 7874
Qy	1552	AGAG 1556
Db	7875	ATAGG 7879
RESULT 6		
LOCUS	BD161892	10501 bp DNA linear PAT 17-JAN-2003
DEFINITION	Nonhuman primate model of acquired immunodeficiency syndrome.	
ACCESSION	BD161892	
VERSION	BD161892.1 GI:27867650	
KEYWORDS	JP 2002159296-A/1.	
SOURCE	Simian-Human immunodeficiency virus	
ORGANISM	Simian-Human immunodeficiency virus	
REFERENCE	1 (bases 1 to 10501)	
AUTHORS	Shinohara, K., Sakai, K. and Honda, M.	
TITLE	Nonhuman primate model of acquired immunodeficiency syndrome	
JOURNAL	Patent: JP 2002159296-A 1 04-JUN-2002;	
COMMENT	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH	
	OS Simian-human immunodeficiency virus	
	PN JP 2002159296-A/1	
	PD 04-JUN-2002	
	PF 27-NOV-2000 JP 2000360274	
	PI KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA	

PC C12N15/09,A01K67/027,C12N7/00,C12N7/02,G01N33/15,G01N33/50//
PC G01N33/569,
PC (C12N7/00,C12R1:93),(C12N7/02,C12R1:93),C12N15/00 CC genomic
DNA

CC strain='SHIV-C2/1'

CC derived from SIVmac239

CC 5' long terminal repeat

CC U3 region

CC R region

CC U5 region

CC gag

CC pol

CC vif

CC vpx

CC vpr

CC derived from HIV-1

CC tat

CC rev

CC vpu

CC env

CC derived from SIVmac239

CC nef

CC 3' long terminal repeat

CC U3 region

CC R region

CC U5 region

PH Key Location/Qualifiers

FT source (1)..(10501)

FT source (1)..(6455)

FT LTR (1)..(818)

FT misc_feature (1)..(517)

FT repeat_region (518)..(694)

FT misc_feature (695)..(818)

FT gene (1053)..(2585)

FT gene (<2228)..(5410)

FT gene (5340)..(5984)

FT gene (5812)..(6150)

FT gene (6151)..(6456)

FT source (6456)..(9292)

FT gene (6465)..(9097)

FT gene (6604)..(9278)

FT gene (6696)..(6941)

FT gene (6856)..(9465)

FT source (9293)..(10501)

FT gene (9299)..(10090)

FT LTR (9684)..(10501)

FT misc_feature (9684)..(10200)

FT repeat_region (10201)..(10377)

FT misc_feature (10378)..(10501).

FEATURES

source

1..10501

/organism='Simian-Human immunodeficiency virus'

/mol_type='genomic DNA'

/db_xref='taxon:57667'

ORIGIN

Query Match 65.8%; Score 1453.8; DB 6; Length 10501;

Best Local Similarity 97.9%; Pred. No. 3e-297;

Matches 1473; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAA 111

Db 6892 TGGGGTGGAGATGGGGCCACCATGCTCCTTGGGATTTGATGATCTGTAGTCTACAGNA 6951

QY 112 AAAATTGGGGTCAAGTCTATTATGGGTAACCTGTGTGGAGAGAGCAACCACTCTTA 171

Db 6952 AAAATTGGGGTCAAGTCTATTATGGGTAACCTGTGTGGAGAGAGCAACCACTCTTA 7011

QY 172 TTTTGTGCATCAGATCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231

Db 7012 TTTTGTGCATCAGATCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 7071

QY 232 GCCTGTGTACCCACAGACCCCAACCAAGAAAGTAGTATTGGGAAATGTGACAGAAAT 291

Db 7072 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAT 7131

QY 292 TTTAACATGTGGAAAAATACATCGTAGATCAGATGCATGAGGATATATCAATCAGTTTATGG 351

Db 7132 TTTAACATGTGGAAAAATACATCGTAGATCAGATGCATGAGGATATATCAATCAGTTTATGG 7191

QY 352 GATGAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTCTGTGTACTTTAAATTCGACT 411

Db 7192 GATGAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTCTGTGTACTTTAAATTCGACT 7251

QY 412 AATTGGAATATCACTAAGAATATCTAATCCCACTAGTAGCAGCTGGGGAAATGATGAG 471

Db 7252 AATTGGAATATCACTAAGAATATCTAATCCCACTAGTAGCAGCTGGGGAAATGATGAG 7311

QY 472 AAAGGAGNAATAAAAAATTTGCTCTTCTATATCACCACAAGCATAAGAAATAAGTAAAG 531

Db 7312 GAAGGAGAAATAAAAAATTTGCTCTTCTATATCACCACAAGCATAAGAAATAAGTAAAG 7371

QY 532 AAAGAATATGCACCTTTTAAATAGACTTGTAGTACCCTAGAGAAATACCTAATAATACT 591

Db 7372 AAAGNATATGCACCTTTTAAATAGACTTGTAGTACCCTAGAGAAATACCTAATAATACT 7431

QY 592 AAGTATAGTTAATAAGTTGTAAACACCTCAGTCAATTAACAGGCTGTCCAAAGGTATCC 651

Db 7432 AAGTATAGTTAATAAGTTGTAAACACCTCAGTCAATTAACAGGCTGTCCAAAGGTATCC 7491

QY 652 TTTGAGCAATTTCCCATACATTTTGTGTCCTGCGCTGGTTTGGGATCTCTAAAGTGAAC 711

Db 7492 TTTGAGCAATTTCCCATACATTTTGTGTCCTGCGCTGGTTTGGGATCTCTAAAGTGAAC 7551

QY 712 AATAAGACATTTCAATGGATCAGGACCAATGTGACACAAATGTGACACAGTACAATGTACACAT 771

Db 7552 AATAAGACATTTCAATGGATCAGGACCAATGTGACACAAATGTGACACAGTACAATGTACACAT 7611

QY 772 GGAATTTAGGCCAGTGGTGTCAACTCACTGCTGTTAAATGGGAGTCTAGCAGAAAGAAC 831

Db 7612 GGAATTTAGGCCAGTGGTGTCAACTCACTGCTGTTAAATGGGAGTCTAGCAGAAAGAAC 7671

QY 832 ATAGTAATAGATCTGAAATTTTACACACAAATGTGACACAAATGTGACACAGTACAATGTACACAT 891

Db 7672 ATAGTAATAGATCTGAAATTTTACACACAAATGTGACACAAATGTGACACAGTACAATGTACACAT 7731

QY 892 GAATCTGTAGTAATTTAATTTGTACAGACCCCAACCAATACAAGAGAAAGGTTATCTATA 951

Db 7732 GAATCTGTAGTAATTTAATTTGTACAGACCCCAACCAATACAAGAGAAAGGTTATCTATA 7791

QY 952 GGACGAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAGACACACAT 1011

Db 7792 GGACGAGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAGACACACAT 7851

QY 1012 TGTACATTTAGGAGCAAAATGGAATAACACTTTTACACAGATAGTTTATAAATTAAGA 1071

Db 7852 TGTACATTTAGGAGCAAAATGGAATAACACTTTTACACAGATAGTTTATAAATTAAGA 7911

QY 1072 GAAAAATTTAGGAATAAAAAATAGCCTTTTAAATCAATCCTCAGGAGGGACCCAGAAAT 1131

Db 7912 GAAAAATTTAGGAATAAAAAATAGCCTTTTAAATCAATCCTCAGGAGGGACCCAGAAAT 7971

QY 1132 GTAATGCAAGTTTAAATTTGGAGGGGAAATTTCTTCTACTGTAAATACAGCACAATCTGTT 1191

Db 7972 GTAATGCAAGTTTAAATTTGGAGGGGAAATTTTCTACTGTAAATACAGCACAATCTGTT 8031

QY 1192 AATAGTACTTGGAAATTTTACTGGAGGCAAAATGGCCTGGAAGAAATGACATAATCACA 1251

Db 8032 AATAGTACTTGGAAATTTTCTGGAGGGCAAAATGGCCTGGAAGAAATGACATAATCACA 8091

QY 1252 CTCCAAATGCAGAAATAAAAAATAAATTAATATGTGCGAGAAATAGTAAAGCAATGTAT 1311

Db 8092 CTCCAAATGCAGAAATAAAAAATAAATTAATATGTGCGAGAAATAGTAAAGCAATGTAT 8151

QY 1312 GCCCCTCCCATCAGAGCAAAATTAGATGTTTCATCAATATTTACAGGGCTGCTACTAACA 1371


```
gene
5829..8458
/ gene="tat"
/ join(5829..6042,8370..8458)
/ gene="tat"
/ citation=[2]
/ codon_start=1
/ product="TAT protein"
/ protein_id="AAA81040.1"
/ db_xref="GI:1055034"
/ translation="MEPVNPSLEPWKHPGSPKTCACNYCKKCCFHQCACFITKGLG
ISYGRKRRQRRPPQDSQTHVSLSPSQPRGPTGPKBQKKKVERETDPAVH"
5968..8642
/ gene="rev"
/ join(5968..6042,8370..8642)
/ gene="rev"
/ citation=[2]
/ codon_start=1
/ product="REV protein"
/ protein_id="AAA81041.1"
/ db_xref="GI:1055035"
/ translation="MAGRSGSDDELLKTVLRIKFLVQSPPPSLEGTRQARRRRRW
RERQRQRSISERILGTFLGRFEPVPLPPLPLEKLTLDONEDCGTSGTQGVGSPQL
VESPAILEPGTKE"
6060..6302
/ gene="vpu"
/ gene="vpu"
/ citation=[2]
/ codon_start=1
/ product="VPU protein"
/ protein_id="AAA81042.1"
/ db_xref="GI:1055036"
/ translation="MLSQILAIIVALVVAALIAIIVWSIVIEYRKILRQKIDRLID
RIRREDSGNESEGQDELAALERHLAPWDVDDL"
6223..8784
/ gene="env"
/ gene="env"
/ citation=[2]
/ codon_start=1
/ product="ENV polyprotein precursor"
/ protein_id="AAA81043.2"
/ db_xref="GI:9409798"
/ translation="WRVKEIRKWHQLRGGILLGLMLCSAAKEKTWVTIYGVPMV
REATTLFCASDAKAYDEVNWNWATHACVPTDPNPQEVVLGNVTENFMWKNWVDQ
MHEDIISWDESLKPCVKLPLCVLTNLTNTKNTNPTSSWGMKEGEIKNCSF
YITTSIRNKVKEVALNRLDVPIENTNTKYRLISNTSVITQACPKVSFQPIPIH
YCVPAFAMKLNKNTFNGSGPCNTVSTVQCTHGIRPVVSTQLLINGSLEBIVIRS
ENFTDNATIIIVOLNESVVIINCTRNPNTRRLSLPGRAFVARRNIIGDIRQACHNI
SRKWNLTQIIVIKLREKFNKTIAFNOSSGDPEIIVHSPNCGGEFFYCNTAOLFN
STWNVTGTNGTEGNDITLQCRIKQIINMQKVGKAMAPPIITGQIRCSSNIIGLLL
TRDGNSTETETEIFRPGGDMRDNRSELYKIKVRIEPIGVAPTRAKRRTVQREKR
AVGIGAVFLGLFAGSGTMGAASVTLTQVABLLSLGIVQQNNLLRATIEAQOHLQLT
WVGIKOLQARLALERYLRDQOLMGICWCSGKLICTTSVPWNVSNSKSDVDIWNMT
WMWEREDTNDYTDYLDLEKSOTOEKNKEKELLEKWSLWNWFDITNWLWYIRLF
IMIVGGLIGLIRFAVLSTVNRVQGSPLSFOTLLPASRGPDREPEGTEERGGRRDRD
RSGPLVNGFLALFWDLRNLCLFLYHLRLNLLIVTRIVELLGRGWALKYWNLLQ
YWSQELKNASLSLNLATAIAVABGTRVIRKIVQVACRAIRNIPTRIOGLERALL"
6223..7746
/ gene="env"
/ product="glycoprotein 120"
/ citation=[2]
7747..8781
/ gene="env"
/ product="glycoprotein 41"
/ citation=[2]
8786..9400
/ gene="nef"
/ gene="nef"
/ citation=[2]
1029
/ codon_start=1
```

```
/product="NEF protein"
/protein_id="AAA81044.1"

Query Match      65.6%; Score 1448; DB 14; Length 9713;
Best Local Similarity 98.8%; Pred. No. 5.1e-296;
Matches 1470; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

Qy 72 CATGCTCCTTTGGGATATTGATGATCTGTAGTGGCT---ACAGAAAAATTTGGGTGTCACAGT 128
Db 6273 CTTGCTCCTTTGGGATGTTGATGATCTGTAGTGTGCAAAAGAAAAAGCGTGGGTGACAAAT 6332
Qy 129 CTATTATGGGGTACTGTGTGGAGAGAGAACACACACTCTATTATTGTGTGATCAGATGC 188
Db 6333 CTATTATGGGGTACTGTGTGGAGAGAGAACACACACTCTATTATTGTGTGATCAGATGC 6392
Qy 189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 248
Db 6393 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 6452
Qy 249 CCCCAACCCACAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAA 308
Db 6453 CCCCAACCCACAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAA 6512
Qy 309 TAAACATGGTAGATCAGATGCAATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCC 368
Db 6513 TAAACATGGTAGATCAGATGCAATGAGGATATAATCAGTTTATGGGATGAAAGCCTAAAGCC 6572
Qy 369 ATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTTGCACACTAATTTGAATATCACTAA 428
Db 6573 ATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTTGCACACTAATTTGAATATCACTAA 6632
Qy 429 GAATACTACTAATCCCACTAGTAGCAGCTGGGGGAATGATGAGAGAAAGAGAGAAATAAAAAA 488
Db 6633 GAATACTACTAATCCCACTAGTAGCAGCTGGGGGAATGATGAGAGAAAGAGAGAAATAAAAAA 6692
Qy 489 TTGCTCTTTTATATACCAACAGCATAGAATAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 548
Db 6693 TTGCTCTTTTATATACCAACAGCATAGAATAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 6752
Qy 549 TAATAGACTTGTAGTAGTACCAATAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 608
Db 6753 TAATAGACTTGTAGTAGTACCAATAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 6812
Qy 609 TTGTAACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCCTTTACAGCAATTCCTCAT 668
Db 6813 TTGTAACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCCTTTACAGCAATTCCTCAT 6872
Qy 669 ACATTATTGTGTCGGCGCTGGGTTTGGATGCTTAAAGTGTAAACATAAGACATTCCAATGG 728
Db 6873 ACATTATTGTGTCGGCGCTGGGTTTGGATGCTTAAAGTGTAAACATAAGACATTCCAATGG 6932
Qy 729 ATCAGGACCATGCACAAATGTACACAGTACAAATGTACATGGAATTAGGCCAGTGGT 788
Db 6933 ATCAGGACCATGCACAAATGTACACAGTACAAATGTACATGGAATTAGGCCAGTGGT 6992
Qy 789 GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTAGATCTGA 848
Db 6993 GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTAGATCTGA 7052
Qy 849 AAATTTTCACAGCAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTAGTAAATTA 908
Db 7053 AAATTTTCACAGCAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTAGTAAATTA 7112
Qy 909 TTGTACAGACCCACACAAATACAGAGAGAGGTTTCTTATAGGACACAGGAGAGACATT 968
Db 7113 TTGTACAGACCCACACAAATACAGAGAGAGGTTTCTTATAGGACACAGGAGAGACATT 7172
Qy 969 TTATGCAAGAGAGAAACATAATAGGAGATATAAGACACACATTCATTAATTAGTAGAGC 1028
Db 7173 TTATGCAAGAGAGAAACATAATAGGAGATATAAGACACACATTCATTAATTAGTAGAGC 7232
Qy 1029 AAATGGAAATACACTTTTACACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAATAA 1088
Db 1029 AAATGGAAATACACTTTTACACAGATAGTTATATAAAATTAAGAGAAAAATTTAGGAATAA 1088
```

Db 7233 AAAATGGAAATAACACTTTTACAACAGATAGTTATATAAAATTAAGAGAAAAATTTTAGGAATAA 7292

Qy 1089 AACAAATAGCCTTTAAATCAATCCTCAGGAGGGACCCAGAAAATTTGAATGCAAGTTTAA 1148

Db 7293 AACAAATAGCCTTTAAATCAATCCTCAGGAGGGACCCAGAAAATTTGAATGCAAGTTTAA 7352

Qy 1149 TTGTGGAGGGGAATTTCTTACTACTTAATACAGCAAACTGTTTAATAGTACTTGGAAATGT 1208

Db 7353 TTGTGGAGGGGAATTTTCTACTGTAAATACAGCAAACTGTTTAATAGTACTTGGAAATGT 7412

Qy 1209 TACTCGAGGGACAAATGSCACCTGAAGGAAATGACATAATACACATCCCAATGCGAGAAATAA 1268

Db 7413 TACTCGAGGGACAAATGSCACCTGAAGGAAATGACATAATACACATCCCAATGCGAGAAATAA 7472

Qy 1269 ACAAAATTATAATATGTGGCGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1328

Db 7473 ACAAAATTATAATATGTGGCGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 7532

Qy 1329 ACAAAATTAGATGTTCAATCAATATTTACAGGGCTGCTACTTAACAGAGATGGAGTAAATAG 1388

Db 7533 ACAAAATTAGATGTTCAATCAATATTTACAGGGCTGCTACTTAACAGAGATGGAGTAAATAG 7592

Qy 1389 TACTCAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGAGATATGAGGCAAAATTTGGAG 1448

Db 7593 TACTCAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGAGATATGAGGCAAAATTTGGAG 7652

Qy 1449 AAGTGAATTTATATAATATAAGTAGTAAGAAATTTGAACCAATGAGATAGGAGTAGCACCCACAG 1508

Db 7653 AAGTGAATTTATATAATATAAGTAGTAAGAAATTTGAACCAATGAGATAGGAGTAGCACCCACAG 7712

Qy 1509 GGCAAAGAGAGAAACAGTGCAAGAGAAAAAAGACCGGATCCAAGAAG 1556

Db 7713 GGCAAAGAGAGAAACAGTGCAAGAGAAAAAAGACCGGATCCAAGAAG 7760

RESULT 8

CO753923

LOCUS CO753923 2010 bp DNA linear PAT 01-MAR-2004

DEFINITION Sequence 28 from Patent WO2004001051.

ACCESSION CO753923

VERSION CO753923.1 GI:44845222

KEYWORDS Human immunodeficiency virus 1 (HIV-1)

SOURCE Human immunodeficiency virus 1

ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE 1

AUTHORS Tangy,F., Lorin,C., Mollet,L. and Delebecque,F.

TITLE Recombinant measles viruses expressing epitopes of antigens of rna viruses - use for the preparation of vaccine compositions

JOURNAL Patent: WO 2004001051-A 28 31-DEC-2003; INSTITUT PASTEUR (FR)

FEATURES

Location/Qualifiers

1..2010

/organism="Human immunodeficiency virus 1"

/mol_type="unassigned DNA"

/db_xref="taxon:11676"

ORIGIN

Query Match 60.7%; Score 1339.8; DB 6; Length 2010;

Best Local Similarity 94.2%; Pred. No. 4.8e-273;

Matches 1417; Conservative 0; Mismatches 52; Indels 36; Gaps 1;

Qy 52 TGGATCTCGGCTTCAGATCCATGCTCCTGGGATATTGATGATCTGTAGTGCTACAGAA 111

Db 37 TGGGGGTGGAGATGGGGCACCACCTGCTCTGGGATGTTGATGATCTGTAGTGCTACAGAA 96

Qy 112 AAAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 171

Db 97 AAAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 156

Qy 172 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231

Db 157 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216

Qy 232 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTTGGGAAATGTGACAGAAAAT 291

Db 217 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTTGGGAAATGTGACAGAAAAT 276

Qy 292 TTTAAATCTGTGGAAAAATAACATGTTGATAGATCAGATGCGATGAGGATATATATCATGTTATGG 351

Db 277 TTTAAATCTGTGGAAAAATAACATGTTGATAGATCAGATGCGATGAGGATATATATCATGTTATGG 336

Qy 352 GATGAAGCCCTAAAGCCATGTTAAATTTAACCCCACTCTGTGTGTTTAAATTTGCACT 411

Db 337 GATGAAGCCCTAAAGCCATGTTAAATTTAACCCCACTCTGTGTGTTTAAATTTGCACT 396

Qy 412 AATTGTAATATCACTAAGAAATCTACTAATCCCCTAGTAGCAGCTGGGGAATGATGGAG 471

Db 397 AATTGTAATATCACTAAGAAATCTACTAATCCCCTAGTAGCAGCTGGGGAATGATGGAG 456

Qy 472 AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATTAAGAAATAAGGTAAG 531

Db 457 GAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATTAAGAAATAAGGTAAG 516

Qy 532 AAAGAATATGCACTTTTAAATAGACTTGATCTAGTACCATAAGAAAAATCTAAATAACT 591

Db 517 AAAGATATGCACTTTTAAATAGACTTGATCTAGTACCATAAGAAAAATCTAGTAACT 576

Qy 592 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTATCC 651

Db 577 AAGTATAGGTTAATAAGTTGTAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTATCC 636

Qy 652 TTTGAGCCAAATCCCATACATATTGTCGCCGCTGGGTTTGGATGCTTAAAGTGTAAAC 711

Db 637 TTTGAGCCAAATCCCATACATATTGTCGCCGCTGGGTTTGGATGCTTAAAGTGTAAAC 696

Qy 712 AATAAGCATTCAATGGATCAGGACCATGCAACAAATGTCAGCACAGTACAATGTACACAT 771

Db 697 AATAAGCATTCAATGGATCAGGACCATGCAACAAATGTCAGCACAGTACAATGTACACAT 756

Qy 772 GGAATTAGGCGAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 831

Db 757 GGAATTAGGCGAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 816

Qy 832 ATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTTAAACCAATATAGTACAGTAAAT 891

Db 817 ATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTTAAACCAATATAGTACAGTAAAT 876

Qy 892 GAATCTGTAGTAATTAATTGTACAAGCCCAACCAATACAAAGAGAGGTTATCTATA 951

Db 877 GAATCTGTAGTAATTAATTGTACAAGCCCAACCAATACAAAGAGGTTATCTATA 917

Qy 952 GGACCAGGGAGAGCATTTTATGCAAGAGAAACATAATAGGAGATATAGAGCAAGCACAT 1011

Db 918 -----TGCAGAAATTGGATAATGGGCAAGTCTGCAAGACAAGCACAT 960

Qy 1012 TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTAAACAGATAGTTATAAAATTAAGA 1071

Db 961 TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTAAACAGATAGTTATAAAATTAAGA 1020

Qy 1072 GAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 1131

Db 1021 GAAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAAT 1080

Qy 1132 GTAATGCAAGTAAATTTGAGGGGAAATTTCTTACTGTATAACAGCAACTGTTT 1191

Db 1081 GTAATGCAAGTAAATTTGAGGGGAAATTTCTTACTGTATAACAGCAACTGTTT 1140

Qy 1192 AATAGTACTTGGAAATGTTA CTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACA 1251

Db 1141 AATAGTACTTGGAAATGTTGCTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACA 1200

Qy 1252 CTCCAATGCAGATAAACAATAATTAATATGTCGAGAGAAATAGGAAAGGCAATGAT 1311

Db 1201 CTCCAATGCAGATAAACAATAATTAATATGTCGAGAGAAATAGGAAAGGCAATGAT 1260

QY	1141	AGTTTAAATTTGGAGGGGAATCTTCTACTATAACAGCACAACTCTTTAATAGTACT	1200
Db	1117		1176
QY	1201	TGGAATGTTACTGGAGGACAAATGGCACTGAAGGAAATGACATATACAACTCCAATGCG	1260
Db	1177	TGGAATGTTACTGAAGGTCAAATAAAGCTGAAGGAAATATACAACTCACACTCCCATGCG	1236
QY	1261	AGAATAAACAAATTTATAATATATGGCAGAAAGTAGGAAAGCAATGTATGCCCTCC	1320
Db	1237	AGATAAACAAATTTATAACATGTGGCAGGAAGTAGGAAAGCAATGTATGCCCTCC	1296
QY	1321	ATCAGAGACAAATTTAGATGTTTCATCAATATTACAGGCGTCTACTAACAGAGATGGA	1380
Db	1297	ATCAGAGACAAATTTAGATGTTTCATCAATATTACAGGCGTCTATTAAACAGAGATGGT	1356
QY	1381	GGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC	1440
Db	1357	GGTAA--TAACGAGAGCGAGACCGAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC	1413
QY	1441	AATTCGAGAAGTGAATTTATAAATATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA	1500
Db	1414	AATTCGAGAAGTGAATTTATAAATATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA	1473
QY	1501	CCCACAGGCGAAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1556
Db	1474	CCCACAGGCGAAGAGAGAGAGTGGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1529
RESULT 11			
AY426111		2568 bp DNA linear VRL 28-JUN-2004	
LOCUS		HIV-1 clone Bal-1p isolate Bal from USA envelope glycoprotein (env)	
DEFINITION		gene, complete cds.	
ACCESSION	AY426111		
VERSION	AY426111.1	GI:37962967	
KEYWORDS			
SOURCE		Human immunodeficiency virus 1 (HIV-1)	
ORGANISM		Viruses; Retroviridae; Retroviridae; Lentivirus; Primate	
REFERENCE		1 (bases 1 to 2568)	
AUTHORS		Pastore,C., Ramos,A. and Mosier,D.E.	
TITLE		Intrinsic Obstacles to Human Immunodeficiency Virus Type 1	
JOURNAL		Coreceptor Switching	
PUBMED		J. Virol. 78 (14), 7565-7574 (2004)	
AUTHORS		15220431	
TITLE		2 (bases 1 to 2568)	
JOURNAL		Pastore,C., Ramos,A. and Mosier,D.E.	
PUBMED		Direct Submission	
AUTHORS		Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research	
TITLE		Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA	
JOURNAL		Location/Qualifiers	
FEATURES		1..2568	
source		/organism="Human immunodeficiency virus 1"	
		/proviral	
		/mol_type="genomic DNA"	
		/isolate="Bal"	
		multiple passages in CXCR4 expressing cells"	
		/db_xref="taxon:11676"	
		/clone="Bal-1p"	
		/country="USA"	
gene		1..2568	
CDS		/gene="env"	
		1..2568	
		/gene="env"	
		/codon_start=1	
		/product="envelope glycoprotein"	
		/protein_id="AA05835.1"	
		/db_xref="GI:37962968"	
		/translation="NRVKEKYQHLWRGWRGWTMLGLMICSATEKLWVTYYGVVP	

WKEATTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVELENVTENFNNWKNMVE
OMHED11SLNDOSLPCVKGLPCLVTLNCTDLRNTTNDNTNTSSRMMGGBEMKPI
CSFKITINRGKQKEVALFYKLDIVPIDNNNNRYRLISCNVTSTVITQACPKISPEPI
PIHYCAPAGFAILKCKDKKNGKPCSNVSTVQCTHGRPVVSTQLLNGSLABEUV
IRSNFADNKTIIIVOLNESVEINCTRNPNNTKSIHIGPRALYITGKIIGDIRQAH
CNLSRAKNDTLANKIVIKLEQFNKTIIVFKHSSGGDEIVTHSPNCGGEFFYCNSTQ
LFTNWTNVTESNNVTNNITLPIKIQIIMNKVKGRAMYAPP IRQOIFCNSNITG
LLLPDGGPDKNTKTEVPRPGGDMRDNRSELYKVKVIEPLGVAPTKAKRRVVORE
KRAVIGAVLLGFLGAAGSTMGASMTLTVOARLLLSGIVQOQNNLLRAIEAOHLLQ
LTVWGIKOLQARVLAVERYLDRDQQLGIGWCSGKLICTTAVFWNASKNLSKILWIK
MTNWEIRENNYTSIIYSLEESQOQEKNEQELLEDKWSLWNNWSEITTEWLYIK
IFIMIGGLIGLIRIVFVSLIMNRVQYSPSLFQTHLPVSGRDPDRPGIIEBEGED
RDRGRVLNGSLALIWDLRSLCLFSYHRLRLDLLIVTRIVELLGRGWEALKYWNAL
LQYWSQLKNSAVSLNATAIAVAEGTDRVIEVVQGCACRAIRHIPRRIRQGLERILL"

ORIGIN

Query Match	56.3%	Score 1242.6;	DB 14;	Length 2568;
Best Local Similarity	89.9%	Pred. No. 1.7e-252;		
Mismatches	1358;	Conservative	0;	Mismatches 144;
Indels	9;	Gaps	2;	
QY	52	TGGATCTCGGCTTCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAA	111	
Db	37	TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTGTACAGAA	96	
QY	112	AAATTTGGGGTCACAGTCTATTATGGGGTACTCTGTGGAGAGAGCAACACCACCTCTA	171	
Db	97	AAATTTGGGGTCACAGTCTATTATGGGGTACTCTGTGGAGAGAGCAACACCACCTCTA	156	
QY	172	TTTTGTGCATCAGATGCTTAAAGCCTATGATACAGAGGTACATATATGTTTGGGCCACAT	231	
Db	157	TTTTGTGCATCAGATGCTTAAAGCATATGATACAGAGGTACATATATGTTTGGGCCACAT	216	
QY	232	GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGCACAGAAAT	291	
Db	217	GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGAATTTGGAATAATGTGCACAGAAAT	276	
QY	292	TTTAAACATGTGGAAAAATAACATGGTAGATCAGATGATGAGGATATATCAAGTTTATGG	351	
Db	277	TTTAAACATGTGGAAAAATAACATGGTAGACAGATGATGAGGATATATCAAGTTTATGG	336	
QY	352	GATGAAAGCCTTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTTACTTTAAATTCGACT	411	
Db	337	GATCAAGCCTTAAAGCCATGTGTAAATTAACCTCCACTCTGTGTTTACTTTAAATTCGACT	396	
QY	412	AATTTGAATATCACTA-----AGNATCTACTAATCCACTAGTAGCAGCTGGGGAATG	465	
Db	397	GATTTGAGGAATATCTACTTAATGGGAATGACATATACCTAGTAGTAGCAGGGAATG	456	
QY	466	ATGGAGAAAGGAGAAATAAAAAATTTGCTTTCTATATACCAACAGCATAGAAATTAAG	525	
Db	457	ATGGGGGAGAGAGAAATAAAAAATTTGCTTTCAAAATCACCACAAACATAAGAGGTAAAG	516	
QY	526	GTAAGAAGAATAATGCACTTTTAAATAGACTGTATGATAGTAGTACCAATAGAAAATCTAAT	585	
Db	517	GTGCAGAAAATAATGCACTTTTAAATAGACTGTATGATAGTAGTACCAATAGAAAATCTAAT	576	
QY	586	AATACTAAGTATAGTTAATAGTTGTAAACCTCAGCTCATTACACAGCCCTGTCCCAAG	645	
Db	577	AATACTAAGTATAGTTAATAGTTGTAAACCTCAGCTCATTACACAGCCCTGTCCCAAG	636	
QY	646	GTATCTTTTACGCCAAATTTCCCATACATATTATGTGTCCCGGCTGGGTTTGCAGTCTAAG	705	
Db	637	ATATCTTTTACGCCAAATTTCCCATACATATTATGTGTCCCGGCTGGGTTTGCAGTCTAAG	696	
QY	706	TGTAAACAATAAGACATTTCAATGGATCAGGACCATGCAAAATGTGCAGCACAGTACAAATGT	765	
Db	697	TGTAAACAATAAGACATTTCAATGGAAAGGACCATGTTCAAAATGTGCAGCACAGTACAAATGT	756	
QY	766	ACACATGGAATTTAGGCCAGTGTGTCAACTCACTCACTGTTTAAATGGCAGTCTAGCAGAA	825	
Db	757	ACACATGGAATTTAGGCCAGTGTGTCAACTCACTCACTGTTTAAATGGCAGTCTAGCAGAA	816	
QY	826	GAAGACATAGTAATTTAGATCTGAAAAATTTTACAGACAATAGTCTAAAAACCATATAATAGTACAG	885	

MTWWEWDREINNTYSIIYSLIEESQOQKNEQELLEDKWSLWNNFEITELWLYIK
IFIMITGLGILRIVFSVLIMNRVQYSPISFOTHPASPRGDPGGTIEEGERD
LDYSGRLVNSGALIWDDLRSLCULFSYHRRLDVLIVTRIVELLGRGWEALKYWNL
LOYWSELKNSAVSLINATAVGAETDRVIEVQCAIRIHRIPRIRQSLERILLI
R

ORIGIN

Query Match 56.1%; Score 1237.8; DB 14; Length 2568;

Query Match	89.7%	Pred. NO. 1.8e-251;	Indels	9;	Gaps	2;
Best Local Similarity	89.7%		Mismatches	147;		
Matches 1355;	Conservative	0;				

[illegible]

		/db_xref="taxon:11676"				
		/clone="BaL-1B"				
		/country="USA"				
gene	CDS	1..2568				
		/gene="env"				
		1..2568				
		/gene="env"				
/codon_start=1						
/product="envelope glycoprotein"						
/protein_id="AAR05837.1"						
/db_xref="GI:37962972"						
/translation="MRVKSEKIQHLRWGRWGTMLGLMICSATEKLWTVYGVVPV WKEATTLPCASDAKAYDEVHNVWATHACVPTDPNPQOELENVTFENFWKNVVE QMHEDIISLWQSLKPCVKLPTCLVTLNCTDLRNTNGDNTTSSSEMGGMGEMKN CSFKITINIRWQKKEYALFYKLDIVPIDNNNNRRLISQNTSVITQACPKISPEPI PIHYCAPAGFALCKDKFKNGKPCSNVSTVQCTHGRIPVYSTQLLNGSLABEEVV IRSENFADNAKIIIVQLNESVIEINCRNNNTKRSIHIGPGRKIYTTGKIIGDIRQAH CNLSRAKNDTLNKIVIKLRQFGNKTIIVFKHSSGGDEIIVTHSPNCGEFPYCNSTC LPNSTWNVTEESNTVENNTITLPCRILQIINMQKVGKRAMYAPPIRQIRCSNITG LLLTDRGGPEDNKTEVFRPGGDMRDNSELYIKYKVKIPLGVAFTPAKRRVVQRE KRAVGIVALLGFAGAGSTWGAASMTLTVQARLSLSGIVQOQNNLLRAIEAQOHLLO LTVWIKQIQLARLAVLRDQQLIGWCGSGKLICTTAVPMNASNKSINKIWN MTWMDREINNYTSIIYSLIEESONQOEKNEOELLELDKWSLWNNPFIETELWYIK IFMTIGLIGLRIVFVSLIMNRVQGYPLSPOTHLPASRGDPGPIBEEGGERD RDRGRUWNGSLALIWDLRSICLPSYHRLRDLILLIIVRIVELLGRGWEALKYWNIL LQYWSQELXNSAVSLNATAIAVAEGTDURVIEVVOGACRAIRHPRIRQGLERILL"						
		ORIGIN				
		Query Match		56.1%; Score 1237.8; DB 14; Length 2568;		
		Best Local Similarity		89.7%; Pred. No. 1.8e-251;		
		Matches 1355; Conservative		0; Mismatches 147; Indels 9; Gaps 2;		
Qy	52	TTGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111			
Db	37	TGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAA	96			
Qy	112	AAATTTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA	171			
Db	97	AAATTTGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTA	156			
Qy	172	TTTTTTGTCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231			
Db	157	TTTTTTGTCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAT	216			
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAAT	291			
Db	217	GCCTGTGTACCCACAGACCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAAT	276			
Qy	292	TTTAAACATGTGGAAAAATAACATGTGTAGATCGATGAGGATATTAATCAGTTTATGG	351			
Db	277	TTTAAACATGTGGAAAAATAACATGTGTAGATCGATGAGGATATTAATCAGTTTATGG	336			
Qy	352	GATGAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	411			
Db	337	GATGAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACT	396			
Qy	412	AATTTGAATATCACTA-----AGAAATACATACTAATCCCACTAGTAGCAGCTGGGGAATG	465			
Db	397	GATTTGAGGNATACTACTAATGGGAATGACACTAATACCACTAGTAGTAGCAGGGAATG	456			
Qy	466	ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTCTATATCACCAAGCATTAAGAAATTAAG	525			
Db	457	ATGGGGGAGAGAAATGAAAAATTTGCTTCTTCAAAATCACCAAAACATTAAGAGGTAAAG	516			
Qy	526	GTAAAGAAAGATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAATACTAAT	585			
Db	517	GTGCAAGAAAGATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAATACTAAT	576			
Qy	586	AATACTAGTATAGTAAATAGTTGTAAACACCTCAGTCATTACACAGGCTGTCCCAAAG	645			
Db	577	AATATAAGTATAGTAAATAGTTGTAAACACCTCAGTCATTACACAGGCTGTCCCAAAG	636			
Qy	646	GTATCCTTTACGCCAAATTTCCCATACATTTATGTGTCCCGGCTGGGTTTGGCATGCTAAAG	705			
Db	637	ATATCTCTTTGAGGCAATTTCCCATACATTTATGTGTCCCGGCTGGTTTTGGCATGCTTAAAG	696			
Qy	706	TGTAACAATTAAGACATTTCAATGATCAGGACCAATGCACAAATGCTCAGCACAGTACAAATGT	765			
Db	697	TGTAAGAATTAAGAGTTTCAATGGAAAAGGACCAATGTTTCAATGTCAGCACAGTACAAATGT	756			
Qy	766	ACACATGGAATTAGGCAGGTGTTGTCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAA	825			
Db	757	ACATATGGGATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAA	816			
Qy	826	GAAGACATAGTAAATTAGATCTGAAAATTTTCACAGACAAATGCTTAAAAACCATTAATAGTACAG	885			
Db	817	GAAGAGGTAGTAAATTAGATCCGAAAAATTCGCGGCACAATGCTTAAAAACCATTAATAGTACAG	876			
Qy	886	CTAAATGAATCTGTAGTAAATTAATTTGTCACAGACCCCAACCAACATACAGAGAGAAGGTTA	945			
Db	877	CTGAATGAATCTGTAGAAATTAATTTGTCACAGACCCCAACCAACATACAGAAAAAGTATA	936			
Qy	946	TCATATAGGACACGGGAGAGCATTTTATGCAAGAAGAAAAATATATAGGAGATATAAGACAA	1005			
Db	937	CATATAGGACACGGCAGAAAAATATATATACACAGGAAAAATATATAGGAGATATAAGACAA	996			
Qy	1006	GCACATTGTAACATTAGTAGAGCAAAATGGAATAACTTTTCAACACAGATAGTTTATAAAA	1065			
Db	997	GCACATTGTAACCTTAGTAGAGCAAAATGGAATGACACTTTTAAATAGATAGTTTATAAAA	1055			
Qy	1066	TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTTAATCAATCTCTCAGAGGGGACCCA	1125			
Db	1057	TTAAGAGAACAAATTTGGGAATAAAAACAATAGTCTTTTAAGCAITTTCTCTCAGAGGGGACCCA	1115			
Qy	1126	GAAATTTGTAATGCACAGTTTTTAATTTGGGAGGGAATTTCTTCTACTGTAATACAGCACAA	1185			
Db	1117	GAAATTTGTGACGACACAGTTTTTAATTTGGGAGGGAATTTTCTTCTACTGTAATCAACACAA	1175			
Qy	1186	CTGTTTAAATAGTACTTTGGAAATGTTACTGGAGGACAAATGGCACTCGAAGAAATGCATA	1245			
Db	1177	CTGTTTAAATAGTACTTTGGAAATGTTACTGAGAGGTCAATAACACTGTGAAAAATAACACA	1235			
Qy	1246	ATCACACTCCAATGCGAGATAAAACAAAATTTATAAATATGTGGCAGAAAAGTAGGAAAAGCA	1305			
Db	1237	ATCACACTCCCATGCGAGATAAAACAAAATTTATAAACATGTGGCAGAAAAGTAGGAAAGCA	1295			
Qy	1306	ATGTATGCCCTCCCATGACAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTA	1365			
Db	1297	ATGTATGCCCTCCCATGACAGGACAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTA	1355			
Qy	1366	CTAACAGAGATGGAGTAACTAGTACTGAGACTGAGACTGAGATCTTCAGACTCTGGAGCA	1425			
Db	1357	TTAACAGAGATGGTGG---TCCAGAGGACCAACAGACCGAGGTCTTCAGACTCTGGAGCA	1415			
Qy	1426	GGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAAAATATAAAGTAGTAAAGAAATTGAA	1485			
Db	1414	GGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAAATATAAAGTAGTAAAAATTGAA	1475			
Qy	1486	CCAATAGGAGTAGCACCCACCGGCAAAAGAGAGAACAGTGCACAAAGAAAAAGACCG	1545			
Db	1474	CCATTAGGAGTAGCACCCCAAGGCAAGAGAGAGTGTGTCAGAGAGAAAAAAGAGCA	1535			
Qy	1546	GATCCCAAGAG 1556				
Db	1534	GTGGGAATAGG 1544				

Search completed: November 12, 2004, 07:54:29

Job time : 6350.94 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 11, 2004, 15:28:44 ; Search time 724.277 Seconds
(without alignments)
16003.167 Million cell updates/sec

Title: US-09-687-864A-13
Perfect score: 2208
Sequence: 1 aagcttgccgcatctgtta.....aactcgagtgataatctaga 2208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2208	100.0	2209	4	AAF82929	Aaf82929 HIV-1 gp1
2	2152.8	97.5	2252	4	AAF82928	Aaf82928 HIV-1 gp1
3	1866	84.5	2070	4	AAF82930	Aaf82930 HIV-1 gp1
4	1838	83.2	2028	4	AAF82931	Aaf82931 HIV-1 gp1
5	1453.8	65.8	2046	12	ACA63265	ACA63265 HIV-1 imm
6	1453.8	65.8	2610	12	ACA63266	ACA63266 HIV-1 imm
7	1448	65.6	2051	10	AAL56171	Aal56171 HIV trunct
8	1448	65.6	2562	10	AAL56170	Aal56170 Human imm
9	1339.8	60.7	2010	12	ACA63267	ACA63267 HIV-1 imm
10	1339.8	60.7	2574	12	ACA63268	ACA63268 HIV-1 imm
11	1225.8	55.5	3806	2	AAX04767	Aax04767 Env gene
12	1225.8	55.5	3807	2	AAT58551	Aat58551 Human imm
13	1222.2	55.4	9540	12	AD052562	Ado52562 Human imm
14	1222.2	55.4	9540	12	ADP20074	Adp20074 Human imm
15	1219	55.2	3807	2	AAQ14753	Aaq14753 HIV-1 BA-
16	1207.8	54.7	2553	1	Aan80949	Aan80949 HIV prote
17	1199.2	54.3	2612	12	ADJ92821	Adj92821 Human imm
18	1199.2	54.3	8896	12	ADP20082	Adp20082 Human imm
19	1197	54.2	1512	5	Aaf87100	Aaf87100 HIV-1 gp1
20	1179.8	53.4	1422	12	ADP74731	Adp74731 HIV-1 iso
c 21	1174.2	53.2	3808	2	AAV58244	Avs58244 Insert re

c	22	1174.2	53.2	3808	2	AAV60252	Aav60252 Insert re
	23	1173	53.1	2553	2	AAQ76018	Aaq76018 DNA encod
	24	1172.2	53.1	2571	2	AAT09010	Aat09010 HIV-1 str
	25	1172.2	53.1	2571	2	AAZ08741	Aaz08741 HIV-1 MN
	26	1172.2	53.1	2571	3	AAZ08741	Aaz08741 HIV-1 MN
	27	1172.2	53.1	2571	3	AAZ08741	Aaz08741 HIV-1 MN
	28	1172.2	53.1	2571	4	AAZ08741	Aaz08741 HIV-1 MN
	29	1172.2	53.1	2571	5	AAZ08741	Aaz08741 HIV-1 MN
	30	1172.2	53.1	2571	8	ABX14499	Abx14499 Human imm
	31	1172.2	53.1	2571	9	ADA50072	Ada50072 Human imm
	32	1172.2	53.1	2571	10	ADG92081	Adg92081 HIV rev/e
	33	1172.2	53.1	2571	12	ADG92081	Adg92081 HIV rev/e
	34	1172.2	53.1	6474	2	AAQ40300	Aaq40300 Sequence
	35	1172.2	53.1	6474	3	AAZ08741	Aaz08741 HIV-1 MN
	36	1172.2	53.1	6926	4	AAQ40281	Aaq40281 Sequence
	37	1172.2	53.1	6926	3	AAZ08741	Aaz08741 HIV-1 MN
	38	1172.2	53.1	6926	4	AAZ08741	Aaz08741 HIV-1 MN
	39	1172.2	53.1	6926	4	AAZ08741	Aaz08741 HIV-1 MN
	40	1172.2	53.1	9738	2	AAZ08741	Aaz08741 HIV-1 MN
	41	1172.2	53.1	9745	2	AAZ08741	Aaz08741 HIV-1 MN
	42	1172.2	53.1	9746	2	AAQ14752	Aaq14752 HIV-1 (MN-
	43	1172.2	53.1	9746	2	AAZ08741	Aaz08741 HIV-1 MN
	44	1169.8	53.0	2574	2	AAQ76019	Aaq76019 DNA encod
	45	1168.8	52.9	4527	2	AAZ08741	Aaz08741 HIV-1 MN

ALIGNMENTS

RESULT 1

AAF82929

ID AAF82929 standard; cDNA; 2209 BP.

XX AAF82929;

XX 11-SEP-2003 (revised)

DT 29-JUN-2001 (first entry)

XX HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.

XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;

XX acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;

XX HIV-1; gp120; human; CD154; fusion protein; ss.

XX Human immunodeficiency virus 1.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 13..2209

FT sig_peptide /*tag= a

FT /*tag= b

FT /*tag= c

FT /*tag= d

FT /*tag= e

FT /*tag= f

FT /*tag= g

FT /*tag= h

FT /*tag= i

FT /*tag= j

FT /*tag= k

FT /*tag= l

FT /*tag= m

FT /*tag= n

FT /*tag= o

FT /*tag= p

FT /*tag= q

FT /*tag= r

FT /*tag= s

FT /*tag= t

FT /*tag= u

FT /*tag= v

FT /*tag= w

FT /*tag= x

FT /*tag= y

FT /*tag= z

FT /*tag= AA

FT /*tag= AB

FT /*tag= AC

FT /*tag= AD

FT /*tag= AE

FT /*tag= AF

FT /*tag= AG

FT /*tag= AH

FT /*tag= AI

FT /*tag= AJ

FT /*tag= AK

FT /*tag= AL

FT /*tag= AM

FT /*tag= AN

FT /*tag= AO

FT /*tag= AP

FT /*tag= AQ

FT /*tag= AR

FT /*tag= AS

FT /*tag= AT

FT /*tag= AU

FT /*tag= AV

FT /*tag= AW

FT /*tag= AX

FT /*tag= AY

FT /*tag= AZ

FT /*tag= BA

FT /*tag= BB

FT /*tag= BC

FT /*tag= BD

FT /*tag= BE

FT /*tag= BF

FT /*tag= BG

FT /*tag= BH

FT /*tag= BI

FT /*tag= BJ

FT /*tag= BK

FT /*tag= BL

FT /*tag= BM

FT /*tag= BN

FT /*tag= BO

FT /*tag= BP

FT /*tag= BQ

FT /*tag= BR

FT /*tag= BS

FT /*tag= BT

FT /*tag= BU

FT /*tag= BV

FT /*tag= BW

FT /*tag= BX

FT /*tag= BY

FT /*tag= BZ

FT /*tag= CA

FT /*tag= CB

FT /*tag= CC

FT /*tag= CD

FT /*tag= CE

FT /*tag= CF

FT /*tag= CG

FT /*tag= CH

FT /*tag= CI

FT /*tag= CJ

FT /*tag= CK

FT /*tag= CL

FT /*tag= CM

FT /*tag= CN

FT /*tag= CO

FT /*tag= CP

FT /*tag= CQ

FT /*tag= CR

FT /*tag= CS

FT /*tag= CT

FT /*tag= CU

FT /*tag= CV

FT /*tag= CW

FT /*tag= CX

FT /*tag= CY

FT /*tag= CZ

FT /*tag= DA

FT /*tag= DB

FT /*tag= DC

FT /*tag= DD

FT /*tag= DE

FT /*tag= DF

FT /*tag= DG

FT /*tag= DH

FT /*tag= DI

FT /*tag= DJ

FT /*tag= DK

FT /*tag= DL

FT /*tag= DM

FT /*tag= DN

FT /*tag= DO

FT /*tag= DP

FT /*tag= DQ

FT /*tag= DR

FT /*tag= DS

FT /*tag= DT

FT /*tag= DU

FT /*tag= DV

FT /*tag= DW

FT /*tag= DX

FT /*tag= DY

FT /*tag= DZ

FT /*tag= EA

FT /*tag= EB

FT /*tag= EC

FT /*tag= ED

FT /*tag= EE

FT /*tag= EF

FT /*tag= EG

FT /*tag= EH

FT /*tag= EI

FT /*tag= EJ

FT /*tag= EK

FT /*tag= EL

FT /*tag= EM

FT /*tag= EN

FT /*tag= EO

FT /*tag= EP

FT /*tag= EQ

FT /*tag= ER

FT /*tag= ES

FT /*tag= ET

FT /*tag= EU

FT /*tag= EV

FT /*tag= EW

FT /*tag= EX

FT /*tag= EY

FT /*tag= EZ

FT /*tag= FA

FT /*tag= FB

FT /*tag= FC

FT /*tag= FD

FT /*tag= FE

FT /*tag= FF

FT /*tag= FG

FT /*tag= FH

FT /*tag= FI

FT /*tag= FJ

FT /*tag= FK

FT /*tag= FL

FT /*tag= FM

FT /*tag= FN

FT /*tag= FO

FT /*tag= FP

FT /*tag= FQ

FT /*tag= FR

FT /*tag= FS

FT /*tag= FT

FT /*tag= FU

FT /*tag= FV

FT /*tag= FW

FT /*tag= FX

FT /*tag= FY

FT /*tag= FZ

FT /*tag= GA

FT /*tag= GB

FT /*tag= GC

FT /*tag= GD

FT /*tag= GE

FT /*tag= GF

FT /*tag= GG

FT /*tag= GH

FT /*tag= GI

FT /*tag= GJ

FT /*tag= GK

Db 1741 TTTGAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCACATGTCTAAGTGAGGCC 1800
Qy 1801 ACCAGTAAACACACTCTGTGTTACAGTGGGCTGAAAAAGGATGACTACACCATGAGCAAC 1860
Db 1801 AGCAGTAAACACACTCTGTGTTACAGTGGGCTGAAAAAGGATGACTACACCATGAGCAAC 1860
Qy 1861 AACTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAGGACTCTATTAT 1920
Db 1861 AACTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAGGACTCTATTAT 1920
Qy 1921 ATCTATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCATTATTA 1980
Db 1921 ATCTATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCATTATTA 1980
Qy 1981 GCCAGCTCTGCTTAAAGTCCCGGTAGATTGCGAGAGAACTTACTCAGAGCTGCAAAAT 2040
Db 1981 GCCAGCTCTGCTTAAAGTCCCGGTAGATTGCGAGAGAACTTACTCAGAGCTGCAAAAT 2040
Qy 2041 ACCCAGAGTTCGCGCAAACTTGGCGGCAACAATCCATTCATCTTGGGAGGAGTATTGAA 2100
Db 2041 ACCCAGAGTTCGCGCAAACTTGGCGGCAACAATCCATTCATCTTGGGAGGAGTATTGAA 2100
Qy 2101 TTGCAACAGAGTCTTGGGTGTTCTCAATGTGACTGATCCAAAGCAAGTGAGCCATGCG 2160
Db 2101 TTGCAACAGAGTCTTGGGTGTTCTCAATGTGACTGATCCAAAGCAAGTGAGCCATGCG 2160
Qy 2161 ACTGGCTTCACGCTCTTTGGCTTACTCAAACCTCGAGTGATATCTAGA 2208
Db 2161 ACTGGCTTCACGCTCTTTGGCTTACTCAAACCTCGAGTGATATCTAGA 2208

RESULT 2

AAF82928
ID AAF82928 standard; cdna; 2252 BP.
XX AAF82928;
AC AAF82928;
XX AAF82928;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX HIV-1 gp120-human CD154 long form extracellular domain fusion cdna.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 13..2252
FT sig_peptide 13..72
FT FT /tag= a
FT FT /tag= b
FT FT /note= "synthetic secretory signal peptide"
FT FT 73..1542
FT FT /tag= c
FT FT /note= "HIV-1 gp120 domain coding sequence"
FT FT 1543..1593
FT FT /tag= d
FT FT /note= "[Gly4Ser]3 linker coding sequence"
FT FT 1594..2252
FT FT /tag= e
FT FT /note= "human CD154 long form extracellular domain coding sequence"
XX WO200126608-A2.
PN 19-APR-2001.
XX 13-OCT-2000; 2000WO-US028414.
XX 14-OCT-1999; 99US-0159690P.

XX (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
XX
PI Ledbetter JA, Hayden-Ledbetter MS;
XX
DR WPI; 2001-281790/29.
DR P-PSDB; AAB62333.
XX
PT DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
PS Example 1; Fig 3A; 55pp; English.
XX
CC The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC long form extracellular domain fusion protein linked by (Gly4Ser)3
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;
Query Match 97.5%; Score 2152.8; DB 4; Length 2252;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2206; Conservative 0; Mismatches 2; Indels 42; Gaps 1;
Qy 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCCATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGG 120
Db 61 GCTTCGAGATCTATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGG 120
Qy 121 GTCACAGTCTATTATTTGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA 180
Db 121 GTCACAGTCTATTATTTGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGTGCA 180
Qy 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTTGGGCCACACATGCTGTGTA 240
Db 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTTGGGCCACACATGCTGTGTA 240
Qy 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATG 300
Db 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATG 300
Qy 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Db 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Qy 361 CTAAGCCATGTTAAATTAACCCCACTCTGTGTACTTTTAAATGACATTAATTGAT 420
Db 361 CTAAGCCATGTTAAATTAACCCCACTCTGTGTACTTTTAAATGACATTAATTGAT 420
Qy 421 ATCACTAAGATAGTACTACTTAATCCCACTAGTAGCAGCTGGGAAATGATGAGAGAGAGAA 480
Db 421 ATCACTAAGATAGTACTACTTAATCCCACTAGTAGCAGCTGGGAAATGATGAGAGAGAGAA 480
Qy 481 ATAAAAAATTTCTCTTTCTATATACCAACAGCATTAAGAAATTAAGTAAAGAAAGATAT 540
Db 481 ATAAAAAATTTCTCTTTCTATATACCAACAGCATTAAGAAATTAAGTAAAGAAAGATAT 540
Qy 541 GCACCTTTTAAATAGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 GCACCTTTTAAATAGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 601 TTAATAGTTTCAACCTCAGTATTACAGAGCTCTCCAAAGGATATCTTTTCAGGCA 660
Db 601 TTAATAGTTTCAACCTCAGTATTACAGAGCTCTCCAAAGGATATCTTTTCAGGCA 660

```
QY 661 ATTCCATACATTATTGTGTCCTGGCTGGGTTTGGATGCTAAAGTGTAACAATAAGACA 720
Db 661 ATTCCATACATTATTGTGTCCTGGCTGGGTTTGGATGCTAAAGTGTAACAATAAGACA 720
QY 721 TTCAATGATCAGGACCAATGCACAAATGTCTAGCAGCAGTACAAATGTACACATGGAATTAGG 780
Db 721 TTCAATGATCAGGACCAATGCACAAATGTCTAGCAGCAGTACAAATGTACACATGGAATTAGG 780
QY 781 CCAATGATGTCACCTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
Db 781 CCAATGATGTCACCTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
QY 841 AGATCTGAAATTTTACAGACCAATGCTTAAACCCATAATAGTACAGCTAAATGAAATCTGTA 900
Db 841 AGATCTGAAATTTTACAGACCAATGCTTAAACCCATAATAGTACAGCTAAATGAAATCTGTA 900
QY 901 GTAATTAATTTGTAAGACCCCAACAAATACAAAGAAAGGTTTATCTATAGGACCGGG 960
Db 901 GTAATTAATTTGTAAGACCCCAACAAATACAAAGAAAGGTTTATCTATAGGACCGGG 960
QY 961 AGAGCAATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGCAAGCAATTTGTAACATT 1020
Db 961 AGAGCAATTTTATGCAAGAAAGAAACATAATAGGAGATATAAGCAAGCAATTTGTAACATT 1020
QY 1021 AGTAGCAGAAATGGAATTAACACTTTTCAACAGATAGTTATATAAATTAAGAGAAAAATTT 1080
Db 1021 AGTAGCAGAAATGGAATTAACACTTTTCAACAGATAGTTATATAAATTAAGAGAAAAATTT 1080
QY 1081 AGGAATAAAACAAATAGCCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTTGTAATGCAC 1140
Db 1081 AGGAATAAAACAAATAGCCCTTTAATCAATCCTCAGGAGGGGCCCAAGAAATTTGTAATGCAC 1140
QY 1141 AGTTTAAATTTGAGAGGGAATTTCTTCTACTGTGTAATAACAGCAAACTGTTTAAATAGTACT 1200
Db 1141 AGTTTAAATTTGAGAGGGAATTTCTTCTACTGTGTAATAACAGCAAACTGTTTAAATAGTACT 1200
QY 1201 TGGATGTTTACTGGAGGACAAATGGCACTGAGGAATGACATATCACACTCCAATGC 1260
Db 1201 TGGATGTTTACTGGAGGACAAATGGCACTGAGGAATGACATATCACACTCCAATGC 1260
QY 1261 AGAATAAAACAAATTAATAATGTGCGAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
Db 1261 AGAATAAAACAAATTAATAATGTGCGAGAAAGTAGGAAAGCAATGTATGCCCTCCC 1320
QY 1321 ATCAGAGCAAAATTAGATGTTTCATCAATATTAACAGGCTGCTACTAACAGAGATGGA 1380
Db 1321 ATCAGAGCAAAATTAGATGTTTCATCAATATTAACAGGCTGCTACTAACAGAGATGGA 1380
QY 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTTGGAGGAGATATAGGGAC 1440
Db 1381 GGTAAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTTGGAGGAGATATAGGGAC 1440
QY 1441 AATCGAGAGTGAATTAATAATATAAAGTAGTAAGAAATGAAACCAATAGGATAGCA 1500
Db 1441 AATCGAGAGTGAATTAATAATATAAAGTAGTAAGAAATGAAACCAATAGGATAGCA 1500
QY 1501 CCCACAGGGCAAGAGAGAAACAGTGCAGAAAGAAAAAGAGGGGGAGCGGTTTCAGGA 1560
Db 1501 CCCACAGGGCAAGAGAGAAACAGTGCAGAAAGAAAAAGAGGGGGAGCGGTTTCAGGA 1560
QY 1541 -----GACCGGATCCAAGAGGTTTGGCAAGATAGAAGTGA 1578
Db 1561 GGTGAGGTTTCTGGAGGTGGCGGATCCGAGTCCAGAGGTTTGGCAAGATAGAAGTGA 1620
QY 1579 AGGAATCTTCATGAAGATTTTGTATTCATGAAACGATACAGAGTGCACACAGGAGAA 1638
Db 1621 AGGAATCTTCATGAAGATTTTGTATTCATGAAACGATACAGAGTGCACACAGGAGAA 1680
QY 1639 AGATCCTTATCCTTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAG 1698
Db 1681 AGATCCTTATCCTTACTGAACCTGTGAGGAGATTAAGAAAGCCAGTTTGAAGGCTTTGTGAAG 1740
PN WO200126608-A2.
```

```
QY 1699 GATATAATGTTAAACAAAGAGGAGACGAAGAAAGAAAAACAGCTTTGAAATCCAAAAAGGT 1758
Db 1741 GATATAATGTTAAACAAAGAGGAGACGAAGAAAGAAAAACAGCTTTGAAATCCAAAAAGGT 1800
QY 1759 GATCAGAAATCCTCAAAATTTGCGGCACATGTCTAATAGTGAGGCCAGCAGTAAACACATCT 1818
Db 1801 GATCAGAAATCCTCAAAATTTGCGGCACATGTCTAATAGTGAGGCCAGCAGTAAACACATCT 1860
QY 1819 GTGTTTACAGTGGGCTGAAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTCGGAA 1878
Db 1861 GTGTTTACAGTGGGCTGAAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTCGGAA 1920
QY 1879 AATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1938
Db 1921 AATGGGAAACAGCTGACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACC 1980
QY 1939 TTCTGTTTCCAATCGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTGCCTAAAG 1998
Db 1981 TTCTGTTTCCAATCGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTGCCTAAAG 2040
QY 1999 TCCCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAATACCCACAGTTTCGCCCAA 2058
Db 2041 TCCCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGCAATACCCACAGTTTCGCCCAA 2100
QY 2059 CTTTGGCGGCAACAAATCCATTCACTTTGGGAGGAGTATTGAAATTCGAACCCAGGTGCTTCG 2118
Db 2101 CTTTGGCGGCAACAAATCCATTCACTTTGGGAGGAGTATTGAAATTCGAACCCAGGTGCTTCG 2160
QY 2119 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAAGCCATGGCCTTACGTCCTTT 2178
Db 2161 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAAGCCATGGCCTTACGTCCTTT 2220
QY 2179 GGCTTACTCAAACTCGAGTGAATCTAGA 2208
Db 2221 GGCTTACTCAAACTCGAGTGAATCTAGA 2250

RESULT 3
AAF82930
ID AAF82930 standard; cDNA; 2070 BP.
XX
XX AAF82930;
XX
XX 11-SEP-2003 (revised)
XX 29-JUN-2001 (first entry)
XX
XX HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
XX acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
XX HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 13..2070
XX FT /*tag= a
XX FT sig_peptide 13..72
XX FT /note= "synthetic secretory signal peptide"
XX FT misc_feature 73..1542
XX FT /tag= c
XX FT /note= "HIV-1 gp120 domain coding sequence"
XX FT misc_feature 1543..1593
XX FT /tag= d
XX FT /note= "[Gly4Ser]3 linker coding sequence"
XX FT misc_feature 1594..2070
XX FT /tag= e
XX FT /note= "human CD154 short form extracellular domain coding sequence"
XX
PN WO200126608-A2.
```

XX 19-APR-2001.
XX 13-OCT-2000; 2000WO-US028414.
XX 14-OCT-1999; 99US-0159690P.
XX (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
XX
XX Ledbetter JA, Hayden-Ledbetter MS;
PI WPI: 2001-281790/29.
DR P-PSDB; AAB62335.
XX
XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
XX Example 1; Fig 3B; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC short form extracellular domain fusion protein linked by (Gly4Ser)3
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;
SQ
Query Match 84.5%; Score 1866; DB 4; Length 2070;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 35; Indels 138; Gaps 1;
QY 1 AAGCTTGGCGCCATGCTGATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG 60
DB 1 AAGCTTGGCGCCATGCTGATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG 60
QY 61 GCTTCGAGATCCTGCTCGGATATTGATGATCTGAGTGTACAGAAAAATTGTGG 120
DB 61 GCTTCGAGATCCTGCTCGGATATTGATGATCTGAGTGTACAGAAAAATTGTGG 120
QY 121 GTCACAGTCTATTATGGGTACTCTGTGTGAGAGAGCAACCACTCTATTTTGTGCA 180
DB 121 GTCACAGTCTATTATGGGTACTCTGTGTGAGAGAGCAACCACTCTATTTTGTGCA 180
QY 181 TCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTCTGTGA 240
DB 181 TCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTCTGTGA 240
QY 241 CCCACAGACCCCAACCCCAAGAGTATGTTGGGAAATGTACAGAAAAATTAAACATG 300
DB 241 CCCACAGACCCCAACCCCAAGAGTATGTTGGGAAATGTACAGAAAAATTAAACATG 300
QY 301 TGGAAAAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 301 TGGAAAAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 CTTAAAGCCATGTGTAATAATTAACCCCACTCTGTTTAAATTTGCACTAAATTTGAAT 420
DB 361 CTTAAAGCCATGTGTAATAATTAACCCCACTCTGTTTAAATTTGCACTAAATTTGAAT 420
QY 421 ATCACTAAGAAATTAACCTAGTACAGTGTAGGAAATGATGAGAGAAAGAGNA 480
DB 421 ATCACTAAGAAATTAACCTAGTACAGTGTAGGAAATGATGAGAGAAAGAGNA 480
QY 481 ATAAAAAATTTGCTCTTTCTATATCAACCAAGCATAAGAAATTAAGTAAAGAAATAT 540
DB 481 ATAAAAAATTTGCTCTTTCTATATCAACCAAGCATAAGAAATTAAGTAAAGAAATAT 540
QY 541 GCACCTTTTAAATAGACTTGTAGTACCAATAGAAAAATACCTAATAACTAAGTATAGG 600

DB 541 GCACCTTTTAAATAGACTTGTAGTACCAATAGAAAAATCTAATAACTAAGTATAGG 600
QY 601 TTAATAAGTTGTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCTTTTCAGCCA 660
DB 601 TTAATAAGTTGTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCTTTTCAGCCA 660
QY 661 ATTCCATACATATTATTGTGCTCGGCTGGGTGGATGCTTAAAGTAAACATTAAGACA 720
DB 661 ATTCCATACATATTATTGTGCTCGGCTGGGTGGATGCTTAAAGTAAACATTAAGACA 720
QY 721 TTCAATGATCAGGACCATGACAAATGTGACAGCAGTACAAATGTACACATGCAATTAGG 780
DB 721 TTCAATGATCAGGACCATGACAAATGTGACAGCAGTACAAATGTACACATGCAATTAGG 780
QY 781 CCAGTGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
DB 781 CCAGTGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
QY 841 AGATCTGAAAAATTTACAGACAAATGCTAAAACCAATAATAGTACAGTAAATGTAATCTGTA 900
DB 841 AGATCTGAAAAATTTACAGACAAATGCTAAAACCAATAATAGTACAGTAAATGTAATCTGTA 900
QY 901 GTAATTAATTTGACAGACCCCAACCAATACAAAGAGGTTATCTATAGGACAGGG 960
DB 901 GTAATTAATTTGACAGACCCCAACCAATACAAAGAGGTTATCTATAGGACAGGG 960
QY 961 AGAGCATTTTATGCAAGAGAAAAATATAATAGAGATATAAGCAACAGCATTGTAACTT 1020
DB 961 AGAGCATTTTATGCAAGAGAAAAATATAATAGAGATATAAGCAACAGCATTGTAACTT 1020
QY 1021 AGTAGACAAAATGGAATAACACTTTTCAACAGATAGTTATAAATTAAGAGAAAAATTT 1080
DB 1021 AGTAGACAAAATGGAATAACACTTTTCAACAGATAGTTATAAATTAAGAGAAAAATTT 1080
QY 1081 AGGAATAAAACAATAGCTTTTAAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCAC 1140
DB 1081 AGGAATAAAACAATAGCTTTTAAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCAC 1140
QY 1141 AGTTTAAATTTGAGAGGGAAATTTCTTCTACTGTATAACAGCAACTGTTTAAATAGTACT 1200
DB 1141 AGTTTAAATTTGAGAGGGAAATTTCTTCTACTGTATAACAGCAACTGTTTAAATAGTACT 1200
QY 1201 TGGAAATTTCTGAGAGGACAAATGGCACTGAAAGAAATGACATTAATCACTCCAAATGC 1260
DB 1201 TGGAAATTTCTGAGAGGACAAATGGCACTGAAAGAAATGACATTAATCACTCCAAATGC 1260
QY 1261 AGAATAAAACAATTTAATAATATGTCAGAGAAATAGGAAAGCAATGTTATGCCCTCCC 1320
DB 1261 AGAATAAAACAATTTAATAATATGTCAGAGAAATAGGAAAGCAATGTTATGCCCTCCC 1320
QY 1321 ATCAGAGCAAAATTAGATGTTTCAATCAATATTACAGGGCTGCTACTAACAGAGATGGA 1380
DB 1321 ATCAGAGCAAAATTAGATGTTTCAATCAATATTACAGGGCTGCTACTAACAGAGATGGA 1380
QY 1381 GGTAAATAGTACTGAGACTGAGATCTGAGATCTTCAAGCTGAGAGGAGGATATGAGGAC 1440
DB 1381 GGTAAATAGTACTGAGACTGAGATCTGAGATCTTCAAGCTGAGAGGAGGATATGAGGAC 1440
QY 1441 AATTGGAGAGTGAATTTAATAATATAAAGTAGTAAGNATTTGAACCAATAGGACTAGCA 1500
DB 1441 AATTGGAGAGTGAATTTAATAATATAAAGTAGTAAGNATTTGAACCAATAGGACTAGCA 1500
QY 1501 CCCACAGGGCAAGAGAGAAACAGTGCAGAGAGAAAGAGGGG----- 1545
DB 1501 CCCACAGGGCAAGAGAGAAACAGTGCAGAGAGAAAGAGGGG----- 1545
QY 1561 GACAGATAGAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCATGAAAAACGATACAG 1620
DB 1546 ----- 1545
QY 1621 AGATGCAACACAGGAGAAAGATCTTATCTTCTGAACTGTGAGGAGATTAAGGCCAG 1680

QY 541 GCACCTTTTAAATAGACTTGTAGTACCAATAGAAAAATACATAAATCTAAAGTATAGG 600
DB 541 GCACCTTTTAAATAGACTTGTAGTACCAATAGAAAAATACATAAATCTAAAGTATAGG 600
QY 601 TTAATAAGTGTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCTTTTCAGCCA 660
DB 601 TTAATAAGTGTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCTTTTCAGCCA 660
QY 661 ATTCCATACATATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA 720
DB 661 ATTCCATACATATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA 720
QY 721 TTCAATGATCAGGACCAATGCAAAATGTACAGCAAGTACAAATGTACACATGGAATTAGG 780
DB 721 TTCAATGATCAGGACCAATGCAAAATGTACAGCAAGTACAAATGTACACATGGAATTAGG 780
QY 781 CCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
DB 781 CCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATT 840
QY 841 AGATCTGAAAAATTTTACAGACAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTA 900
DB 841 AGATCTGAAAAATTTTACAGACAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTA 900
QY 901 GTAATTAATTGTACAAGACCCCAACAATACAAAGAAAGGTTATCTATAGGACCAAGG 960
DB 901 GTAATTAATTGTACAAGACCCCAACAATACAAAGAAAGGTTATCTATAGGACCAAGG 960
QY 961 AGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAGCACATGTGAACATT 1020
DB 961 AGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAGCACATGTGAACATT 1020
QY 1021 AGTAGACAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAAGAGAAAAATTT 1080
DB 1021 AGTAGACAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAAGAGAAAAATTT 1080
QY 1081 AGGAATAAAAACAATAGCTTTTAATCAATCTCAGAGGGGACCCAGAAATTTGTAATGCAC 1140
DB 1081 AGGAATAAAAACAATAGCTTTTAATCAATCTCAGAGGGGACCCAGAAATTTGTAATGCAC 1140
QY 1141 AGTTTAAATTTGGAGGGGAATCTTCTACTGTATATACAGCACACTGTTTAAATAGTACT 1200
DB 1141 AGTTTAAATTTGGAGGGGAATCTTCTACTGTATATACAGCACACTGTTTAAATAGTACT 1200
QY 1201 TGGAAATGTTTACTGGAGGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGC 1260
DB 1201 TGGAAATGTTTACTGGAGGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGC 1260
QY 1261 AGAATAAAAACAATTTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320
DB 1261 AGAATAAAAACAATTTATAAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320
QY 1321 ATCAGAGACAAATTTAGATGTTTCATCAATATTACAGGCTGCTACTAACAGAGATGGA 1380
DB 1321 ATCAGAGACAAATTTAGATGTTTCATCAATATTACAGGCTGCTACTAACAGAGATGGA 1380
QY 1381 GGTAAATAGTACTGAGACTGAGACTCAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC 1440
DB 1381 GGTAAATAGTACTGAGACTGAGACTCAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC 1440
QY 1441 AATTGGAGAGTGAATTTATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500
DB 1441 AATTGGAGAGTGAATTTATAAATATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500
QY 1501 CCCACCGGCAAGAGAGAAACAGTGCAAAGAGAAAAAGACCCGGATCCCAAGAGGTTG 1560
DB 1501 CCCACCGGCAAGAGAGAAACAGTGCAAAGAGAAAAAGACCCGGATCC----- 1550
QY 1561 GACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCATGAACGATACAG 1620
DB 1551 ----- 1550

QY 1621 AGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAATCTGTAGGAGATTAAAGCCAG 1680
DB 1551 ----- 1550
QY 1681 TTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAAGAAAGAAAAACAGC 1740
DB 1551 -----AGNAAACAGC 1560
QY 1741 TTTGAATGCAAAAAGAGTGATCAGAAATCCTCAAAATTTGGGACACATGTATAGTGAGGCC 1800
DB 1561 TTTGAATGCAAAAAGAGTGATCAGAAATCCTCAAAATTTGGGACACATGTATAGTGAGGCC 1620
QY 1801 AGCAGTAAAAACAATCTGTGTACAGTGGGCTGAAAAGGATACTACACCATGAGCAAC 1860
DB 1621 AGCAGTAAAAACAATCTGTGTACAGTGGGCTGAAAAGGATACTACACCATGAGCAAC 1680
QY 1861 AACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAAGGACTCTATTAT 1920
DB 1681 AACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACAAAGGACTCTATTAT 1740
QY 1921 ATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1980
DB 1741 ATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1800
QY 1981 GCCAGCTCTGCCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACTCAGAGCTCAAAAT 2040
DB 1801 GCCAGCTCTGCCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACTCAGAGCTCAAAAT 1860
QY 2041 ACCACAGTTCGGGCAAAACCTTGGGGCAACAAATCATTCTTCTGGGAGGAGTATTGAA 2100
DB 1861 ACCACAGTTCGGGCAAAACCTTGGGGCAACAAATCATTCTTCTGGGAGGAGTATTGAA 1920
QY 2101 TTGCAACACAGTGTCTCGGTGTTTGTCAATGTGATGTATCCAAAGCCAAAGTGAGCCATGCG 2160
DB 1921 TTGCAACACAGTGTCTCGGTGTTTGTCAATGTGATGTATCCAAAGCCAAAGTGAGCCATGCG 1980
QY 2161 ACTGGCTTCACTGCTTTGGCTTACTCAAACTCGAGTCAATCTAGA 2208
DB 1981 ACTGGCTTCACTGCTTTGGCTTACTCAAACTCGAGTCAATCTAGA 2028

RESULT 5

ACAG3265
ID ACA63265 standard; DNA; 2046 BP.

AC ACA63265;

XX AC ACA63265;

DT 22-APR-2004 (first entry)

XX HIV-1 immunogenic sequence #1.

DE Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;

XX immunogenic; virucide; ds.

XX Human immunodeficiency virus type 1.

OS WO2004001051-A2.

PN 31-DEC-2003.

PD 20-JUN-2003; 2003WO-EP007146.

PF 20-JUN-2002; 2002EP-00291550.

XX (INSP) INST PASTEUR.

XX (CNRS) CENT NAT RECH SCI.

PA Tangy F, Loxin C, Mollet L, Delebecque F;

XX WPI; 2004-082508/08.

XX New recombinant mononegavirales measles virus expressing a heterologous

PT amino acid, useful for preparing immunogenic or vaccine composition for

the prophylaxis or treatment of measles.

Disclosure; Fig 16A; Opp; English.

The present invention relates to a recombinant monogavirales measles virus expressing a heterologous amino acid, which is capable of eliciting a humoral and/or cellular immune response against the heterologous amino acid sequence including in individuals having pre-existing measles virus immunity. The recombinant virus is useful for preparing immunogenic or vaccine composition for the prophylaxis or treatment of measles. The present sequence is a HIV immunogenic sequence shown in the exemplification of the invention

Sequence 2046 BP; 741 A; 328 C; 475 G; 502 T; 0 U; 0 Other;

Query Match 65.8%; Score 1453.8; DB 12; Length 2046;
Best Local Similarity 97.9%; Pred. No. 1e-286;
Matches 1473; Conservative 0; Mismatches 32; Indels 0;

Qy	52	TG	ATCTCGGCTTCGAGATCCCATGCTCTCTTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	37	TG	GGGTGGAGATGGGGCACCATGCTCTCTTGGGATGTTGATCATCTGTAGTGCTACAGAA	96
Qy	112	AA	ATTGTGGGTACAGTCTTATATGGGCTACTCTGTGGAGAGACACCACTCTTA	171
Db	97	AA	ATTGTGGGTACAGTCTTATATGGGCTACTCTGTGGAGAGACCACTCTTA	156
Qy	172	TT	TGTGTCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	157	TT	TGTGTCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACACAT	216
Qy	232	GC	TGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTCGGAAATGTGACAGAAAT	291
Db	217	GC	TGTGTACCCACAGACCCCAACCCCAAGAAGTAGTATTCGGAAATGTGACAGAAAT	276
Qy	292	TT	TAAATGTTGGAAAAATAACATGTTAGATCAGATGTCATGAGGATATATCAGTTTATGG	351
Db	277	TT	TAAATGTTGGAAAAATAACATGTTAGATCAGATGTCATGAGGATATATCAGTTTATGG	336
Qy	352	GAT	GAAGCCTTAAGCCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATGTCAT	411
Db	337	GAT	GAAGCCTTAAGCCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATGTCAT	396
Qy	412	AA	TTTGAATATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	471
Db	397	AA	TTTGAATATCATAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	456
Qy	472	AA	AGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAGAATAAGGTTAAAG	531
Db	457	GA	AGAGAAATAAAAAATTGCTCTTTCTATATCACCAAGCATAGAATAAGGTTAAAG	516
Qy	532	AA	AGAAATATGCATCTTTTAAATAGACTGATGTAGTACCAATAGAAATACTAATACT	591
Db	517	AA	AGAAATATGCATCTTTTAAATAGACTGATGTAGTACCAATAGAAATACTAATACT	576
Qy	592	AA	GATAGGTTAAATAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTATCC	651
Db	577	AA	GATAGGTTAAATAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTATCC	636
Qy	652	TT	TACGCCAATCCCATATATTGTGTCCCGGCTGGGTTTGCATGCTAAAGTGTAAAC	711
Db	637	TT	TACGCCAATCCCATATATTGTGTCCCGGCTGGGTTTGCATGCTAAAGTGTAAAC	696
Qy	712	AA	TAGACATTCAAATGGATCAGGACCATGCACAAATGTGACACAGTACAATGTACACAT	771
Db	697	AA	TAGACATTCAAATGGATCAGGACCATGCACAAATGTGACACAGTACAATGTACACAT	756
Qy	772	GG	AATTAGGCCAGTGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAGAC	831
Db	757	GG	AATTAGGCCAGTGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAGAC	816
Qy	832	AT	AGTAAATTAGATCTGAAATTTTCAGACAAATGCTTAAACCATTAATAGTACAGCTAAAT	891

XX Human immunodeficiency virus.
OS
FH Key Location/Qualifiers
FT CDS 1..2001
FT /*tag= a
FT /product= "truncated gp 160"
XX
XX WO2003077838-A2.
XX
XX 25-SEP-2003.
XX
XX 05-MAR-2002; 2002WO-US007144.
XX
XX 05-MAR-2002; 2002WO-US007144.
XX
XX (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.
XX
XX Dimitrov DS, Chow Y, Phogat SK, Broder CC;
XX
XX WPI; 2003-779074/73.
XX
XX P-PSDB; ABU64219.
XX
XX New HIV antigenic composition comprising an HIV envelope glycoprotein 160
XX having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
XX subunit useful for protecting a human from HIV infection.
XX
XX Disclosure; Page 62-63; 65pp; English.
XX
XX The present invention relates to an HIV antigenic composition, comprising
XX an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
XX subunit, where the carboxy-terminal end of gp120 is covalently linked
XX through a peptide linker of at least 5 amino acids, to the amino-terminal
XX end of gp41. The HIV antigenic composition is useful for protecting a
XX human from HIV infection, potentially in the form of a vaccine. The
XX present sequence is the HIV truncated gp160 coding sequence
XX
XX Sequence 2051 BP; 749 A; 333 C; 467 G; 502 T; 0 U; 0 Other;
XX
XX Query Match 65.6%; Score 1448; DB 10; Length 2051;
XX Best Local Similarity 98.8%; Pred. No. 1.6e-285;
XX Matches 1470; Conservative 0; Mismatches 15; Indels 3; Gaps 1;
XX
XX 72 CATGCTCTGGGATATTGATGATCTGTAGTGCT---ACAGAAAATTTGGGTCACAGT 128
XX 51 CTGCTCTCTGGGATGTTGATGATCTGTAGTGCTGCCAAAAGAAAACGTGGGTCAAT 110
XX
XX 129 CTATTATGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTATTTGTGCATCAGATGC 188
XX 111 CTATTATGGGTACCTGTGTGGAGAGAAGCAACCACTCTATTATTTGTGCATCAGATGC 170
XX
XX 189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 248
XX
XX 171 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 230
XX
XX 249 CCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAATA 308
XX 231 CCCCAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAATA 290
XX
XX 309 TAAACATGTTAGATCAGATGTCATGAGGATATATATCAGTTTATGGGATGAAAGCCTAAAGCC 368
XX
XX 291 TAAACATGTTAGATCAGATGTCATGAGGATATATATCAGTTTATGGGATGAAAGCCTAAAGCC 350
XX
XX 369 ATGTGTAATAATTAACCCCACTCTGTGTTACTTTAAATTTGCACTAATTTGAATATCACTAA 428
XX
XX 351 ATGTGTAATAATTAACCCCACTCTGTGTTACTTTAAATTTGCACTAATTTGAATATCACTAA 410
XX
XX 429 GAATACTACTATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAGGAGGAATAAAAAA 488
XX 411 GAATACTACTATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAGGAGGAATAAAAAA 470
XX
XX 489 TTGCTCTTTCTATATCACCACAGCATAGAATAAGGTAAAGAGAAATATGCACTTTT 548

Db 471 TTGCTCTTTCTATATCACCACAAGCATAAGAAATAAGGTAAGAAAGAAATATGCACTTTT 530
Qy 549 TAATAGACTTGTATGTAGTACCAATAGAAAATACATAATAATAGTATAGTATAGTAAATAG 608
Db 531 TAATAGACTTGTATGTAGTACCAATAGAAAATACATAATAATAGTATAGTATAGTAAATAG 590
Qy 609 TTGTAACACCTCAGTCAATTTACACAGGCTGTCCAAAAGGTATCCTTTACGCCAATTTCCCAT 668
Db 591 TTGTAACACCTCAGTCAATTTACACAGGCTGTCCAAAAGGTATCCTTTACGCCAATTTCCCAT 650
Qy 669 ACATTTATGTTGTCCTGGCTGGGTTTGGATGCTCTAAAAGTGTAAACAATAAGACATTTCAATGG 728
Db 651 ACATTTATGTTGTCCTGGCTGGGTTTGGATGCTCTAAAAGTGTAAACAATAAGACATTTCAATGG 710
Qy 729 ATCAGGACCATGCACAAATGTACACAGTACAAATGTACACATGCAATTTAGGCCAGTGGT 788
Db 711 ATCAGGACCATGCACAAATGTACACAGTACAAATGTACACATGCAATTTAGGCCAGTGGT 770
Qy 789 GTCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAGAAGACATAGTAAATTTAGATCTGA 848
Db 771 GTCAACTCAACTGCTGTTAAATGGCAGTCTTAGCAGAGAAGACATAGTAAATTTAGATCTGA 830
Qy 849 AAATTTACAGACAAATGCTAAACCATTAATAGTACAGCTAAATGATCTGTAGTAATTA 908
Db 831 AAATTTACAGACAAATGCTAAACCATTAATAGTACAGCTAAATGATCTGTAGTAATTA 890
Qy 909 TTGTACAGAGCCCAACCAACATACAGAGAGAGGTTATCTATAGGACGAGGAGACATTT 968
Db 891 TTGTACAGAGCCCAACCAACATACAGAGAGAGGTTATCTATAGGACGAGGAGACATTT 950
Qy 969 TTATGCAAGAGAACAATAATAGGAGATATTAAGACAAGCACATTTGTAACATTAGTAGAGC 1028
Db 951 TTATGCAAGAGAACAATAATAGGAGATATTAAGACAAGCACATTTGTAACATTAGTAGAGC 1010
Qy 1029 AAAATGGGAATAACTTTTACAAAGATAGTTATATAAATAAGAGAAAATTTAGGAATAA 1088
Db 1011 AAAATGGGAATAACTTTTACAAAGATAGTTATATAAATAAGAGAAAATTTAGGAATAA 1070
Qy 1089 AACATAGCCTTTAATCAATCCTCAGGAGGGAGCCAGAAAATTTGTAATGACAGTTTAA 1148
Db 1071 AACATAGCCTTTAATCAATCCTCAGGAGGGAGCCAGAAAATTTGTAATGACAGTTTAA 1130
Qy 1149 TTGTGGAGGGGAATTTCTTACTGTAAATACAGCACTGTTTAAATAGTACTTGGAAATGT 1208
Db 1131 TTGTGGAGGGGAATTTTCTTACTGTAAATACAGCACTGTTTAAATAGTACTTGGAAATGT 1190
Qy 1209 TACTGGAGGGAACAATGGCACTGAAGGAAATGACATATCACTCCCAATGCAAGATAA 1268
Db 1191 TACTGGAGGGAACAATGGCACTGAAGGAAATGACATATCACTCCCAATGCAAGATAA 1250
Qy 1269 ACAATTTAATAATATGTGCGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1328
Db 1251 ACAATTTAATAATATGTGCGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCACAGG 1310
Qy 1329 ACAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTTAAACAAGATGAGGTAATAG 1388
Db 1311 ACAATTTAGATGTTTCATCAAAATATTACAGGCTGCTACTTAAACAAGATGAGGTAATAG 1370
Qy 1389 TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGAATTTGGAG 1448
Db 1371 TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGAATTTGGAG 1430
Qy 1449 AAGTGAATTTATATAATATAAGTAGTAAGAAATTCGAACCAATAGGAGTAGCACCCACAG 1508
Db 1431 AAGTGAATTTATATAATATAAGTAGTAAGAAATTCGAACCAATAGGAGTAGCACCCACAG 1490
Qy 1509 GCGAAGAGAGAGAAACAGTGCGAAGAGAAAAAGACCCGGATCCAGAAG 1556
Db 1491 GCGAAGAGAGAGAAACAGTGCGAAGAGAAAAAGACAGCAGTGGGAATAGG 1538

RESULT 8
AAL56170

Db 1431 AAGTGAATTATATAATAATAAAGTAGTAAGAAATTGAACCAATAGGATAGCACCCACCAG 1490
Qy 1509 GCRAAGAGAGAACAGTGCRAAGAGRAAARAGACCGGATCCAAGAAG 1556
Db 1491 GCRAAAGAGAGAACAGTGCRAAAGAGAGAAAGAACAGCAGTGGGAATAGG 1538
RESULT 9
ACA63267
ID ACA63267 standard; DNA; 2010 BP.
XX AC
XX ACA63267;
XX DT 22-APR-2004 (first entry)
XX DE HIV-1 immunogenic sequence #3.
XX KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;
XX KW immunogenic; virucide; ds.
XX OS Human immunodeficiency virus type 1.
XX XX WO2004001051-A2.
XX PD 31-DEC-2003.
XX PF 20-JUN-2003; 2003WO-EP007146.
XX PR 20-JUN-2002; 2002EP-00291550.
XX PA (INSP) INST PASTEUR.
XX PA (CNRS) CENT NAT RECH SCI.
XX XX
XX PI Tangy F, Lorin C, Mollet L, Delebecque F;
XX DR WPI; 2004-082508/08.
XX PT New recombinant mononegavirales measles virus expressing a heterologous
PT amino acid, useful for preparing immunogenic or vaccine composition for
PT the prophylaxis or treatment of measles.
XX PS Disclosure; Fig 16E; Opp; English.
XX CC The present invention relates to a recombinant mononegavirales measles
CC virus expressing a heterologous amino acid, which is capable of eliciting
CC a humoral and/or cellular immune response against the heterologous amino
CC acid sequence including in individuals having pre-existing measles virus
CC immunity. The recombinant virus is useful for preparing immunogenic or
CC vaccine composition for the prophylaxis or treatment of measles. The
CC present sequence is a HIV immunogenic sequence shown in the
CC exemplification of the invention
XX SQ Sequence 2010 BP; 720 A; 326 C; 469 G; 495 T; 0 U; 0 Other;
Query Match 60.7%; Score 1339.8; DB 12; Length 2010;
Best Local Similarity 94.2%; Pred No. 1.8e-263;
Matches 1417; Conservative 0; Mismatches 52; Indels 36; Gaps 1;
Qy 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAA 111
Db 37 TGGGGTGGAGATGGGGCACCACCTGCTCTGGGATGTTGATGATCTGTAGTGCTACAGAA 96
Qy 112 AATTTGGGTCACAGTCTATTATATGGGTACTGTGTGGAGAGAGCAACCACTCTA 171
Db 97 AATTTGGGTCACAGTCTATTATGGGTACTGTGTGGAGAGAGCAACCACTCTA 156
Qy 172 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAAATGTTGGGCCACACAT 231
Db 157 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAAATGTTGGGCCACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAT 291

Db 217 GCCTGTGTATCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAT 276
Qy 292 TTTTAACATGTGGAATAATAACATGCTAGATCAGATGCATGAGGATATATAATCAGTTTATGG 351
Db 277 TTTTAACATGTGGAATAATAACATGCTAGATGCATGAGGATATATAATCAGTTTATGG 336
Qy 352 GATGAAGCCCTAAAGCCATGTGTAAATTAACCCCACTCTCTGTGTACTTTAAATTCGACT 411
Db 337 GATGAAGCCCTAAAGCCATGTGTAAATTAACCCCACTCTCTGTGTACTTTAAATTCGACT 396
Qy 412 AATTTGAATATCACTAAGAATFACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 471
Db 397 AATTTGAATATCACTAAGAATFACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 456
Qy 472 AAAGGAGAAATAAATAATTTGCTCTTCTATATCACCACAAGCATAAAGAAATAAGGTAAG 531
Db 457 GAAGGAGAAATAAATAATTTGCTCTTCTATATCACCACAAGCATAAAGAAATAAGGTAAG 516
Qy 532 AAAGAATATGCACCTTTTAAATAGACTTGTATGTAGTACCCTAATAGAAAATACTAATAATACT 591
Db 517 AAAGAATATGCACCTTTTAAATAGACTTGTATGTAGTACCCTAATAGAAAATACTAATAATACT 576
Qy 592 AAGTATAGGTTAAATAGTTGTAAACACCTCAGTCATTACACAGGCTGTCCAAAAGTATCC 651
Db 577 AAGTATAGGTTAAATAGTTGTAAACACCTCAGTCATTACACAGGCTGTCCAAAAGTATCC 636
Qy 652 TTTTCAGCAATTTCCCATACATTTTGTGTCGCGCTGGGTTTGGCATGCTTAAAGTGTAAAC 711
Db 637 TTTTCAGCAATTTCCCATACATTTTGTGTCGCGCTGGGTTTGGCATGCTTAAAGTGTAAAC 696
Qy 712 AATAAGACATTTCAATGGATCAGGACCATGCACAATGTGCAGCACAGTACAATGTACACAT 771
Db 697 AATAAGACATTTCAATGGATCAGGACCATGCACAATGTGCAGCACAGTACAATGTACACAT 756
Qy 772 GGAATTAGCCAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAAC 831
Db 757 GGAATTAGCCAGTGGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAAC 816
Qy 832 ATAGTAAATTAGATCTGAAAAATTTTTCACAGACAAATGCTAAAAACATAATAGTACAGTAAAT 891
Db 817 ATAGTAAATTAGATCTGAAAGATTTTTCACAGACAAATGTTAAACCATTAATAGTACAGTAAAT 876
Qy 892 GAATCTGTAGTAAATTAATTTGTAAGACCCCAACCAATACAAGAGAAGGTTATCTATA 951
Db 877 GAATCTGTAGTAAATTAATTTGTAAGACCCCAACCAATAGC----- 917
Qy 952 GGACAGGAGAGCATTTTATGCAAGAAAGAAACATAATAGGAGATATTAAGACAACACAT 1011
Db 918 -----TGCAGAAATTGGATAAATGGGCAAGTGTCTGCAAGACAAGCACAT 960
Qy 1012 TGTAACTTACTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATATAAATTAAAGA 1071
Db 961 TGTAACTTACTAGAGCAAAATGGAATAACACTTTTACAACAGATAGTTATATAAATTAAAGA 1020
Qy 1072 GAAAAATTTAGGAATFAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAAT 1131
Db 1021 GAAAAATTTAGGAATFAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAAT 1080
Qy 1132 GTAATGCACAGTTTAAATTTGAGGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTT 1191
Db 1081 GTAATGCACAGTTTAAATTTGAGGGGGAATTTTCTACTGTAATACAGCACAACTGTTT 1140
Qy 1192 AATAGTACTTGGAAATTTTACTTGGAGGGGCAAAATGSCACTGAAGGAAATGACATAATCACA 1251
Db 1141 AATAGTACTTGGAAATTTTCTTGGAGGGGCAAAATGSCACTGAAGGAAATGACATAATCACA 1200
Qy 1252 CTCCAATGCAGAAATAAACAATAATTAATATGTGGCAAGAAAGTAGGAAAAAGCAATGTAT 1311
Db 1201 CTCCAATGCAGAAATAAACAATAATTAATATGTGGCAAGAAAGTAGGAAAAAGCAATGTAT 1260
Qy 1312 GCCCTTCCCATCAGAGCAAAATTTAGATGTTTCATCAAAATATACAGGCTGCTACTACA 1371
Db 1261 GCCCTTCCCATCAGAGCAAAATTTAGATGTTTCATCAAAATATACAGGCTGCTACTACA 1320


```

Db 1540 TAAATTGTACAGACCAACAAATACAGAAAAAGTATACATATAGCAGGAGCAGC 1599
Qy 966 ATTTTATGCAAGAAACATATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG 1025
Db 1600 ATTTTATACACAGAGAAATATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG 1659
Qy 1026 AGCAAAATGGAATAACATTTTACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAA 1085
Db 1660 AGCAAAATGGAATGACACTTTAAATTAAGATAGTTATAAAATTAAGAGAAATTTGGGAA 1719
Qy 1086 TAAACAATAGCTTTTAAATCAATCTCAGGAGGAGCCAGCAAAATGTAATGACAGTTT 1145
Db 1720 TAAACAATAGTCTTTTAAAGCACTCTCAGGAGGAGCCAGCAAAATGTAAGCGCACAGTTT 1779
Qy 1146 TAAATTGTGAGGGGAATCTTCTACTGTAATACAGCAACAATGTTTAAATAGTACTTGAA 1205
Db 1780 TAAATTGTGAGGGGAATTTTCTACTGTAATTAACACACACTGTTTAAATAGTACTTGAA 1839
Qy 1206 TGTACTGAGGAGCAAAATGGCACTGGAAGAAATGACATAATCACATCCCAATGAGAAAT 1265
Db 1840 TGTACTGAAGAGTCAAAATAACACTGTAGAAAAATAACCAATCACACTCCCATGCAGAAT 1899
Qy 1266 AAAAAAATTAATATATGTCAGAAAGTAGGAAAGCAATGTATGCCCTCCATCAC 1325
Db 1900 AAAAAAATTAATAATGTCAGAAAGTAGGAAAGCAATGTATGCCCTCCATCAC 1959
Qy 1326 AGGCAAAATTAGATGCTCATCAATATTACAGGGCTGCTACTAAACAAGAGATGAGGTAA 1385
Db 1960 AGGCAAAATTAGATGCTCATCAATATTACAGGGCTGCTTAAACAAGAGATGAGGTAA 2016
Qy 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGCAATTTG 1445
Db 2017 TCCTGAGGACAAACAGCGAGGCTTCAGACCTGGAGGAGAGATATGAGGGCAATTTG 2076
Qy 1446 GAGAGTGAATTAATAATATAAGTAGTAAGAAATGGAACCAATAGAGTAGCACCCAC 1505
Db 2077 GAGAGTGAATTAATAATATAAGTAGTAAGAAATGGAACCAATAGAGTAGCACCCAC 2136
Qy 1506 CAGGCAAGAGAGAACAGTGCAGAGAGAAAAAGAGCGGATCCAGAAAG 1556
Db 2137 CAGGCAAGAGAGAGAGTGGTCAGAGAGAAAAAGAGCAGTGGGAATAGG 2187

RESULT 12
AAT58551
ID AAT58551 standard; cDNA; 3807 BP.
XX AC AAT58551;
XX DT 17-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 25-MAR-1997 (first entry)
XX DE Human Immunodeficiency Virus-1 strain BA-L env gene.
XX KW Acquired immune deficiency syndrome; AIDS; envelope protein; env gene;
XX KW vaccine; ds.
XX OS Human immunodeficiency virus 1; (strain BA-L).
XX FH Location/Qualifiers
XX FT 648..3215
XX FT /*tag= a
XX FT /product= "envelope_protein"
XX FN US5576000-A.
XX PD 19-NOV-1996.
XX PF 15-FEB-1995; 95US-00388809.
XX PR 17-OCT-1990; 90US-00599491.

```

```

PR 25-FEB-1993; 93US-00022835.
XX (USSH ) US DBPT HEALTH & HUMAN SERVICES.
XX Gallo RC, Franchini G, Lori FC, Popovic M, Reitz MS, Gartner S;
XX Markham PD;
XX WPI; 1997-011206/01.
XX DR P-PSDB; AAW11581.
XX PT New isolated envelope protein of HIV-1 strain BA-L and recombinant
XX PT equivalents - useful as immunogens for vaccines and antibody prodn.,
XX PT typical of US clinical isolates.
XX PS Example; Fig 8; 86pp; English.
XX CC A HindIII fragment of unintegrated viral DNA representing the BA-L genome
XX CC was cloned into lambda phage Charon 28 DNA from total DNA of peripheral
XX CC blood lymphocytes infected with and producing HIV-1(BA-L). A positive
XX CC clone was selected by hybridisation using a HIV-1 env probe. This clone,
XX CC designated BA-L1, was found to contain the entire gene for the envelope
XX CC protein on a 2.8 kb HindIII-XbaI fragment and a 0.4 kb EcoRI-HindIII
XX CC fragment. When cloned together these fragments comprise the env gene, as
XX CC well as the coding regions for rev and the rev-responsive element of env,
XX CC both necessary for efficient expression in eukaryotic cells. The claimed
XX CC recombinantly produced envelope protein can be used as an immunogen for
XX CC raising antibodies against HIV. (Updated on 25-MAR-2003 to correct PF
XX CC field.) (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 3807 BP; 1307 A; 662 C; 937 G; 901 T; 0 U; 0 Other;

Query Match 55.5%; Score 1225.8; DB 2; Length 3807;
Best Local Similarity 89.9%; Pred. No. 3.4e-240;
Matches 1340; Conservative 0; Mismatches 142; Indels 9; Gaps 2;

Qy 72 CATGCTCTCTGGGATATGATGATCTGTAGTGTACAGAAAAATTTGGGTGCACAGTCTA 131
Db 701 CATGCTCTCTGGGATATTAATGATGCTGTAAAGAAAAATTTGGGTGCACAGTCTA 760
Qy 132 TTATGGGTACTCTGTGGAGAGAACCAACACACTCTATTTTGTGATCAGATGCTAA 191
Db 761 TTATGGGTACTCTGTGGAGAGAACCAACACACTCTATTTTGTGATCAGATGCTAA 820
Qy 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 251
Db 821 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 880
Qy 252 CAACCCACAGAGTAGTATTTGGGAATGTGCACAGAAAAATTTTAACTGTGGAAAAATAA 311
Db 881 CAACCCACAGAGTAGTATTTGGGAATGTGCACAGAAAAATTTTAACTGTGGAAAAATAA 940
Qy 312 CATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCCATG 371
Db 941 CATGCTAGACAAATGATGAGGATATAATCAGTTTATGGGATCAAGCCCTAAAGCCATG 1000
Qy 372 TGTAAATTAACCCCACTCTGTGTGTACTTTAAATTGCACTAATTTGA-----ATATCAC 425
Db 1001 TGTAAATTAACCCCACTCTGTGTGTACTTTAAATTGCACTAATTTGAGGAATGCTACTAA 1060
Qy 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAAGAGAGGAATAAA 485
Db 1061 TGGGAATGACACTAATACCACTAGTAGCAGGGAATGTTGGGGGAGAGGAATAAA 1120
Qy 486 AAATTTGCTCTTTTATATCACCACAGCATAAAGAAATAAGGTAAAGAAAGAAATATGCACT 545
Db 1121 AAATTTGCTCTTTTCAATATCACCACAGCATAAAGGTAAAGGTGCAAGAAAGAAATATGCACT 1180
Qy 546 TTTTAAATAGACTTGTAGTACCAATAGAAAAATACTAATAATAGTACTAGTAGGTAAAT 605
Db 1181 TTTTAAATAGACTTGTAGTACCAATAGAAAAATACTAATAATAGTACTAGTAGGTAAAT 1240
Qy 606 AAGTTGTAAACACCTCAGTCATTACAGGCGCTGTCCAAAGGTATCTCTTTAGCCAAATCC 665

```

Db 1241 AAGTTGTAACACCTCAGTCATTACACAGGCGCTGCCAAAGGTATCTTTGAGCCAATTCC 1300
Qy 666 CATACATTATTTGTTCCCGCTGGTTTGCATGCTAAAGTGAACATTAAGACATTCAA 725
Db 1301 CATACATTATTTGTTCCCGCTGGTTTGGCAITCTTAAAGTGAAGATAAGAGTTCAA 1360
Qy 726 TGGATCAGGACCATGSCACAAATGTCAGCACAGTACAAATGTACACATGGAAATTAGGCCAGT 785
Db 1361 TGGAAAGGACATGTACAAATGTCAGCACAGTACAAATGTACACATGGAAATTAGGCCAGT 1420
Qy 786 GGTGTCACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGACATAGTAATTAGATC 845
Db 1421 AGTATCACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATC 1480
Qy 846 TGAATAATTCACAGACAAATGCTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAAT 905
Db 1481 CGCCAAATTTCCGGACATGCTAAAGTCATTAATAGTACAGCTGAATGAATCTGTAGAAAT 1540
Qy 906 TAAATGTACAAGACCCCAACAATACAAAGAGAGGTTATCTATAGGACCAGGAGAGC 965
Db 1541 TAAATGTACAAGACCCCAACAATACAAAGAGAGTTATCTATAGGACCAGGAGAGC 1600
Qy 966 ATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAG 1025
Db 1601 ATTTTATACAAGAGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACCTTAGTAG 1660
Qy 1026 AGCAAAATGGAATTAACCTTTACACAGATAGTTATATAAATTAAGAGAAAAATTTAGGAA 1085
Db 1661 AGCAAAATGGAATGACACTTTTAAATAGATAGTTATATAAATTAAGAGAACAAATTTGGAA 1720
Qy 1086 TAAACCAATACGCTTTAATCAATCCTCAGGAGGGAGCCAGAAATGTAATGCACAGTTT 1145
Db 1721 TAAACCAATAGTCTTTAGACACTCTCTCAGGAGGGAGCCAGAAATGTCAGCACAGTTT 1780
Qy 1146 TAAATGTGGAGGGGAATCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTGGAA 1205
Db 1781 TAAATGTGGAGGGGAATTTTCTACTGTAATTCACACAACTGTTTAAATAGTACTTGGAA 1840
Qy 1206 TGTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATATATCACTCCCAATGCAGNAT 1265
Db 1841 TGTACTGAAGAGTCAAAATAACACTGTGTAGAAAATAACACAATCACTCCCATGCAGNAT 1900
Qy 1266 AAAACAAATTAATAATATGTGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1325
Db 1901 AAAACAAATTAATAATATGTGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAG 1960
Qy 1326 AGGCAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTTAAACAAGAGATGGAGTAA 1385
Db 1961 AGGCAAAATTAGATGTTTCATCAAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGG-- 2017
Qy 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGNATAGGGGACAAATTG 1445
Db 2017 TCCTGAGGACAAACAGACCGAGGCTTCAGACCTGGAGGAGAGATAGGGGATAATTG 2077
Qy 1446 GAGAGTCAATTAATAATATAAGTAGTAAGATTGCAACCAATAGGAGTAGCACCCAC 1505
Db 2078 GAGAGTGAATTAATAATATAAGTAGTAAGATTGCAACCAATAGGAGTAGCACCCAC 2137
Qy 1506 CAGGCAAGAGAGAAGACAGTGCAAAGAGAAAAAGACCGGATCCAAAGAG 1556
Db 2138 CAAGCAAGAGAGAGTGGTGCAGAGAGAAAAAGAGACAGTGGGAATAGG 2188

RESULT 13
AD052562
ID AD052562 standard; DNA; 9540 BP.
XX
AC AD052562;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human immunodeficiency virus 1 parent JRCSF DNA.
XX

KW Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy;
XX vaccine; ds.
OS Human immunodeficiency virus 1.
XX US2004101823-A1.
XX 27-MAY-2004.
XX 19-DEC-2002; 2002US-00325468.
XX 21-DEC-2001; 2001US-0343524P.
XX (MAXY-) MAXYGEN INC.
XX Soong NW, Pekrun K, Shibata R;
PI WPI; 2004-399670/37.
XX GENBANK; M38429.
XX New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a
PT composition for treating or preventing infection caused by HIV-1.
XX Disclosure; SEQ ID NO 46; 310pp; English.
CC The present invention relates to human immunodeficiency virus 1 (HIV-1)
CC viral variants and nucleic acids and polypeptides thereof having improved
CC replication properties for development of suitable animal models for the
CC study of HIV-1 pathogenesis. The invention is useful for treating and
CC preventing HIV-1 infection. The invention is also useful in gene therapy
CC and in the preparation of vaccines. The present sequence is human
CC immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the
CC invention.
XX
SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;
Query Match 55.4%; Score 1222.2; DB 12; Length 9540;
Best Local Similarity 90.0%; Pred. No. 2.1e-239;
Matches 1337; Conservative 0; Mismatches 133; Indels 15; Gaps 2;
Qy 72 CATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGGTACAGTCTA 131
Db 6289 CTTGCTCTTGGGACATTAATGATCTGTAGTGTAGAAAAAGTTGTGGGTACAGTCTA 6348
Qy 132 TTATGGGGTACTCTGTGGAGAGCAACCAACCACTCTATTTTGTGATCAGATGCTAA 191
Db 6349 TTATGGGGTACTCTGTGGAGAGCAACCAACCACTCTATTTTGTGATCAGATGCTAA 6408
Qy 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCC 251
Db 6409 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCC 6468
Qy 252 CAACCCCAAGAAGTAGTATTGGGAAATGTGCAGAAAAATTTTAACTGTGGAAAAATAA 311
Db 6469 CAACCCCAAGAAGTAGTATTGGGAAATGTGCAGAAAAATTTTAACTGTGGAAAAATAA 6528
Qy 312 CATGTAGATCAGATGATGAGGATATTAATCAGTTTATGGGATGAAGCCCTAAAGCCATG 371
Db 6529 CATGTAGACAGATGACAGGAGGATGTAATCAATTTATGGGATCAAGCTTAAAGCCATG 6588
Qy 372 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAAATTTGAATATCACTAAGAA 431
Db 6589 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCAAGATGT-----GAA 6636
Qy 432 TACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAGAGAAAGAGAGAAATAAAAAATTG 491
Db 6637 TGCTACTAATACCCTAGTAGTAGGGAATGATGAGAGAGAGAGAGAAATAAAAAACTG 6696
Qy 492 CTCCTTCTATATCACCAAGCATAAGAAATAAGTAAAGAAAGAAATATGACATTTTAA 551
Db 6697 CTCCTTCAATATCACCAAGCATAAGAGATAAGGTGCGAGAGAAATATGCTCTTTTTA 6756
Qy 552 TAGACTTGTATGTACCAATAGAAAAATACATAATAACTAAGTATAGGTTTAATAAGTTG 611

Db 6757 TAACTGGATGTAGTACCAATAGATTAATAGAAATATACAAATATAGGTTTAAATAGTTG 6816
Qy 612 TAACACCTCAGTCATTACACAGSCCTGTCCAAAGGTATCCTTTTCAGCCAAATTTCCCATACA 671
Db 6817 TAACACCTCAGTCATTACACAGSCCTGTCCAAAGGTATCCTTTGAACCAATTTCCCATACA 6876
Qy 672 TTATGTGTCCCGCTGGGTTCGATGCTAAAGTGTAAACATTAAGACATTTCAATGGATC 731
Db 6877 TTATGTGTCCCGCTGGGTTCGATGCTAAAGTGTAAACATTAAGACATTTCAATGGAAA 6936
Qy 732 AGGACCATGCACAAATGTCCAGACAGTACAATGTACACATGGAATTTAGGCCAGTGTGTC 791
Db 6937 AGACAAATGTAAATGTCCAGACAGTACAATGTACACATGGAATTTAGGCCAGTGTATC 6996
Qy 792 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAGACATAGTAATTTAGATCTGAAAA 851
Db 6997 AACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAGAGTGTGAATTTAGATCTGACAA 7056
Qy 852 TTTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAAATTTG 911
Db 7057 TTTTACGGCAATGCTTAAACCATTAATAGTACAGCTGAATGAATCTGTAAAAATTAATTTG 7116
Qy 912 TACAAGACCCCAACAATACAGAGAGAGGTTTATCTATAGGACAGGAGAGCATTTTA 971
Db 7117 TACAAGGCCCAACAATACAGAGAGAGTATACATATAGGACAGGAGAGCATTTTA 7176
Qy 972 TGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGATAGTAGGACAAA 1031
Db 7177 TACACAGGAGAATAATAGGAGATATAAGACAAGCACATTTGATAGTAGGACACA 7236
Qy 1032 ATGGAATAACACTTTACACAGATGTTATAAAATTAAGAGAAAAATTTAGGAATAAAMC 1091
Db 7237 ATGGAATAACACTTTAAACACAGATGTTAAAAATTAAGAGAACAAATTTAATAAATAAAC 7296
Qy 1092 ATAGCCTTTAATCAATCCTCAGGAGGACCCAGAAATGTAATGCACAGTTTAAATTTG 1151
Db 7297 AATAGTCCTTACTCCTCAGGAGGGGATCCAGAAATGTAATGCACAGTTTAAATTTG 7356
Qy 1152 TGGAGGGGAATTTCTTACTGTAATACACACAATGTTTAAATAGTACTTGGAAATGTTAC 1211
Db 7357 TGGAGGGGAATTTTCTACTGTAATACACACAATGTTTAAATAGTACTTGGAAATGATAC 7416
Qy 1212 TGGAGGGCAAAATGGCACTGGAAGGAATGACATAATCACATCTCCAATGCAGAAATAAACA 1271
Db 7417 TGAAAAAGTCAAGTGGCACTGGAAGGAATGACACCATCATCTCCCATGCAGAAATAAACA 7476
Qy 1272 AATTATTAATATGTGCAGAAAGTAGGAAAGCAATGTAATGCTCCCTCCCATCACAGGACA 1331
Db 7477 AATTATTAACATGTGGCAGGAATGGGAAAGCAATGTAATGCTCCCTCCCATTAAGGAGACA 7536
Qy 1332 AATTAGATGTTTCAATCAATATTACAGGCTGCTACTTAACAAGAGATGGAGGTAATAGTAC 1391
Db 7537 AATTAGATGTTTCAATCAATATTACAGGCTGCTACTTAACAAGAGATGGTGTAA---AAA 7593
Qy 1392 TGAGACTGAGCTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGAACAATTTGAGAGAG 1451
Db 7594 TGAGAGTGGAGTGGAGATCTTCAGACCTGGAGGAGGAGACATGAGGGAACAATTTGAGAGAG 7653
Qy 1452 TGAATATATAATATAAGTAGTAGAATTTGAACCAATAGAGTAGACCCACCCAGGCGC 1511
Db 7654 TGAATATATAATATAAGTAGTAGAATTTGAACCAATAGAGTAGACCCACCCAGGCGC 7713
Qy 1512 AAAGAAGAACAAGTGCAGGAAGAAAAAAGACCGGATCCAGGAAG 1556
Db 7714 AAAGAAGAAGTGGTGCAAGAGAAAAAAGACAGTGGGAATAGG 7758

RESULT 14

ADP20074

ID ADP20074 standard; DNA; 9540 BP.

XX

AC ADP20074;

XX DT 09-SEP-2004 (first entry)
XX DE Human immunodeficiency virus 1 isolate JRCSF nucleotide sequence.
XX KW immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSF;
KW gene; ds.
XX OS Human immunodeficiency virus 1.
XX PH Key Location/Qualifiers
FT LTR 1..635
FT /tag= a
FT /partial
FT 790..2304
FT /tag= b
FT /product= "gag"
FT 2085..5108
FT /tag= c
FT /product= "pol"
FT 5053..5631
FT /tag= d
FT /product= "vif"
FT 5571..5861
FT /tag= e
FT /product= "vpr"
FT 6073..6318
FT /tag= f
FT /product= "vpu"
FT 6236..8782
FT /tag= g
FT /product= "env"
FT 8784..9434
FT /tag= h
FT /product= "nef"
FT 9103..9540
FT /tag= i
FT /partial
XX WO2004053100-A2.
XX 24-JUN-2004.
XX 11-DEC-2003; 2003WO-US039534.
XX 11-DEC-2002; 2002US-0432869P.
XX 24-APR-2003; 2003US-0465350P.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Wilson I, Pantophlet R;
XX WPI; 2004-480933/45.
XX P-P8DB; ADP20067, ADP20068, ADP20069, ADP20070, ADP20071, ADP20072,
XX ADP20073.
XX GENBANK; M38429.
XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against
XX the polypeptide, useful preventing or treating human immunodeficiency
XX virus (HIV) infection, especially HIV-1 infection.
XX Disclosure; Page 139-141; 149pp; English.
XX
XX The present invention describes an immunogenic mutant HIV gp120
XX polypeptide that can stimulate a neutralising antibody response against a
XX human immunodeficiency virus (HIV). Also described: (i) an immunogenic
XX mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising
XX antibody response against a panel of HIV-1 comprising HIV-1 primary
XX isolates of at least two different clades, where the mutant gp120 has at
XX least one amino acid mutation in at least one epitope of the HIV-1 gp120
XX polypeptide specifically bound by a neutralising antibody, which reduces

CC binding affinity of the non-neutralising antibody; (2) an immunogenic
CC mutant HIV-1 gp120 polypeptide (Ib) having at least one amino acid
CC mutation in at least one epitope of the gp120 polypeptide specifically
CC bound by a non-neutralising antibody; (3) a vaccine (II) comprising one
CC or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5)
CC an isolated HIV neutralising antibody (IV) fraction obtained by using
CC (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V)
CC obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in
CC a subject, by administering an HIV neutralising antibody produced in
CC response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV
CC -1 infection in a human subject, involves administering HIV-1
CC neutralising antibodies to the subject, where the HIV-1 neutralising
CC antibodies comprise antibodies stimulated in response to (II); (9) HIV
CC neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV
CC neutralising antibodies (VII) obtained by using (Ib); and (11) isolated
CC HIV-1 neutralising antibodies obtained by harvesting spleen and lymph
CC nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV
CC activities, and can be used in vaccines and in HIV binding agents. (Ia)
CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1
CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1
CC which involves immunising a subject with a (Ia) or (Ib). The antibodies
CC are useful for preventing or ameliorating HIV, especially HIV-1,
CC infection in a subject. The present sequence represents an HIV-1 isolate
CC JRC5F genomic nucleotide sequence, which is given in the exemplification
CC of the present invention.

SQ Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;

Query Match 55.4%; Score 1222.2; DB 12; Length 9540;
Best Local Similarity 90.0%; Pred. No. 2.1e-239;
Matches 1337; Conservative 0; Mismatches 133; Indels 15; Gaps 2;

QY	72	CATGCTCCTGGGATTTGATGATCTGTAGTGTACAGAAAATTTGGGTCCACAGTCTA	131
DB	6299	CTTGCTCCTGGGACATTAATGATCTGTAGTGTGTAGAAAAGTTGGGTCCACAGTCTA	6348
QY	132	TTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA	191
DB	6349	TTATGGGGTACCTGTGTGGAGAGAAACCAACCACTCTATTTTGTGCATCAGATGCTAA	6408
QY	192	AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGACC	251
DB	6409	AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGACC	6468
QY	252	CAACCCACAGAGTGTATTTGGGAATGTGCAGAAAATTTTACATGTGGAANAATAA	311
DB	6469	CAACCCACAGAGTGTATTTGGGAATGTGAACAAATTTTAACTGTGGAANAATAA	6528
QY	312	CATGCTAGATCAGATGTCATGAGGATATATCAGTTTATGGGATGAAAGCTTAAAGCCATG	371
DB	6529	CATGCTAGACAGATGTCAGGAGATGTAATCAATTTATGGGATCAAGCTTAAAGCCATG	6588
QY	372	TGTAAATTTAACCCCACTCTGTGTTACTTTTAAATTTGCACATAATTTGAATATCATAAGAA	431
DB	6589	TGTAAATTTAACCCCACTCTGTGTTACTTTTAAATTTGCAAGATGT-----GAA	6636
QY	432	TACTACTAATCCACTAGTACAGCTGGGATGTGGAGAACGAGAAATTAATAATTTG	491
DB	6637	TGCTACTAATACCACTAGTGTAGTGTGGGAATGTATGGAGAGAGAGAAATTAATAATTTG	6696
QY	492	CTCTCTTCTATATCACCACAGCATTAAGAAATTAAGGTAAAGAAAGAAATATGCACTTTTAA	551
DB	6697	CTCTTCTCAATATACCAANAAGCATTAAGATTAAGGTGCGAAGAAATATGCTCTTTTAA	6756
QY	552	TAGACTTGTAGTACCAATAGAAAATCTAATAATACTAAGTATAGGTTAATAAGTTG	611
DB	6757	TAAACTGGATGTAGTACCAATAGAAAATTAAGAAATTAATAACCAATATAGGTTAATAAGTTG	6816
QY	612	TAAACCTCAGTCATTACACAGCCCTGTCCAAGGTATCTTTTCAGCCAAATTTCCCATACA	671
DB	6817	TAAACCTCAGTCATTACACAGCCCTGTCCAAGGTATCTTTTCAGCCAAATTTCCCATACA	6876
QY	672	TTATGTTGTCCCGGTGGGTTTGGCATGTCTAAAGTGTAAACAATAAGACATTTCAATGGATC	731

DB	6877	TTATGTTGCCCGGCTGGTTTTGGCATTTCTAAAGTGTAAATAAAGACATTTCAATGGAAA	6936
QY	732	AGGACCATGCAACAATGTTCAGCACAGTACATGTACACATGGAATTTAGCCAGTGGTCTC	791
DB	6937	AGGCAATGTATAAATGTTCAGCACAGTACATGTACACATGGAATTTAGCCAGTGGTCTC	6996
QY	792	AACCTCAACTGCTGTTTAAATGTCAGTCTAGCAGAAGACACATAGTAATTTAGATCTGAAA	851
DB	6997	AACCTCAACTGCTGTTTAAATGTCAGTCTAGCAGAAGACACATAGTAATTTAGATCTGAAA	7056
QY	852	TTTTCACAGCAATGCTTAAACCATATAATAGTACAGCTAAATGAATCTGTAGTAATTAATG	911
DB	7057	TTTTAGGACAATGCTTAAACCATATAATAGTACAGCTGAATGAATCTGTAAATAATTAATG	7116
QY	912	TACAAGACCCCAACAACAATACAGAAGAAAGTTTATCTATAGACACAGGAGAGCAATTTA	971
DB	7117	TACAAGGCCCCAGCAACAATACAGAAGAAAGTTTATACATATAGACACAGGAGAGCAATTTA	7176
QY	972	TGCAAGAAGAAACAATAATAGGAGATATTAAGACAAGCACATTTGTAACATTTAGTAGCAAA	1031
DB	7177	TACAACAGGAGAAATATAGGAGATATTAAGACAAGCACATTTGTAACATTTAGTAGCAAA	7236
QY	1032	ATGGAATAACACTTTTACACACAGATAGTTTATAAATAAAGAGAAAAAATTTAGGAATAAAC	1091
DB	7237	ATGGAATAACACTTTTAAACACAGATAGTTTAAATAAAGAGAAAAAATTTAATAATAAAC	7296
QY	1092	AATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCACAGTTTAATG	1151
DB	7297	AATAGTCTTTTACTCACTCCTCAGGAGGGGATCCAGAAAATTTGTAATGCACAGTTTAATG	7356
QY	1152	TGGAGGGGAAATTTCTTCTACTGTAAATACAGCACAACTGTTTAAATAGTACTTTGGAATGTTAC	1211
DB	7357	TGGAGGGGAAATTTTCTTCTACTGTAAATCAACACAACTGTTTAAATAGTACTTTGGAATGTTAC	7416
QY	1212	TGGAGGGGCAAAATGSCACTGGAAGGAAATGACATAATCACTCCCAATGCAGAAATAAACAA	1271
DB	7417	TGAAAAGTCAAGTGGCACTGGAAGGAAATGACACCAATCATCTCCCATGCAGAAATAAACAA	7476
QY	1272	AATTATAATATGCGGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCTCCATCAGAGGACA	1331
DB	7477	AATTATAAACATGTGCGGAGGAAAGTAGGAAAAGCAATGTATGCTCTCCATTTAAAGGACA	7536
QY	1332	AATTAGATGTTTCATCAAAATATTACAGGCTGCTACTATAACAAGAGATGGAGGTAATAGTAC	1391
DB	7537	AATTAGATGTTTCATCAAAATATTACAGGCTGCTACTATAACAAGAGATGGGTTAA---AAA	7593
QY	1392	TCAGACTCAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGAACAATTTGAGAGAG	1451
DB	7594	TGAGAGTCAGATCGAGATCTTCAGACCTGGAGGAGAGACATGAGGGAACAATTTGAGAGAG	7653
QY	1452	TGAATTTATATAAATAAAGTAGTAAGAAATTTGAACCAATAGAGTAGCACCCACCCAGGC	1511
DB	7654	TGAATTTATATAAATAAAGTAGTAAGAAATTTGAACCAATTTAGGAGTAGCACCCACCCAGGC	7713
QY	1512	AAAGAGAGAGAACAGTGCACAAAGAGAAAAAGACCCGATCCAGAAAG	1556
DB	7714	AAAGAGAGAGAGTGGTGCACAAAGAGAAAAAGACCCAGTGGGAATAGG	7758

RESULT 15

AAQ14753

ID AAQ14753 standard; DNA; 3807 BP.

XX AAQ14753;

XX

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 05-FEB-1992 (first entry)

XX HIV-1 BA-L clone.

XX human immunodeficiency virus; United States; MN isolate; AIDS;

KW envelope protein; ss.
 XX Human immunodeficiency virus 1.
 XX
 FH Key Location/Qualifiers
 FT CDS 394..476
 FT /*tag= b
 FT /product= "rev"
 FT 648..3215
 FT /*tag= a
 FT /product= "env"
 XX
 XX USN7599491-N.
 PN 15-OCT-1991.
 XX
 XX 17-OCT-1990; 90US-00183830.
 PF
 XX 17-OCT-1990; 90US-00599491.
 PR
 XX (USSH) NAT INST OF HEALTH.
 PA
 XX Reitz M;
 XX
 XX WPI; 1991-346752/47.
 DR P-PSDB; AAR14905.
 XX
 XX US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in
 PT therapeutics, vaccines and diagnostic tests.
 XX
 XX Example 3; Fig 8; 61pp; English.
 PS
 XX A HindIII fragment of unintegrated viral DNA representing the HIV-1 (BA-
 CC L) genome was cloned by standard techniques into lambda phage Charon 28
 CC DNA from total DNA of peripheral blood macrophages infected with and
 CC producing HIV-1 (BA-L). A positive clone was selected by hybridisation
 CC using a HIV-1 envelope probe. This clone, designated BA-L1, contained the
 CC entire env gene. The insert was subcloned and sequenced. The BA-L1 plasmid
 CC clone has been deposited as ATCC 40890. The sequence also contains the
 CC coding region for the rev protein which is needed for efficient
 CC expression of the envelope protein in eukaryotic cells. (Note: Revised
 CC entry submitted to correct the patent number format of US Government-
 CC owned NTIS applications to prevent clashes with ongoing US granted patent
 CC numbers. For further information please visit the Derwent web site at
 CC www.derwent.com/dwpi/updates/ntis us.html.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;
 Query Match 55.2%; Score 1219; DB 2; Length 3807;
 Best Local Similarity 89.7%; Pred. No. 8.2e-239;
 Matches 1335; Conservative 0; Mismatches 145; Indels 9; Gaps 2;
 QY 72 CATGCTCTGGGATATTGATGATCTGTAGTGTACAGAAAATTTGGTGGTCAAGTCTA 131
 DB 701 CATGCTCTGGGATATTGATGATCTGTAGTGTACAGAAAATTTGGTGGTCAAGTCTA 760
 QY 132 TTATGGGGTACCTGTGTGAGAGAGCAACACCACTCTATTCTGTGATCAGATGCTAA 191
 DB 761 TTATGGGGTACCTGTGTGAGAGAGCAACCACTCTATTCTGTGATCAGATGCTAA 820
 QY 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 251
 DB 821 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 880
 QY 252 CAACCCACAGAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAAAATAA 311
 DB 881 CAACCCACAGAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAAAATAA 940
 QY 312 CATGGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 371
 DB 941 CATGGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1000

QY 372 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGA-----ATATCAC 425
 DB 1001 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAAGAAATGCTACTAA 1060
 QY 426 TAAGAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAAGAAATGCTACTAA 485
 DB 1061 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAAGAAATGCTACTAA 1120
 QY 486 AAATTTGCTCTTTTAT 545
 DB 1121 AAATTTGCTCTTTTAT 1180
 QY 546 TTTTAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAAGAAATGCTACTAA 605
 DB 1181 TTTTAAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAAGAAATGCTACTAA 1240
 QY 606 AAGTTGTAACACCTCAGTCATTTACACAGGCTGTCCAAAGGTATCTTTTACGCCAATTTCC 665
 DB 1241 AAGTTGTAACACCTCAGTCATTTACACAGGCTGTCCAAAGGTATCTTTTACGCCAATTTCC 1300
 QY 666 CATACATTTATTTGTCCTGGCTGGTGTTCGATGCTAAAGTGTAAACAATAGACATTTCAA 725
 DB 1301 CATACATTTATTTGTCCTGGCTGGTGTTCGATGCTAAAGTGTAAACAATAGACATTTCAA 1360
 QY 726 TGGATCAGGACCATGACAAATGTACACACAGTACAAATGTACACATGGAATTTAGCCAGT 785
 DB 1361 TGGAAAAGGACCATGACAAATGTACACACAGTACAAATGTACACATGGAATTTAGCCAGT 1420
 QY 786 GGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGACATAGTAATTTAGATC 845
 DB 1421 AGTATCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGACATAGTAATTTAGATC 1480
 QY 846 TGAATAATTTACAGCAATGCTTAAACCATATATAGTACAGCTTAAATGAATCTGTAGTAA 905
 DB 1481 CGCCAAATTTTCGCGACCAATGCTTAAAGTCTAATATAGTACAGCTTAAATGAATCTGTAGTAA 1540
 QY 906 TAATTTGTAACAGACCAACCAATATACAGAGAGGTTATCTATAGACACAGGAGAGC 965
 DB 1541 TAATTTGTAACAGACCAACCAATATACAGAGAGGTTATCTATAGACACAGGAGAGC 1600
 QY 966 ATTTTATGCAAGAGAAACATAATAGGAGATATAGACAGACACATTTGTAACATTAGTAG 1025
 DB 1601 ATTTTATGCAAGAGAAATATAGGAGATATAGACAGACACATTTGTAACATTAGTAG 1660
 QY 1026 AGCAAAATGGAATAACACTTTTACACAGATAGTTATATAAATTAAGAGAAAAATTTAGGAA 1085
 DB 1661 AGCAAAATGGAATAACACTTTTACACAGATAGTTATATAAATTAAGAGAAAAATTTAGGAA 1720
 QY 1086 TAAACAAATAGCTTTTAAATCAATCTCAGGAGGGGACCCAGAAAATTTGTAATGACACATTT 1145
 DB 1721 TAAACAAATAGCTTTTAAATCAATCTCAGGAGGGGACCCAGAAAATTTGTAATGACACATTT 1780
 QY 1146 TAAATTTGGAGGGGAATTTCTTACTGTAAATACAGCACTCTTAAATAGTACTTTGGAA 1205
 DB 1781 TAAATTTGGAGGGGAATTTCTTACTGTAAATACAGCACTCTTAAATAGTACTTTGGAA 1840
 QY 1206 TGTACTTGAGGGGACCAATGTCCTGAGAGGAAATGACATAATCACTCCCAATGCGAAT 1265
 DB 1841 TGTACTTGAGGGGACCAATGTCCTGAGAGGAAATGACATAATCACTCCCAATGCGAAT 1900
 QY 1266 AAAACAAATTAATAATATGTCGCGAGAAAGTATAGGAAAAGCAATGTATGCCCTCCCATCAC 1325
 DB 1901 AAAACAAATTAATAATATGTCGCGAGAAAGTATAGGAAAAGCAATGTATGCCCTCCCATCAC 1960
 QY 1326 AGGCAAAATTAATAATATGTCGCGAGAAAGTATAGGAAAAGCAATGTATGCCCTCCCATCAC 1385
 DB 1961 AGGCAAAATTAATAATATGTCGCGAGAAAGTATAGGAAAAGCAATGTATGCCCTCCCATCAC 2017
 QY 1386 TAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGAGATATAGGAGGAAATTTG 1445
 DB 2018 TCCTGAGGACCAACAGACCGAGGCTTCAGACCTGGAGGAGAGATATAGGAGGAAATTTG 2077
 QY 1446 GAGAAAGTGAATTAATAATAATTAAGTAGTAAGAAATTTGAACCAATAGGAGTAGACCCAC 1505

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 128.864 Seconds
(without alignments)
12178.890 Million cell updates/sec

Title: US-09-687-864A-13
Perfect score: 2208
Sequence: 1 aagtttgcgcgcgtctgtg.....aactcgagtgataatctaga 2208

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225.8	55.5	3807	1	US-08-022-835-5
2	1225.8	55.5	3807	1	US-08-388-809-5
3	1225.8	55.5	3807	2	US-08-647-714-5
c 4	1174.2	53.2	3807	2	US-08-417-210A-78
c 5	1174.2	53.2	3807	4	US-09-136-159A-78
6	1173	53.1	2552	2	US-08-448-603A-27
7	1173	53.1	2552	3	US-09-134-075-27
8	1173	53.1	2552	3	US-09-492-739-27
9	1172.2	53.1	2571	1	US-08-254-358-3
10	1172.2	53.1	2571	1	US-08-475-391-3
11	1172.2	53.1	2571	2	US-08-709-609-3
12	1172.2	53.1	2571	4	US-09-552-950-3
13	1172.2	53.1	2571	4	US-09-936-572-3
14	1172.2	53.1	2571	5	PCT-US95-07178-3
c 15	1172.2	53.1	6474	3	US-08-651-472-66
c 16	1172.2	53.1	6474	3	US-08-358-928-66
17	1172.2	53.1	6926	3	US-08-651-472-69
18	1172.2	53.1	6926	3	US-08-358-928-69
19	1172.2	53.1	9739	1	US-08-022-835-1
20	1172.2	53.1	9739	1	US-08-388-809-1
21	1172.2	53.1	9739	2	US-08-647-714-1
22	1172.2	53.1	9746	1	US-08-022-835-3
23	1172.2	53.1	9746	2	US-08-388-809-3
24	1172.2	53.1	9746	2	US-08-647-714-3
25	1171.4	53.1	1539	3	US-07-956-483-21
26	1171.4	53.1	1539	3	US-08-472-240A-13
27	1169.8	53.0	2573	2	US-08-448-603A-29

28	1169.8	53.0	2573	3	US-09-134-075-29	Sequence 29, Appl
29	1169.8	53.0	2573	3	US-09-492-739-29	Sequence 29, Appl
30	1168.8	52.9	4527	2	US-08-944-449-8	Sequence 8, Appl
31	1168.8	52.9	4527	3	US-09-353-362-8	Sequence 15, Appl
32	1168.6	52.9	1532	2	US-08-037-816A-15	Sequence 15, Appl
33	1168.6	52.9	1532	2	US-08-530-146-15	Sequence 15, Appl
34	1165.4	52.8	1532	2	US-08-037-816A-27	Sequence 27, Appl
35	1165.4	52.8	1532	2	US-08-530-146-27	Sequence 27, Appl
36	1161.8	52.6	1932	4	US-09-475-515-31	Sequence 31, Appl
37	1161.8	52.6	2457	4	US-09-475-515-32	Sequence 32, Appl
38	1161.6	52.6	2570	2	US-08-448-603A-31	Sequence 31, Appl
39	1161.6	52.6	2570	3	US-09-134-075-31	Sequence 31, Appl
40	1161.6	52.6	2570	3	US-09-492-739-31	Sequence 31, Appl
41	1161	52.6	1419	4	US-09-475-515-30	Sequence 30, Appl
42	1160.8	52.6	9737	3	US-08-944-449-7	Sequence 7, Appl
43	1160.8	52.6	9737	3	US-09-353-362-7	Sequence 12, Appl
44	1160.4	52.6	1929	4	US-09-602-864-12	Sequence 12, Appl
45	1160	52.5	1527	3	US-07-956-483-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-022-835-5
; Sequence 5, Application US/08022835
; Patent No. 5420030
; GENERAL INFORMATION:
; APPLICANT: Reitz Jr., Marvin S.
; APPLICANT: Franchini, Genoveffa
; APPLICANT: Markham, Phillip D.
; APPLICANT: Gallo, Robert C.
; APPLICANT: Lori, Franco C.
; APPLICANT: Popovic, Mikulas
; APPLICANT: Gainter, Suzanne
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,835
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

[illegible]

TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 648..3215
US-08-388-809-5

Query Match 55.5%; Score 1225.8; DB 1; Length 3807;
Best Local Similarity 89.9%; Pred. No. 1.3e-289;
Matches 1340; Conservative 0; Mismatches 142; Indels 9; Gaps 2;

QY 72 CATGCTCTCGGATATTGATGATCTAGTGTCTACAGAAAATTTGGGTCAAGTCTA 131
DB CATGCTCTCGGATATTGATGATCTAGTGTCTAGAAAATTTGGGTCAAGTCTA 760
QY 132 TTATGGGGTACTGTGTGGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA 191
DB TTATGGGGTACTGTGTGGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA 820
QY 192 AGCCTATGATCAGAGGTACATAATTTTGGGCCACACATGCTGTGTACCCAGAGCCC 251
DB AGCATATGATCAGAGGTACATAATTTTGGGCCACACATGCTGTGTACCCAGAGCCC 880
QY 252 CAACCCCAAGAGTAGTATTGGGAAATGTGCAGAAAATTTTAACTGTGGAAAATAA 311
DB CAACCCCAAGAGTAGTATTGGGAAATGTGCAGAAAATTTTAACTGTGGAAAATAA 940
QY 312 CATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCCATG 371
DB CATGCTAGAACAAATGATGAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCCATG 1000
QY 372 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTGA-----ATATCAC 425
DB TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTGAAGGAATGCTACTAA 1060
QY 426 TAAGNATCTACTAATCCCATGTAGTACAGCTGGGATGATGGAGAAGGAGAAATAA 485
DB TGGGAATGACACTAATACCTAGTGTAGTACAGGGGAATGGTGGGGGAGGAGAAATGAA 1120
QY 486 AAATGTCTCTTCTATATACCAAGCATAAAGAAATAGGTAAAGAAAGAAATATGCACT 545
DB AAATGTCTCTTCTATATACCAAGCATAAAGAAATAGGTAAAGAAAGAAATATGCACT 1180
QY 546 TTTTAAATAGACTGTATGTAGTACCAATAGAAAATACTAATAATCTAAGTATAGTTAAT 605
DB TTTTAAATAGACTGTATGTAGTACCAATAGAAAATACTAATAATCTAAGTATAGTTAAT 1240
QY 606 AAGTTGTAACACTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCCAATCC 665
DB AAGTTGTAACACTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCCAATCC 1300
QY 666 CATACATTATTGTGTCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 725
DB CATACATTATTGTGTCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1360
QY 726 TGGATCAGGACCATGACAAAATGTGACGACAGTACAAATGTACATGGAATTTAGGCCAGT 785
DB TGGAAAAGGACCATGACAAAATGTGACGACAGTACAAATGTACATGGAATTTAGGCCAGT 1420
QY 786 GGTGTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATAGATC 845
DB AGTATCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATAGATC 1480
QY 846 TGAATAATTTCAAGCAATGCTTAAACCATATAGTACAGCTTAAATGATCTGTAGTAAT 905
DB CGCAATTTTCGGGCAATGCTTAAAGTCATTAATAGTACAGCTTAAATGATCTGTAGTAAT 1540

QY 906 TAAATTGTACAGACCCCAACAACATACAGAAAGAGGTATTCTATAGACCCAGGAGAGC 965
DB TAAATTGTACAGACCCCAACAACATACAGAAAGAGGTATTCTATAGACCCAGGAGAGC 1600
QY 966 ATTTTATGCAAGAGAAACATAAATAGGAGATATAAGCAAGCACATTGTAACATTAGTAG 1025
DB ATTTTATGCAAGAGAAACATAAATAGGAGATATAAGCAAGCACATTGTAACATTAGTAG 1660
QY 1026 AGCAAAATGGAAATAACACTTTTCAACAGATAGTTTATAAAATTAAGAGAAAATTTAGGAA 1085
DB AGCAAAATGGAAATGACACTTTTAAATTAAGATAGTTTATAAAATTAAGAGAAAATTTGGGAA 1720
QY 1086 TAAACAATAGCTTTTAACTCCTCAGAGGGGAGCCAGAAAATTTGTAATGCACAGTTT 1145
DB TAAACAATAGCTTTTAACTCCTCCTCAGAGGGGAGCCAGAAAATTTGTAATGCACAGTTT 1780
QY 1146 TAAATTGTGGGGGAAATTTCTTCTACTGTAAATACAGCACAACTGTTTAAATAGTACTTGGAA 1205
DB TAAATTGTGGGGGAAATTTTCTTCTACTGTAAATTAACACAACTGTTTAAATAGTACTTGGAA 1840
QY 1206 TGTTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATCACTCCCAATGCAGAA 1265
DB TGTTACTGAAGAGTCAAAATTAACACTGTAGAAAATAACACAAATCACTCCCAATGCAGAA 1900
QY 1266 AAAACAAATTAATAATATGTGGGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1325
DB AAAACAAATTAATAACATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1960
QY 1326 AGGCAAAATAGATGTTTCATCAAAATATTACAGGCTGTCTACTAAACAGAGATGGAGGTAA 1385
DB AGGCAAAATAGATGTTTCATCAAAATATTACAGGCTGTCTACTAAACAGAGATGGAGGTAA 2017
QY 1386 TAGTACTGAGACTGAGACTTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 1445
DB TCCTTGAGGACAAACAGACCCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 2077
QY 1446 GAGAAAGTGAATTTATATAATATAAAGTAGTAAGAAATTTGAACCAATAGAGTAGACCCAC 1505
DB GAGAAAGTGAATTTATATAATATAAAGTAGTAAGAAATTTGAACCAATAGAGTAGACCCAC 2137
QY 1506 CAGGGCAAGAGAGAAACAGTCGAAAGAGAAAAGACCCGATCCAAAG 1556
DB CAGGGCAAGAGAGAGAGTGGTCAGAGAGAAAAGAGCAGTGGGAATAGG 2188

RESULT 3
US-08-647-714-5
; Sequence 5, Application US/08647714
; Patent No. 5869313
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C. LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,714
; FILING DATE:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4092US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 648..3215
US-08-647-714-5

Query Match 55.5%; Score 1225.8; DB 2; Length 3807;
Best Local Similarity 89.9%; Pred. No. 1.3e-289;
Matches 1340; Conservative 0; Mismatches 142; Indels 9; Gaps 2;

Qy	72	CATGCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTTCACAGTCTA	131
Db	701	CATGCTCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTTCACAGTCTA	760
Qy	132	TTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA	191
Db	761	TTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA	820
Qy	192	AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC	251
Db	821	AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC	880
Qy	252	CAACCCACAGAGTGTGTTGGGAAATGTGACAGAAAAATTTAACTGTGGAAAAATAA	311
Db	881	CAACCCACAGAGTGTGTTGGGAAATGTGACAGAAAAATTTAACTGTGGAAAAATAA	940
Qy	312	CATGTTAGATCAGATGCTAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCATG	371
Db	941	CATGTTAGAACAAATGCTATGAGATATAATCAGTTTATGGGATCAAGCCCTAAAGCCATG	1000
Qy	372	TGTAATAATTAACCCCACTCTGTGTACTTTAAATGGCACTAATTTGA-----ATATCAC	425
Db	1001	TGTAATAATTAACCCCACTCTGTGTACTTTAAATGGCACTAATTTGA-----ATATCAC	1060
Qy	426	TAAAGAACTACTAATATCCCACTAGTAGCAGCTGGGGAATGATGGAGAGAGAGAAATAA	485
Db	1061	TGGGAATGACACTAATACCACTAGTAGTAGCAGGGGAATGTTGGGGGGAGGAGAAATGA	1120
Qy	486	AAATTTGCTTTTCTATATCACCAAGCATAGAAATAAGGTAAAGAGAAATATGCACT	545
Db	1121	AAATTTGCTTTTCTATATCACCAAGCATAGAAATAAGGTAAAGAGAAATATGCACT	1180
Qy	546	TTTTTAATAGACTTGATGTAGTACCAATAGAAATACTAATAATAGTATAGTTAAT	605
Db	1181	TTTTTAATAGACTTGATGTAGTACCAATAGAAATACTAATAATAGTATAGTTAAT	1240
Qy	606	AAATTTGTAACACTCAGTCAATACACAGCCCTGTCCAAAGGTATCTTTTTCAGCCCAATCC	665
Db	1241	AAATTTGTAACACTCAGTCAATACACAGCCCTGTCCAAAGGTATCTTTTTCAGCCCAATCC	1300
Qy	666	CATACATTTATGTTGCCCGCTGGTTTTCGATGCTAAAGTGTAAACAATAGACATTCAA	725
Db	1301	CATACATTTATGTTGCCCGCTGGTTTTCGATGCTAAAGTGTAAACAATAGACATTCAA	1360

Qy	726	TGGATCAGGACCATGCAAAATGTGACACAGTACAATGTACACATGGAATTTAGGCCAGT	785
Db	1361	TGGAAAAGGACCATGTACAAATGTGACACAGTACAATGTACACATGGAATTTAGGCCAGT	1420
Qy	786	GGTCTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAGAACATAGTAATAGATC	845
Db	1421	AGTATCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAGAGAGTGTAAATTAGATC	1480
Qy	846	TGAAAATTTTACACAGCAATGCTTAAACATTAATAGTACAGCTAAATGAATCTGTAGTAAT	905
Db	1481	CGCAATTTTCGCGACCAATGCTTAAAGTCAATTAATAGTACAGCTGAATGAATCTGTAGAAAT	1540
Qy	906	TAAATTGTACAGAGCCCAACCAATACAAGAAAGGTTTCTATAGGACCCAGGAGAGC	965
Db	1541	TAAATTGTACAGAGCCCAACCAATACAAGAAAGGTTTCTATAGGACCCAGGAGAGC	1600
Qy	966	ATTTTATGCAAGAGAAACATAATAGGAGATATTAAGACAAGCACTTGTAACTAGTAG	1025
Db	1601	ATTTTATGCAAGAGAAATAATAGGAGATATTAAGACAAGCACTTGTAACTAGTAG	1660
Qy	1026	AGCAAAATGGAATGACACTTTTAAATTAAGATAGTTTAAATTAAGAGAACTTTGGAA	1085
Db	1661	AGCAAAATGGAATGACACTTTTAAATTAAGATAGTTTAAATTAAGAGAACTTTGGAA	1720
Qy	1086	TAAACAAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCACAGTTT	1145
Db	1721	TAAACAAATAGCCTTTTAAAGCACTCCTCAGGAGGGGACCCAGAAAATTTGTAATGCACAGTTT	1780
Qy	1146	TAAATTGTGGAGGGAAATTTCTTACTGTAAATACAGCACTGTTTAACTAGTACTTGGAA	1205
Db	1781	TAAATTGTGGAGGGAAATTTCTTACTGTAAATTAACCACTGTTTAACTAGTACTTGGAA	1840
Qy	1206	TGTTACTGGAGGGCAAAATGSCACTGAAGGAAATGACATATCACATCCCAATGCAGAAAT	1265
Db	1841	TGTTACTGAAGAGTCAAAATAACACTGTGAGAAAATAACCAATCACTCCCAATGCAGAAAT	1900
Qy	1266	AAAAAAATTAATAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC	1325
Db	1901	AAAAAAATTAATAATATGTGGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC	1960
Qy	1326	AGGCAAAATTAAGATGTTTCAATCAAAATATTAACAGGCTGCTACTAAACAGAGATGGAGTAA	1385
Db	1961	AGGCAAAATTAAGATGTTTCAATCAAAATATTAACAGGCTGCTACTAAACAGAGATGGAGTAA	2017
Qy	1386	TAGTACTGAGACTGAGACTGAGACTTTCAGACCTTGGAGGAGGAGATATGAGGCAATTTG	1445
Db	2018	TCCTGAGGACCAACAGACCCGAGGCTTTCAGACCTTGGAGGAGGAGATATGAGGCAATTTG	2077
Qy	1446	GAGAAATGAAATTAATAATAATAATAAGTAGTAAGAAATTTGAACCAATAGAGTAGCACCCAC	1505
Db	2078	GAGAAATGAAATTAATAATAATAATAAGTAGTAAGAAATTTGAACCAATAGAGTAGCACCCAC	2137
Qy	1506	CAGGCAAGAGAGAGAACACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1556
Db	2138	CAAGCAAGAGAGAGAGAGTGGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2188

RESULT 4
US-08-417-210A-78/c
; Sequence 78, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: FIOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-78

Query Match 53.2%; Score 1174.2; DB 2; Length 3807;
Best Local Similarity 88.1%; Pred. No. 5e-277;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

```
QY 52 TGGATCTGGCTTCGAGATCCATGCTCCTGGGATATTGATGATCTGTAGTGTACAGAA 111
DB 1668 TGGGGGTGGAGATGGGGACCAATGCTCCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609

QY 112 AAATTTGGGTGACAGTCTATTATGGGGTACCTGTGGAGAGAGCAACCACTCTA 171
DB 1608 AAATTTGGGTGACAGTCTATTATGGGGTACCTGTGGAGAGAGCAACCACTCTA 1549

QY 172 TTTTGTGCATGAGTCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
DB 1548 TTTTGTGCATGAGTCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 1489

QY 232 GCCTGTGTACACAGACCCCAACCAAGAGTAGTATTGGGAATGTGACAGAAAT 291
DB 1488 GCCTGTGTACACAGACCCCAACCAAGAGTAGAATTGGTAAATGTGACAGAAAT 1429

QY 292 TTTAACTGTGAAAAATAAATGTTAGATCAGATGATGAGATATATCAATGTTTATGG 351
DB 1428 TTTAACTGTGAAAAATAAATGTTAGATGATGAGATATATCAATGTTTATGG 1369

QY 352 GATGAAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTAAATGCACT 411
DB 1368 GATGAAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTTACTTTAAATGCACT 1309

QY 412 AATTTG-----AATATCACTAAGATATCTAATCCCACTAGTAGCAGCTGG 459
DB 1308 GATTTTGGGAATFACTACTAATACCAATAATAGTATGCTGTAAATAGTAATAGCGAG 1249

QY 460 GGAATGATGGAGAAAGGAGAAATAAATAATTTCTTTCTATATCACCAAGCATAGA 519
DB 1248 GGAACAAATAAGGGAGGAGAAATGAANAATCTCTTTCAATATCACCAAGCATAGA 1189

QY 520 AATAAGGTAAGAAAGATATGCACTTTTAAATAGACTTGTATGATACCAATAGAAAA 579
DB 1188 GATAAGATGCAGAAAGATATGCACTTTTAAATAGACTTGTATGATATGATATCAAT---AAAT 1132

QY 580 ACTAATAATGATAGTATAGTTAATAGTTGTATACCTCAGTCAATACACAGCCTGT 639
DB 1131 AATGATAGTACCAGCTAGTTGATAGTTGATAGTTGATAGTTGATAGTTGATAGTTGAT 1072

QY 640 CCAAGGATATCTTTTCAGCCCAATCCCATACATATTGTCCTCCGCTGGGTTTCGGATG 699
DB 1071 CCAAGGATATCTTTTTCAGCCCAATCCCATACATATTGTCCTCCGCTGGGTTTCGGATG 1012
```

```
QY 700 CTAAGTGTAAACAATAAGACATTCAATGGATCAGGACCATGTCACAAATGTCTAGCACAGTA 759
DB 1011 CTAAGTGTAAACAATAAGATTTAGTGGAAAAAGGATCATGTAAAAATGTCTAGCACAGTA 952

QY 760 CAATGTACACATGGAAATTTAGGCCAGTGTGCTCAACTCACTGCTGTTAAATGGCAGTCTA 819
DB 951 CAATGTACACATGGAAATTTAGGCCAGTGTATCACTCACTGCTGTTAAATGGCAGTCTA 892

QY 820 GCAGAAAGACATAGTAATTTAGATCTGAAATTTTACAGACAAATGCTTAAAAACCAATA 879
DB 891 GCAGAAAGACAGGTAGTAATTTAGATCTGAGAAATTTCAATGATATGCTTAAAAACCAATA 832

QY 880 GTACAGCTAAATGAATCTGTAGTAATTTTGTACAGACCCCAACCAATACAGACAGTA 939
DB 831 GTACATCTGAATGAATCTGTACAAATTTTGTACAGACCCCACTTACAAATAAAAAGAAA 772

QY 940 AGTTTATCTATAGGACACAGGAGAGCATTTTATGCAAGAGAAACATATATAGGAGATATA 999
DB 771 AGGATACATATAGGACACAGGAGAGCATTTTATACACAAATAATATATATAGGAACTATA 712

QY 1000 AGACAAGCACATTTGTAACATTAGTAGACAAATAAGGAATAACATTTTACACAGATAGTT 1059
DB 711 AGACAAGCACATTTGTAACATTAGTAGACAAATAAGGAATAACATTTTAAAGACAGATAGTT 652

QY 1080 ATAAAAATTAAGAGAAAAATTTAGGAAATAAACAATAGCTTTTAAATCAATCCTCAGAGGG 1119
DB 651 AGCAAAATTAAGAGAAAAATTTAGGAAATAAACAATAGCTTTTAAATCAATCCTCAGAGGG 592

QY 1120 GACCAGAAAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATCTTCTACTGTGTAATACA 1179
DB 591 GACCAGAAAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGGAATCTTCTACTGTGTAATACA 532

QY 1180 GCACAATCTGTTTAAATGATGTTTGGAAATGTTTACTGGAGGGGACAAATGGCAGCTGAAGG---A 1236
DB 531 TCACCACCTGTTTAAATGATGTTTGGAAATGTTTACTGGAAATAATACTACAGGGTCA 472

QY 1237 AATGACATAATCACTCACTCAATGACAGATAAACAATAATATTAATATGTTGGCAGAAAGTA 1296
DB 471 AATAACAATATCACACTTCAATGCAAAATAAACAATAATTAACAATGTTGGCAGAAAGTA 412

QY 1297 GGAAGCAATGTTATGCCCCCTCCCATCACAGGACAAATTTAGATGTTTCAATCAATATTACA 1356
DB 411 GGAAGCAATATATGCCCCCTCCCATTTGAAGCAAAATTTAGATGTTTCAATCAATATTACA 352

QY 1357 GGGCTGCTACTAACAAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTTC 1413
DB 351 GGGCTGCTACTAACAAGAGATGGTAAAGACACGGACACGAAACGACACCGAGATCTTC 292

QY 1414 AGACCTGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATATAATATAAGTA 1473
DB 291 AGACCTGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATATAATATAAGTA 232

QY 1474 GTAAGATTGAACCAATAGGAGTAGCACCACCGGCAAGAGAGAACAGTGCAGAAAGA 1533
DB 231 GTAACATTTGAACCAATAGGAGTAGCACCACCGGCAAGAGAGAACAGTGCAGAGTA 172

QY 1534 GAAAAAAGA 1542
DB 171 GAAAAAAGA 163
```

RESULT 5
US-09-136-159A-78/c
; Sequence 78, Application US/09136159A
; Patent No. 6596279
; GENERAL INFORMATION:
; APPLICANT: Viogenetics Corporation
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136,159A

RESULT 7
US-09-134-075-27
; Sequence 27, Application US/09134075
; Patent No. 6042836
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: 3 Embarcadero Center
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,603
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2552
US-09-134-075-27

Query Match 53.1%; Score 1173; DB 3; Length 2552;
Best Local Similarity 88.8%; Pred. No. 8.5e-277; Mismatches 135; Indels 33; Gaps 5;
Matches 1337; Conservative 0;

QY	64	TCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGGGTC	123
Db	46	TGGGCAACCACTCTCTTGGGATTTGATGATCTGTAGTGCTGAGAAAAATTTGGGTC	105
QY	124	ACAGTCTATTATGGGTCCTCTGTGGAGAGAACCAACCACTCTATTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGTCCTCTGTGGAGAGAACCAACCACTCTATTTTGTGCATCA	165
QY	184	GATGCTTAAGCCCTATGATACAGAGTACATATGTTGGGCCACACATGCTGTGACCC	243
Db	166	GATGCTTAAGCCCTATGATACAGAGTACATATGTTGGGCCACACATGCTGTGACCC	225
QY	244	ACAGACCCCAACCCCAAGAGTAGTATTGGAAATGTGACAGAAAAATTTAACATGTGG	303
Db	226	ACAGACCCCAACCCCAAGAGTAGTATTGGAAATGTGACAGAAAAATTTAACATGTGG	285
QY	304	AAAAATAACATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	363
Db	286	AAAAATAACATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	345

QY	364	AAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAATATC	423
Db	346	AAGCCATGTGTAAATTAACCCCACTATGTGTACTTTAAATTCACATAATTTGAATATC	399
QY	424	ACTAAGAATCTACTAATATCCCACTAGTAGCAGCTGGGGAATGTAGGAGAAAGGAGATA	483
Db	400	---AAAAATGCTACTAATATCCCACTAGTAGCAGCTGGGGAATGTAGGAGAGGAGATA	456
QY	484	AAAAATTCCTCTTCTATATACCAACCAAGCATAGAAATAGGTAAAGAAAGATATATCA	543
Db	457	AAAAACTGCTCTTTCAATGTCCACCAAGATATAGAGATAGAGAAATGAATATATCA	516
QY	544	CTTTTAAATAGACTTGTATAGTACCAATAGAAATACTAATAATCTAATAGTATAGGTTA	603
Db	517	CTTTTAAATAGACTTGTATAGTACCAATAGAAATACTAATAATCTAATAGTATAGGTTG	573
QY	604	ATAAGTTGTAAACACTCAGTCATTTACAGAGCTGTCCAAAGGTATCTTTTCAGGCAAT	663
Db	574	ATAAGTTGTAAACACTCAGTCATTTACAGAGCTGTCCAAAGGTATCTTTTCAGGCAAT	633
QY	664	CCCATACATTTATGTCCTCGGCTGTTTCCGATGCTTAAAGTGTAAACAATAGCATTC	723
Db	634	CCCATACATTTATGTCCTCGGCTGTTTCCGATGCTTAAAGTGTAAACAATAGCATTC	693
QY	724	AATGGATCAGGACCATGCAAAATGTGAGCAGTACAAATGTACACATGGAATTAGGCCA	783
Db	694	AACGGAACAGGACCATGTAACAATGTGAGCAGTACAAATGTACACATGGAATTAGGCCA	753
QY	784	GTGTGTCAACTCAACTGCTTTAAATGCGAGTCTAGCAGAGAGAGATAGTAAATAGA	843
Db	754	GTGTGTCAACTCAACTGCTTTAAATGCGAGTCTAGCAGAGAGAGATAGTAAATAGA	813
QY	844	TCTGAAATTTTACAGACAAATGCTTAAACCAATATAGTACAGTAAATGAATCTGTAGTA	903
Db	814	TCTGCAATTTTCTCGGCAATGCTTAAACCAATATAGTACAGTAAATGAATCTGTAGTA	873
QY	904	ATTAATTTGTACAAGACCCCAACAACAATACAAAGAGAGGTTTATCTATAGGACCGGAGA	963
Db	874	ATTAATTTGTACAAGACCCCAACAACAATACAAAGAGAGTATACATATAGGACCGGAGA	933
QY	964	GCATTTTATGCAAGAGAAACATATAGGAGATATAGCAAGCAATGTAACATTAAT	1023
Db	934	GCATTTTATGCAAGAGAGAAATATAGGAGATATAGCAAGCAATGTAACATTAAT	993
QY	1024	AGACCAAAATGGAATTAACACATTTTAAACAGATAGTTTAAAGAGAGAAATTTAGG	1083
Db	994	AGCAAAATGGAATTAACATTTTAAACAGATAGTTTAAAGAGAGAAATTTAGG	1050
QY	1084	AATAAAACATATAGCTTTAATCAATCTCTCAGGAGGAGCCAGAAATTTGTAATGCACAGT	1143
Db	1051	AATAAAACATATAGCTTTAATCAATCTCTCAGGAGGAGCCAGAAATTTGTAATGCACAGT	1110
QY	1144	TTTAATTTGGAGGGGAATTTCTTCTATCTGTAATACAGCAACTGTTTAAATAGTACTGG	1203
Db	1111	TTTAATTTGGAGGGGAATTTCTTCTATCTGTAATACAGCAACTGTTTAAATAGTACTGG	1170
QY	1204	AATGTTCTGAGGAGGACAAATGGCCTCAAGGAAATGA-----CATATATCA	1251
Db	1171	AATATATCTTATCTTGGAAATTAATCTGAAGGTCAAATGACACTGGAGAGAAATATCA	1230
QY	1252	CTCCAATGCAGAAATAAAACAAATTTAATATGTGGCAGAAAGTAGTAAAGCAATGTAT	1311
Db	1231	CTCCAATGCAGAAATAAAACAAATTTAATATGTGGCAGAAAGTAGTAAAGCAATGTAT	1290
QY	1312	GCCCTCCCATCAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	1371
Db	1291	GCCCTCCCATCAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	1350
QY	1372	AGAGATGGAGGTAAATAGTACTGAGACTGAGATCTTTCAGACCTGGAGGAGAGAT	1431
Db	1351	AGAGATGGAGGTAAATAGTACTGAGACTGAGATCTTTCAGACCTGGAGGAGAGAT	1404
QY	1432	ATGAGGACAAATTTGGAGAGAGTGAATTTATATAATATAAGTAGTAGAATTTGAACCAATA	1491

Db 1231 CTCCTCCATCAAGATAAAACAAATTAATAAATGTCGAGGAAGTAGGAAAAGCAATGTAT 1290
Qy 1312 GCCCTCCATCAGAGCAAAATAGATGTTTCATCAAAATATACAGGCTGCTACTACA 1371
Db 1291 GCCCTCCATCAAGAGGCAAAATAGATGCTCATCAAAATATACAGGCTGCTATTACA 1350
Qy 1372 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAT 1431
Db 1351 AGAGATGTTGTAATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAT 1404
Qy 1432 ATGAGGCAAAATGGAGAAGTCAATTAATAATAAAGTAGTAAGAAATTTGAACCAATA 1491
Db 1405 ATGAGGCAAAATGGAGAAGTGAATTAATAATAAAGTAGTAAGAAATTTGAACCAATA 1464
Qy 1492 GGAGTAGCACCACAGGCGAAAGAGAAGACAGTGCAAGAGAAAAAGACCGGATCCA 1551
Db 1465 GGAGTAGCACCACAGGCGAAAGAGAAGAGTGATGCGAGAGAAAAAGAGAGTGCGGA 1524
Qy 1552 AGAAG 1556
Db 1525 ATAGG 1529

RESULT 9

US-08-254-358-3
; Sequence 3, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/254,358
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658785and, Greta E.
; REGISTRATION NUMBER: 35,502
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-254-358-3

Query Match 53.1%; Score 1172.2; DB 1; Length 2571;
Best Local Similarity 87.9%; Pred. No. 1.3e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGTTTCAGATCCATGCTCTTGGGATATTGATGATCTGATGCTACAGAAAAATTG 117
Db 40 TGGGGATGGGCACGATGCTCTTGGGTTATTAAATGATCTGTAGTGTACAGAAAAATTG 99

Qy 118 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACACCTCTATTTTGT 177
Db 100 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACACCTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCACCAAGAGTACTATTGGGAAATGTGACAGAAAAATTTTAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTACTATTGGGAAATGTGACAGAAAAATTTTAAC 279
Qy 298 ATGTGGAAAAATAACATGCTAGATCAGATGATGAGGATATAAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGCTAGATGATGAGGATATAAATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTCTCTTTAAATTTGACATAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTCTCTTTAAATTTGACATAATTG 399
Qy 418 -----AATATCACTAAGATACTACTATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATCTACTTAATACCAATAATAGTACTGCTTAATAACAATAGTATAGCGAGGAACA 459
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAAGCATTAAGAAATAG 525
Db 460 ATAAAGGGAGGAGAAATCAAAAACTGCTCTTTCAATATCACCACAAAGCATTAAGAGATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTGTGATGATGATGATGATGATGATGATGAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTTAAATACTGATATAGTATCAATAG---ATAATGAT 576
Qy 586 AATCTAAGTATAGTTTAATAGTTTAAACACCTCAGTCAATACACAGCCCTGTCCTCAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTTGATAGTTGATAGTTGATAGTTGATAGTTGATAGTTGAT 636
Qy 646 GTATCCTTTTACGCAATTTCCCATACATTTATGTTGTCGCGCTGGGTTTTCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCATTTCCCATACATTTATGTTGCCCCGGCTGTTTTCGATTTCTAATA 696
Qy 706 TGTAACATAAGACATTTCAATGGATCAGGACATGCAACAATGTCAGACAGTACATGAT 765
Db 697 TGTAACGATAAAAAAGTTTCAAGTGGAAAAAGGATCATGTAAAAAATGTCAGACAGTACATG 756
Qy 766 ACATGCAATTAGCCAGTGTGTCACCTCAACTGCTGTTAAATGGCAGTCTACAGAA 825
Db 757 ACATGGAATTAGGCCAGTGTATCAACTCAACTGCTGTTAAATGGCAGTCTACAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAAAATTTTCAGACAAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAGAAATTTTCACTGATATGCTTAAACCATCATAGTACAT 876
Qy 886 CTAATGAATCTGTAGTAAATTAATTTGATCAAGACCCCAACAATATCAAGAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTTAAATTTGTAACAAGACCCCAACTCAATAAAGAAAAAGGATA 936
Qy 946 TCTATAGGACCCAGGAGAGCATTTTATGCAAGAGAAACATATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCCAGGAGAGCATTTTATACAAAAAATAATAATAGGAACTATATAGACAA 996
Qy 1006 GCACATTTGTAACATTAGTAGCAAAAATGGAAATAACACTTTTACACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGTAACATTAGTAGCAAAAATGGAAATGACACTTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCTCAGGAGGAGACCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGTCTTTTAATCAATCTCAGGAGGAGACCA 1116
Qy 1126 GAAATTTGTAATGCAAGTTTAAATTTGTCGAGGGGAATTTCTTCTACTGTAATACACACAA 1185
Db 1117 GAAATTTGTAATGCAAGTTTAAATTTGTCGAGGGGAATTTTCTTCTACTGTAATACACCA 1176

QY 1186 CTGTTTAATAGTACTTGAATG---TTACTGGAGGACAAATGGCACTGAAGGAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGAATGTTGAATTAATTAATCTTGGAAATAATCTACAGGGTCAAATAAC 1236
QY 1243 ATAATCACACTCCAATGACAGATAAAACAAATTAATAATATGTGCGAGAAAGTAGAAAA 1302
Db 1237 AATATCACACTCCAATGACAGATAAAACAAATTAATAATATGTGCGAGAAAGTAGAAAA 1296
QY 1303 GCAATGTATGCCCTCCCATCATCAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATCATCAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTA 1356
QY 1363 CTACTAACAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAAGACACGGACACGAAACGACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAATAATAAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAATAATAAAGTAGTAAGA 1476
QY 1480 ATTGAACCAATAGGATAGCACCCACAGGGGCAAGAGAGAAACAGTGCACAAAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCCACAGGGGCAAGAGAGAAAGTGGTGCAGAGAGAAAA 1536
QY 1540 AGACCGGATCCAGA 1554
Db 1537 AGACGCGATAGGA 1551

RESULT 10

US-08-475-391-3
; Sequence 3, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786211and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-475-391-3

Query Match 53.1%; Score 1172.2; DB 1; Length 2571;
Best Local Similarity 87.9%; Pred. No. 1.3e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
QY 58 TCGGCTTCGAGATCCATGCTCCTCTGGGATATTGATGATCTCTAGTGTCTACAGAAAAATTG 117
Db 40 TGGGGATGGGCGACGATGCTCTCTGGGTATTATGATCTCTAGTGTCTACAGAAAAATTG 99
QY 118 TGGGTCAAGTCTTATTATGGGGTACCTGTGTGGAGAGAACCAACACACTCTATTTTGT 177
Db 100 TGGGTCAAGTCTTATTATGGGGTACCTGTGTGGAGAGAACCAACACACTCTATTTTGT 159
QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTCTGT 219
QY 238 GTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCACAGAGTAGAATTTGGTAATGTGACAGAAAAATTTTAAAC 279
QY 298 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATCAA 339
QY 358 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTG 417
Db 340 AGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTG 399
QY 418 -----AATATCAGTAAAGTACTACTTAACTCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATCAATTAATAGTACTCTTAATCAATAGTATAGCGAGGGAACA 459
QY 466 ATGGAGAAAGGAGAAAAATAAAATTTGCTCTTTCTATATCACCACAGCATAGAATAAG 525
Db 460 ATAAAGGAGGAGAAAAATGAAAACTGCTCTTTCAATATCACCACAGCATAGAATAAG 519
QY 526 GTAAAGAAAGAAATATGCACTTTTAAATAGATCTGATGTAGTACCAATAGAAAAATCAAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTTAAATAGATCTGATGTAGTATCAATAG---ATAATGAT 576
QY 586 AATACTAAGTATAGTTAAATAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCTCAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTTGTAATACCTCAGTCATTACACAGCTTTGTCCTCAAG 636
QY 646 GTATCCTTTTCAGCCAAATTTCCCATACATTTATGTGTCCCGCTGGGTTTTCGATGCTAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACACTATTGTGCCCGCTGGTTTTCGATTTCTAAA 696
QY 706 TGTAAACAAATAGACATTCATGATGATCAGGACCATGCAAAATGTGACGACAGTACAATGT 765
Db 697 TGTAAACGATAAAAGTTTCAAGTGGAAAAAGGATCATGTAAAAATGTGACGACAGTACAATGT 756
QY 766 ACACATGGAATTAGGCCAGTGTCTCACTCACTCACTGTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGTATCACTCACTGTTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATAGTAATTAGATCTGAAAAATTTTACAGACAAATGCTAAAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGATTAATGCTAAAAACCATATAGTACAT 876
QY 886 CTAATGAATCTGTAGTAATTAATTTGAAGAAGCCCAACAAATATCAAGAAAGAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTAATTTGTAAGAGCCCAACTCAATTAAGAAAGAAAGGATA 936
QY 946 TCTATAGGACCGGAGAGCAATTTTATCGAGAGAGAAACATAATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCGGAGAGCAATTTTATACAAACAAAAATATAATAGGAACTATTAGACAA 996
QY 1006 GCACATTGTAACTATTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAA 1065
Db 997 GCACATTGTAACTATTAGTAGAGCAAAATGGAATGACACTTTTACAGACATAGTTAGCAA 1056

```
Qy 1066 TTAAGAGAAAATTTAGGAATAAAACAATACGCTTTAATCAATCCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAACAAATTAAGAAATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGCACAGTTTTAAATTTGTGGAGGGAAATCTTCTACTGTAAATACAGCACAA 1185
Db 1117 GAAATTTGTAATGCACAGTTTTAAATTTGTGGAGGGAAATTTTCTACTGTAAATACATCACA 1176
Qy 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAATGGCAGCTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGTAATTAATCTTGGAAATAATCTACAGGGGTCAAATAAC 1236
Qy 1243 ATAATCACATCCCAATGCAGATAAAACAATTAATAATATGTGCGAGAAAGTAGGAAAA 1302
Db 1237 AATATCACATCTCAATGCAAAATAAAACAATTAATAATGTCGAGAAAGTAGGAAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAAAATATTACAGGGGTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGATGGTGGTAAGGACACCGACACGAACGACACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATTTATATAATAATAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGGACAATTTGGAGAAAGTGAATTTATATAATAATAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCACAGGAGGCAAGAGAGAACAAGTGCACAAAGAGAAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCACAGGAGGCAAGAGAGAACAAGTGCACAGAGAAAAA 1536
Qy 1540 AGACGGATCAAGA 1554
Db 1537 AGACGAGCATAGGA 1551
```

RESULT 11

```
US-08-709-609-3
; Sequence 3, Application US/08709609
; Patent No. 5858775
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858775and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-709-609-3
Query Match
Best Local Similarity 53.1%; Score 1172.2; DB 2; Length 2571;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGCTTCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGGATGGGSCACGATGCTCTCTGGGTATTATGATCTGTAGTGTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACTCTATTGTTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACTCTATTGTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTATGTTTGGGAAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTATGTTTGGTAAATGTGACAGAAAAATTTAAC 279
Qy 298 ATGTGGAAAAATACATGCTGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAA 357
Db 280 ATGTGGAAAAATACATGCTGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATCAA 339
Qy 358 AGCTTAAAGCCATCTGTAAATAATTAACCCCACTCTGTGTGTTACTTTTAAATTTGCACTAATTTG 417
Db 340 AGCTTAAAGCCATCTGTAAATAATTAACCCCACTCTGTGTGTTACTTTTAAATTTGCACTAATTTG 399
Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGTAGTACCAATAGAAAAATG 465
Db 400 AGGAATACTACTAATAAATAGTACTGCTAATAACAATAGTAAATAGGAGGGAACA 459
Qy 466 ATGGAGAAAGGAGAAATTAATAAATTTGCTTCTTCTATATCACCACCAAGCATAGAATAAG 525
Db 460 ATAAAGGGAGGAGAAATGAAAAAATCTGCTTTCAATATATCACCACCAAGCATAGAATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTATAGTAGTACCAATAGAAAAATCTAAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTTATAAATCTGTATATAGTATCAATAG---ATAATGAT 576
Qy 586 AATACTAAGTATAGGTTAAATAGTTGTAACACCTCAGTCAATACAGAGCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCAATACAGAGCTGTGCCAAG 636
Qy 646 GTATCCTTTAGCCCAATTTCCCATACATATTGTTGTCGGCTGGTTTGGCATGCTAAG 705
Db 637 ATATCCTTTAGCCCAATTTCCCATACATATTGTTGTCGGCTGGTTTGGCATGCTAAG 696
Qy 706 TGTAACAATAAGACATTTCAATGGATCAGGACCATGTCACAAATGTGTCAGCACAGTACAAATGT 765
Db 697 TGTAACGATAAAAAGTTTCAGTGGAAAGGATCATGTAAATGTGTCAGCACAGTACAAATGT 756
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTAGTCTGAAATTTTCACAGACATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGTCTGAGAAATTTCTGATAATGCTTAAACCATATAGTACAT 876
Qy 886 CTAATGAATCTGTAGTAATTAATTTGTAACAAGACCCCAACCACTACNATAAAGAAAAAGGATA 945
Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAGAGCCCACTACNATAAAGAAAAAGGATA 936
Qy 946 TCTATAGGACCGAGGAGAGCAATTTTATGCAAGAGAGAAACATAATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCGAGGAGAGCAATTTTATACAAACAAAAAATAATAGGAACTATATAGACAA 996
```

QY 1006 GCACATTGTAACTAGTAGAGCAAAATGGAATAACACCTTTTACACAGATAGTTTAAAA 1065
DB 997 GCACATTGTAACTAGTAGAGCAAAATGGAATAACACCTTTTAAAGACAGATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAACAATAGCCTTTTAACTCAATCCTCAGGAGGGACCCA 1125
DB 1057 TTAAGAGAAAAATTTAGGAATAAACAATAGCCTTTTAACTCAATCCTCAGGAGGGACCCA 1116
QY 1126 GAAATTTGTAATGACACAGTTTAAATTTGTGGAGGGAAATCTTCTACTGTAATACAGACAA 1185
DB 1117 GAAATTTGTAATGACACAGTTTAAATTTGTGGAGGGAAATTTTCTACTGTAATACACCA 1176
QY 1186 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGACAAATGGGCACTGAAGGAAATGAC 1242
DB 1177 CTGTTTAAATAGTACTTTGGAATGGAATGTAATACTTGGAAATACTACAGGGTCAATAAC 1236
QY 1243 ATAAATCACACTCCAATGACAGATAAACAATAATATAAATATCTGGCAGAAAGTAGGAAA 1302
DB 1237 AATATCACACTTCAATGCAAAATAAACAATAATATAAATATCTGGCAGAAAGTAGGAAA 1296
QY 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATCAATATTTACAGGGCTG 1362
DB 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTCAATCAATATTTACAGGGCTA 1356
QY 1363 CTACTAACAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
DB 1357 CTATTAACAAGAGATGGTGAAGGACACGGACACGACGACACGAGATCTTCAGACCT 1416
QY 1420 GGAGAGGAGATATGAGGACAAATTTGGAGAACTGAATTAATAATATAAGTAGTAAGA 1479
DB 1417 GGAGAGGAGATATGAGGACAAATTTGGAGAACTGAATTAATAATATAAGTAGTAAGA 1476
QY 1480 ATTGAACCAATAGGAGTACACCCACCGGCAAGAGAGAAACAGTGCAGAGAGAAAA 1539
DB 1477 ATTGAACCAATAGGAGTACACCCACCGGCAAGAGAGAAAGAGTGGTCAGAGAGAAAA 1536
QY 1540 AGACCGGATCCAAGA 1554
DB 1537 AGACGCGGATAGGA 1551

RESULT 12
US-09-552-950-3
; Sequence 3, Application US/09552950
; Patent No. 6541248
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/09/552,950
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-552-950-3

Query Match 53.1%; Score 1172.2; DB 4; Length 2571;
Best Local Similarity 87.9%; Pred. No. 1.3e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

QY 58 TCGGCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTGAGTACAGAAAAATTTG 117
DB 40 TGGGATGGGCGCAGATGCTCTTGGGTTAATTAATGATCTGTGAGTACAGAAAAATTTG 99
QY 118 TGGGTCACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACCACTCTATTTTGT 177
DB 100 TGGGTCACAGTCTATTATGGGTACTCTGTGGAGAGAGCAACCACTCTATTTTGT 159
QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237

DB 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAAAGCCTGT 219
QY 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAAC 297
DB 220 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGTAAATGTGACAGAAAAATTTTAAAC 279
QY 298 ATGTGGAAAAATAACATCGGTAGATCAGATGCAATGAGGATATTAATCAGTTTATGGGATGAA 357
DB 280 ATGTGGAAAAATAACATCGGTAGAACAGATGATGAGGATATAATCAGTTTATGGGATCAA 339
QY 358 AGCCTAAAGCCATGTGTAATAATTAACCCACTCTCTGTGTTACTTTTAAATGGCACTAATTTG 417
DB 340 AGCCTAAAGCCATGTGTAATAATTAACCCACTCTCTGTGTTACTTTTAAATGGCACTAATTTG 399
QY 418 -----AATATCACTAAAGAAATACTACTAATCCACTAGTAGCAGCTGGGGAATG 465
DB 400 AGGAATACTACTATACCAATAATAGTACTGCTAATTAACATAGTAATAGCGAGGGNACA 459
QY 466 ATGGAGAAAGAGAAATAAAAAATTTGCTTTCTATATCACCAAGCATAGAATAAAG 525
DB 460 ATAAAGGGAGAGAAATGAAAAATCGCTCTTCAATATCACCAAGCATAGAATAAAG 519
QY 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGTATAGTACCATAATAGAAAAATACTAAT 585
DB 520 ATGCAGAAAGAAATATGCACTTTTAAATAGACTTGTATAGTATCAATAG---ATAATGAT 576
QY 586 AATACTAAGTATAGTTAATAAGTTGTAAACCTCAGTCATTTACACAGCCCTGCCAAG 645
DB 577 AGTACCACTATAGTTGATAGTTGTAACTCAGTCATTTACAAAGCTTGTCCAAG 636
QY 646 GTATCCTTTACGCCAATTTCCCATACATTATTGTGTCCCGGCTGGGTTTGCAGATGCTAAAG 705
DB 637 ATATCCTTTGAGCCAAATTTCCCATACACTATTGTGCCCCCGCTGGTTTTCGATTTCTAAAA 696
QY 706 TGTAAACAATAGACATTCOAATGGATCAGGACCATGCAAAATGTGACGACAGTACAAATGT 765
DB 697 TGTAAACGATAAAAAAGTTTCAGTGGAAAAAGGATCATGTAAAAAATGTGACGACAGTACAATGT 756
QY 766 ACACATGGAATTTAGGCCAGTGTGCTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 825
DB 757 ACACATGGAATTTAGGCCAGTGTGCTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 816
QY 826 GAAGACATAGTAATTTAGATCTGAAAAATTTACAGACAAATGCTTAAACCATATAGTACAG 885
DB 817 GAAGAGGTAGTAATTTAGATCTGAGAAATTTCTACTGTAATGCTTAAACCCATCATAGTACAT 876
QY 886 CTAAATGAATCTGTAGTAAATTAATTTGTACAAGACCCAAACAATACAAGAAAGGTTA 945
DB 877 CTGAATGAATCTGTACAAATTAATTTGTACAAGACCCAACTACAAATAAAGAAAAAGGATA 936
QY 946 TCTATAGGACAGGGAGAGCAATTTATGCAAGAGAAACATAATAGGAGATATAGACAA 1005
DB 937 CATATAGGACAGGGAGAGCAATTTTATACAAACAAAAATATAATAGGAACTATATAAGCAA 996
QY 1006 GCACATTGTAACATTTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTTAAAA 1065
DB 997 GCACATTGTAACATTTAGTAGAGCAAAATGGAATAACACTTTTAAAGCAATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAACAATAGCCTTTTAACTCAATCCTCAGGAGGGACCCA 1125
DB 1057 TTAAGAGAAAAATTTAGGAATAAACAATAGCCTTTTAACTCAATCCTCAGGAGGGACCCA 1116
QY 1126 GAAATTTGTAATGACAGTTTAAATTTGTGGAGGGAAATCTTCTACTGTAATACAGACAA 1185
DB 1117 GAAATTTGTAATGACAGTTTAAATTTGTGGAGGGAAATTTTCTACTGTAATACATCAGCA 1176
QY 1186 CTGTTTAAATAGTACTTTGGAATG---TTACTGGAGGACAAATGGCAGTGAAGGAATGAC 1242
DB 1177 CTGTTTAAATAGTACTTTGGAATGGAATTAATAATCTTGGAAATAATCTACAGGGTCAATTAAC 1236
QY 1243 ATAATCACACTCCAATGCAAGATAAACAATAATTAATAATGTTTGGGCCACACATGCTGT 1302

Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTAATAAACATGTGCGAGGAAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATAGATGTTCAATCAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTCAATCAAATATTACAGGGCTA 1356
Qy 1363 CTACTAAACAAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAAGACACGGACGACGACGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGACAAATGGGAGAAGTGAATTTATATAATAATAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATGGGAGAAGTGAATTTATATAATAATAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGAGTAGACCCACAGGCGCAAGAGAGAAACAGTGCACAGAGAAAAA 1539
Db 1477 ATTGAACCAATTAGGAGTAGACCCACCAAGGCAAGAGAGAGAGTGTGTCAGAGAGAAAA 1536
Qy 1540 AGACCGGATCCAAGA 1554
Db 1537 AGACGCGGATAGGA 1551

RESULT 13

US-09-936-572-3
; Sequence 3, Application US/09936572
; Patent No. 6783981
; GENERAL INFORMATION:
; APPLICANT: MITROPHANOUS, KYRIACOS
; TITLE OF INVENTION: ANTI-VIRAL VECTORS
; FILE REFERENCE: 078883/0137
; CURRENT APPLICATION NUMBER: US/09/936,572
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/GB00/01002
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: GB 9906177.2
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-936-572-3

Query Match 53.1%; Score 1172.2; DB 4; Length 2571;
Best Local Similarity 87.9%; Pred. No. 1.3e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCCATGCTCTCGGATATTGGATATTGATGATCTGTAGTGCTACAGAAAAATTG 117
Db 40 TGGGGATGGGCACGATGCTCTCGGTTATTAAATGATCTGTAGTGCTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGTACTGTGTGGAGAGACCAACCACTCTATTATTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACTGTGTGGAAAGAGCAACCACTCTATTATTGT 159
Qy 178 GCATCAGATGCTAAAGCCCTATCATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237
Db 160 GCATCAGATGCTTAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219
Qy 238 GTACCCACAGACCCCAACCAAGAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCAAGAGTATTGGTAAATGTGACAGAAAAATTTAAC 279
Qy 298 ATGTGAAAAAATAACATGTAGATCAGATGCAATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGAAAAAATAACATGTAGATGCAATGAGGATATAATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTGCACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTGCACTAATTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATCAATTAATGTAATCTCTTAATCAATAGTAATAGCGGGAACA 459
Qy 466 ATGGAGAAAGAGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATTAAGAAATAG 525
Db 460 ATAAAGGAGGAGAGAAATGAAAAAATCTGCTCTTTCAATATCACCACAAGCATTAAGAGATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGATGTAGTAGTACCAATAGAAAAATCTAAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT 576
Qy 586 AATACTAAGTATAGTTTAATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTTGTAATACCTCAGTCATTACACAGCTTGTCCAAAG 636
Qy 646 GTATCCTTTACAGCAATTTCCCATACATTTATGTGTCCCGGTGGTTCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACACTATTGTGCCCCGGCTGTTTTCGATTTCTAAAA 696
Qy 706 TGTAAACAATAAGACATTTCAATGGATCAGGACCATGCACAAATGTCAGCACAGTACAATGT 765
Db 697 TGTAAACGATAAAAAAGTTTCAGTGGAAAAAGGATCATGTAAAAATGTGAGCACAGTACAATGT 756
Qy 766 ACATATGGAAATTAGSCCAGTGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTAGTATCACTCACTGCTGTTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAAAATTTTCACAGCAATGCTTAAACCATTAATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAGAAATTTCTACTGATATGCTTAAACCATCATAGTACAT 876
Qy 886 CTAAATGAATCTGTAGTAATTTAATGTACAGAGCCCAACAACAATAACAAGAGAAAGTTA 945
Db 877 CTGAATGAATCTGTACAAATTTAATTTGTAACAAGACCCAACTCAATAAAGAAAAAGGATA 936
Qy 946 TCTATAGGACGAGGAGAGCAATTTATGCAAGAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACGAGGAGAGCAATTTTATACAACAAAAATAATAGGAACTATATAAGACAA 996
Qy 1006 GCACATTTGAACATTAGTAGACAAAAATGGAATAACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGAACATTTAGTAGACAAAAATGGAATGACACTTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAACAATAGCTTTTAAATCAATCTCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAACAATTTAAGAAATAAAAACAATAGTCTTTTAAATCAATCTCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGAATGCAAGTTTAAATTTGTGAGGGGAATTTCTTCTACTGTATAACACACAA 1185
Db 1117 GAAATTTGAATGCAAGTTTAAATTTGTGAGGGGAATTTTCTCTACTGTATAACATACCA 1176
Qy 1186 CTGTTTAATAGTACTTGGAAATG--TTACTGGAGGACAAATGGCACTGGAAGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGGAAATGTAATTAATCTTGGAAATACTACAGGGTCAAATAAC 1236
Qy 1243 ATAAATCACTCCAAATGAGAAATAAAAACAAATTTATAATATGTGCGAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTTCAATGCAAAAAATAAACAATAAATTTAATCATGTGCGAGAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATCAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCAATCAAATATTACAGGGCTA 1356
Qy 1363 CTACTAAACAAGAGATGGAGGTAATAGTACTGA--GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGAGACGACGACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAGAGTGAATTTATATAATAATAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAATAATAAGTAGTAACA 1476

QY 1480 ATTGAACCATAGGATGACCCACAGGCGCAAGAGAGAAAGTGTGCAAGAGAAAA 1539
Db 1477 ATTGAACCATAGGATGACCCACAGGCGCAAGAGAGAAAGTGTGCAAGAGAAAA 1536
QY 1540 AGACCGGATCCAAGA 1554
Db 1537 AGACGAGCATAGGA 1551

RESULT 14

PCT-US95-07178-3
; Sequence 3, Application PC/TUS9507178
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07178
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-07178-3

Query Match 53.1%; Score 1172.2; DB 5; Length 2571;
Best Local Similarity 87.9%; Pred. No. 1.3e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
QY 58 TCGGCTTCGAGATCCATGCTCTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGGATGGGACGATGCTCTGGGTTATTAATGATCTGTAGTGTACAGAAAAATTG 99
QY 118 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGCAACCAACCACTCTATTGTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGCAACCAACCACTCTATTGTGT 159
QY 178 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCTGT 219
QY 238 GTACCCACAGACCCCAACCAAGAGTGTATTGGGAATGTGACAGAAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCAAGAGTGTATTGGTAAATGTGACAGAAAAATTTTAAAC 279
QY 298 ATGTGGAAAAATACATGCTGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAA 357
Db 280 ATGTGGAAAAATACATGCTGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAA 339

QY 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCACTCTGTGTACTTTTAAATTTGCACTAATTG 399
QY 418 -----AATATCACTAAGNATACTACTAATCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTAGTCTGCTAATAACAATAGTAATAGCGAGGAACA 459
QY 466 ATGGAGAAAGGAGAAATAAAAAATTGCTCTTTCTATATCACCACAAGCATAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAAAAAATGCTCTTTCAATATCACCACAAGCATAGAGATAAG 519
QY 526 GTAAAGAAAGATATGCACTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATCTAAT 585
Db 520 ATGCAGAAAGAAATATGCACTTTTAAATAGACTTGTAGTAGTACCAATAGAAAAATCTAAT 576
QY 586 AATCTAGTATAGGTTTAATAGTTGTAAACCACTCAGTCATTTACACAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGATAGTTGTAATACCTCAGTCATTTACACAGCTTGTCCAAAG 636
QY 646 GTATCCTTTTCAGCCAAATCCCATACATTTATGTGTCCCGGCTGGGTTTCCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATCCCATACACTATTGTGCCCCGGCTGGTTTGGGATTTCTAAA 696
QY 706 TGTAAACAATAAGACATTCOAATGGATCAGGACATGCAACAATGTGACACAGTACAATGT 765
Db 697 TGTAAACGATAAAAGTTTCAGTGGAAAGGATCATGTAAAAAATGTGACACAGTACAATGT 756
QY 766 ACACATGGAATTAGCCAGTGTGTCACTCAACTCACTGCTTTAAATGGCAGCTACAGAA 825
Db 757 ACACATGGAATTAGCCAGTGTGTCACTCAACTCACTGCTTTAAATGGCAGTCTACAGAA 816
QY 826 GAAGACATAGTAAATTTAGATCTGAAAAATTTACAGACAATGCTAAAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAAATTTAGATCTGAGAAATTTCTGATGATGCTTAAACCATCATAGTACAT 876
QY 886 CTAATGAATCTGTAGTAAATTTATGTAACAAGACCCAAACAATAACAAGAGAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTTAATGTAACAAGACCCAACTCAATAAAGAAAAAGGATA 936
QY 946 TCTATAGGACCGGAGGAGCAATTTATGCAAGAGAAACATATAGGAGATATAGACAA 1005
Db 937 CATATAGGACCGGAGGAGCAATTTTATACAAACAAAAATATATAGGAACTATATAGACAA 996
QY 1006 GCACATTTGTAACATTTAGTAGCAAAATGGAATTAACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGTAACATTTAGTAGCAAAATGGAATGACACTTTTACACAGATAGTTAGCAAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATPAAAAACAATAGCCTTTTAAATCAATCTCAGGAGGAGCCCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATPAAAAACAATAGTCTTTTAAATCAATCTCAGGAGGAGCCCA 1116
QY 1126 GAAATTTGATGACAGCTTTTAAATTTGGAGGGGAAATTTCTTACTGTATGATACAGACAA 1185
Db 1117 GAAATTTGATGACAGCTTTTAAATTTGGAGGGGAAATTTTCTACTGTAAATACATCACCA 1176
QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAATGGCACTGGAAGGAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGGAATGGAATTAATTAATTAATTAATTAATTAATTAAT 1236
QY 1243 ATAAATCACTCCCAATGCAAGAAATAAAACAAATTAATAATATGTTGGCAAGAAATAGGAAAA 1302
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTTAAACATGTGCGCAAGAAATAGGAAAA 1296
QY 1303 GCAATGATGATGCTCCCTCCCATCAGAGCAAAATTAAGATGTTTCATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGATGATGCTCCCTCCCATGGAAGGCAAAATTAAGATGTTTCATCAAAATATTACAGGGCTA 1356
QY 1363 CTACTCAACAGAGATGGAGGTAATAGTACTCA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAACAGAGATGGTGGTAAGACACGACACGACGACGACGACGACGACGACGACGACGACCT 1416

QY 1420 GGAGGAGGAGATATCAGGCAATTTGGAGAGTGAATTTATATAATATAAAGTAGTAAGA 1479
DB 1417 GGAGGAGGAGATATCAGGCAATTTGGAGAGTGAATTTATATAATATAAAGTAGTAAGA 1476
QY 1480 ATTGAACCAATAGGAGTAGCACCCACAGGCGCAAGAGAGAAACAGTGCACAAAGAGAAAAA 1539
DB 1477 ATTGAACCAATAGGAGTAGCACCCACAGGCGCAAGAGAGAGAGTGGTGCAGAGAGAAAAA 1536
QY 1540 AGACCGGATCCAAGA 1554
DB 1537 AGACGCGGATAGGA 1551

RESULT 15

US-08-651-472-66/c
; Sequence 66, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: psep160M
US-08-651-472-66

Query Match 53.1%; Score 1172.2; DB 3; Length 6474;
Best Local Similarity 87.9%; Pred. No. 1.8e-276;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
QY 58 TCGGCTTCGAGATCCATGCTCTCGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117

DB 3877 TGGGGATGGGCGACGATGCTCTTTGGGTTATTAATGATCTGTAGTGTACAGAAAAATTG 3818
QY 118 TGGGTCACAGTCTATTATTTGGGGTACCTGTGTGGAGAGAACCAACACACCTCTATTTTGT 177
DB 3817 TGGGTCACAGTCTATTATTTGGGGTACCTGTGTGGAGAGAACCAACACACCTCTATTTTGT 3758
QY 178 GCATCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCGCACACATGCCTGT 237
DB 3757 GCATCAGATGCTAAAGCATATGATACAGAGTACATAATGTTTGGGCGCACACAGCCTGT 3698
QY 238 GTACCCACAGACCCCAACCCACAGAGTGTGGGAAATGTGACAGAAAAATTTTAAC 297
DB 3697 GTACCCACAGACCCCAACCCACAGAGTGTGGTAAATGTGACAGAAAAATTTTAAC 3638
QY 298 ATGTGGAAAAATAACATGGTGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAA 357
DB 3637 ATGTGGAAAAATAACATGGTGTAGATCAGATGATGAGGATATAATCAGTTTATGGATCAA 3578
QY 358 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTCTTTTAAATTTGCACTAATTTG 417
DB 3577 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTCTTTTAAATTTGCACTAATTTG 3518
QY 418 -----AATATCACAATAAGTAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
DB 3517 AGGAATACTACTAATAATCAATAATAGTACTGCTTAATAACAATAGTAATAGCGAGGAACA 3458
QY 466 ATGGAGAAAGAGAGAAATTAATAAATTTGCTCTTTCTATATCACCACAGCATAGAATAAG 525
DB 3457 ATAAAGGGAGAGAAATGAAAAAATCTGCTCTTTCAATATCACCACAGCATAGAATAAG 3398
QY 526 GTAAAGAAAGAAATATGCATCTTTTAAATAGACTGTGATGTAGTACCATAAGAAAAATACTAAT 585
DB 3397 ATGCAGAAAGAAATATGCATCTTTTAAATAGACTGTGATGTAGTACCATAAGAAAAATACTAAT 3341
QY 586 AATACTAAGTATAGGTTAATAAGTTGTAAACACCTCAGTCATTACACAGCGCTGTCCAAG 645
DB 3340 AGTACCAGCTATAGTTGATTAAGTTGTAATACCTCAGTCATTACACAGCTGTCCAAG 3281
QY 646 GTATCTTTTCCAGCAATTTCCCATACATTAATTTGTGTCCCGCTGGTTTCCGATGCTAAG 705
DB 3280 ATATCTTTTCCAGCAATTTCCCATACATTAATTTGTGTCCCGCTGGTTTCCGATGCTAAG 3221
QY 706 TGTAAACATAAGACATTCATGGATCAGGACCATGACACAAATGTGACACACAGTACAATGT 765
DB 3220 TGTAAACATAAGAGTTTCAAGTGGAAAGAGTCACTGTAATAATGTGACACACAGTACAATGT 3161
QY 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 825
DB 3160 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTACAGAA 3101
QY 826 GAAGACATAGTAATTAGATCTGAAAAATTTACAGACATGCTTAAACCATTAATAGTACAG 885
DB 3100 GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGTAATAATGCTTAAACCATTAATAGTACAT 3041
QY 886 CTAAATGAATCTGTAGTAATTAATTTGTACAGACCCCAACAAATACAGAGAGAGTTA 945
DB 3040 CTGAATGAATCTGTACAAATTAATTTGTACAGACCCCACTCAATTAAGAAAAAGGATA 2981
QY 946 TCTATAGGACCCAGGAGAGCATTATTCGAAAGAGAAAACATAATAGGAGATATAAGACAA 1005
DB 2980 CATATAGGACCCAGGAGAGCATTATTCGAAAGAGAAAACATAATAGGAGATATAAGACAA 2921
QY 1006 GCACATTTGTAACATTTAGTAGCAAAATGGAATACACTTTTACACAGATAGTTATATAA 1065
DB 2920 GCACATTTGTAACATTTAGTAGCAAAATGGAATGACACTTTTAAAGACAGATAGTTAGCAA 2861
QY 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAAATCAATCTCAGGAGGGACCCA 1125
DB 2860 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAAATCAATCTCAGGAGGGACCCA 2801
QY 1126 GAAATTTGTAATGACACAGTTTAAATTTGTGGAGGGGAATTTCTTCTACTGTAATACAGACAA 1185

Db	2800	GAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTCTACTGTAAATACATCACCA	2741
Qy	1186	CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGGACAAAATGGCACTGAAAGGAAATGAC	1242
Db	2740	CTGTTTAAATAGTACTTGGAAATGTAATAATCTTGGAAATAATCTACAGGGTCAAATAAC	2681
Qy	1243	ATAATCACACTCCCAATGCAGATAAACAATAATATAAATATGTGCGAGAAAAGTAGGAAAA	1302
Db	2680	AATATCACACTTCAATGCAAAATAAACAAAAATTATAAACATGTGGCAGGAAAGTAGGAAAA	2621
Qy	1303	GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTG	1362
Db	2620	GCAATGTATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACAGGGCTA	2561
Qy	1363	CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT	1419
Db	2560	CTATTAAACAAGAGATGGTAAAGGACACGGACACGACACCGAGATCTTCAGACCT	2501
Qy	1420	GGAGGAGAGATATCAGGGACAAATTGGAGAAAGTGAAATTATATAATATAAAGTAGTAAGA	1479
Db	2500	GGAGGAGAGATATCAGGGACAAATTGGAGAAAGTGAAATTATATAATATAAAGTAGTAACA	2441
Qy	1480	ATTGAACCAATAGGAGTAGCACCACAGGGCAAGAGAGAAACAGTGCAAAAGAGAAAAA	1539
Db	2440	ATTGAACCTTAGGAGTAGCACCACCAAGGCCAAGAGAGAGAGAGTGGTGCAGAGAGAAAA	2381
Qy	1540	AGACCGGATCCAAGA	1554
Db	2380	AGAGCAGCGATAGGA	2366

Search completed: November 12, 2004, 12:57:37
Job time : 136.064 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 07:54:46 ; Search time 767.964 Seconds
(without alignments)
15528.563 Million cell updates/sec

Title: US-09-687-864A-13
Perfect score: 2208
Sequence: 1 aagtttgcgcgcgtctgta.....aactcgsagtataatctaga 2208

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1222.2	55.4	9540	17	US-10-325-468-46
2	1199.2	54.3	2612	15	US-10-414-692-20
3	1197.8	54.2	1512	9	US-09-759-841-3
4	1179.8	53.4	1422	18	US-10-728-195-7
5	1174.2	53.2	3807	15	US-10-441-788-78
6	1173	53.1	2552	10	US-09-966-931-27
7	1173	53.1	2552	17	US-10-459-121-27
8	1172.2	53.1	2571	9	US-09-999-183-3
9	1172.2	53.1	2571	13	US-10-077-294-3
10	1172.2	53.1	2571	13	US-10-163-886-3
11	1172.2	53.1	2571	14	US-10-263-127-3
12	1172.2	53.1	2571	15	US-10-375-777-3

13	1172.2	53.1	2571	16	US-10-351-938-3	Sequence 3, Appli
14	1169.8	53.0	2573	10	US-09-966-931-29	Sequence 29, Appl
15	1169.8	53.0	2573	17	US-10-459-121-29	Sequence 29, Appl
16	1166.6	52.8	9704	17	US-10-325-468-40	Sequence 40, Appl
17	1166.6	52.8	9706	17	US-10-325-468-45	Sequence 45, Appl
18	1165.6	52.8	9715	17	US-10-325-468-44	Sequence 44, Appl
19	1165.6	52.8	9715	17	US-10-325-468-44	Sequence 44, Appl
20	1165	52.8	9942	17	US-10-325-468-5	Sequence 5, Appli
21	1165	52.8	9942	17	US-10-325-468-54	Sequence 54, Appl
22	1164.2	52.7	2627	15	US-10-177-390-9	Sequence 9, Appli
23	1163.4	52.7	9942	17	US-10-325-468-1	Sequence 1, Appli
24	1163.4	52.7	9942	17	US-10-325-468-2	Sequence 2, Appli
25	1163.4	52.7	9942	17	US-10-325-468-7	Sequence 7, Appli
26	1163.4	52.7	9942	17	US-10-325-468-50	Sequence 50, Appl
27	1163.4	52.7	9942	17	US-10-325-468-51	Sequence 51, Appl
28	1161.8	52.6	9942	17	US-10-325-468-56	Sequence 56, Appl
29	1161.8	52.6	1932	15	US-10-387-336-31	Sequence 31, Appl
30	1161.8	52.6	2457	15	US-10-387-336-32	Sequence 32, Appl
31	1161.8	52.6	9942	17	US-10-325-468-3	Sequence 3, Appli
32	1161.8	52.6	9942	17	US-10-325-468-52	Sequence 52, Appl
33	1161.6	52.6	2570	10	US-09-966-931-31	Sequence 31, Appl
34	1161.6	52.6	2570	17	US-10-459-121-31	Sequence 31, Appl
35	1160.8	52.6	9737	10	US-10-387-336-30	Sequence 30, Appl
36	1160.8	52.6	9737	14	US-09-827-688-12	Sequence 12, Appl
37	1160.2	52.5	9942	17	US-10-032-162-12	Sequence 6, Appli
38	1160.2	52.5	9942	17	US-10-325-468-6	Sequence 55, Appl
39	1160	52.5	9942	17	US-10-325-468-55	Sequence 13, Appl
40	1148.8	52.0	9181	18	US-10-361-849-13	Sequence 14, Appl
41	1148.8	52.0	9719	9	US-09-737-190A-1	Sequence 1, Appli
42	1148.8	52.0	9719	15	US-10-000-511A-1	Sequence 1, Appli
43	1148.8	52.0	9719	15	US-10-000-511A-2	Sequence 2, Appli
44	1148.8	52.0	9719	17	US-10-325-468-41	Sequence 41, Appl
45	1148.8	52.0	12425	15	US-10-000-511A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-325-468-46
; Sequence 46, Application US/10325468
; Publication No. US20040101823A1
; GENERAL INFORMATION:
; APPLICANT: Soong, Nay Wei
; APPLICANT: Pekrun, Katja
; APPLICANT: Shibata, Riri
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
; FILE REFERENCE: 0166.210US
; CURRENT APPLICATION NUMBER: US/10/325,468
; PRIOR FILING DATE: 2002-12-19
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 9540
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
; FEATURE:
; OTHER INFORMATION: parent JRCSP DNA (GenBank Accession No. M38429)
US-10-325-468-46

Query Match	55.4%	Score 1222.2;	DB 17;	Length 9540;
Best Local Similarity	90.0%;	Pred. No. 1.9e-271;		
Matches 1337;	Conservative 0;	Mismatches 133;	Indels 15;	Gaps 2;
QY	72	CATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGTGCACAGTCTA	131	
Db	6289	CTTGCTCTTGGGACATTAATGATCTGTAGTGTCTAGAAAAAGTTGGTGCACAGTCTA	6348	
QY	132	TTATGGGTACTCTGTGGAGAGCAACCACTCTATTGTGTCATCATGAGCTAA	191	

Db 6349 TTATGGGTACCTGTGTGGAAAGAAACAAACACCACTCTATTTTGTGTCATCAGATGCTAA 6408
Qy 192 AGCCTATGATACAGAGGTACATAATATGTTTGGCCACACATCGCTGTGTACCCACAGACCC 251
Db 6409 AGCATATGATACAGAGGTACATAATATGTTTGGCCACACATCGCTGTGTACCCACAGACCC 6468
Qy 252 CAACCCACAAGAGTAGTATTTGGGAAATGTGCACAGMAAATTTTAACTATGTTGGAAATAA 311
Db 6469 CAACCCACAAGAGTAGTATTTGGGAAATGTGCACAGMAATTTTAACTATGTTGGAAATAA 6528
Qy 312 CATGGTAGATCAGATGCGATGAGGATATAATCAGTTTATGGATGAAGCCCTAAAGCCCATG 371
Db 6529 CATGGTAGATCAGATGCGAGGAGGTATTAATCAATTTATGGGATCAAAAGCTTAAAGCCCATG 6588
Qy 372 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGAAATTTGAAATATCACTAAGAA 431
Db 6589 TGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCAAGATGT-----GAA 6636
Qy 432 TACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAGAAAGGAGAAATAAATAATTTG 491
Db 6637 TGCTACTAATACCCTAGTAGTAGTAGGAGGATGATGGAGAGAGAGAAATTAATAACTG 6696
Qy 492 CTCTTTCTATATCACCAAGCATAAGAAATAAGSTAAAGAAAGAAATATGCACTTTTPAA 551
Db 6697 CTCCTTCAATATCACCAAAAGCATAAGAGATAAGGTGCAGAAAGAAATATGCTCTTTTTTA 6756
Qy 552 TAGACTTGATGTAGTACCAATAGAAATACTAATAACTAAGTATAGTTTAATAAGTTG 611
Db 6757 TAAACTGATGTAGTACCAATAGATAATAAGAAATAATACCAATATATAGTTTAAATAAGTTG 6816
Qy 612 TAAACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTCAGGCCAAATTTCCCATACA 671
Db 6817 TAAACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTCAGGCCAAATTTCCCATACA 6876
Qy 672 TTATTGTCTCCGGTGGGTTTGGGATGCTTAAAGTGAACAATAAGACATTCATTTGGATC 731
Db 6877 TTATTGTCCCGCTGTGTTTGGGATGCTTAAAGTGAACAATAAGACATTCATTTGGAA 6936
Qy 732 AGGACCATGCACAAATGTCAGCACAGTACATGATACATGGAATTAGGCCAGTGGTGC 791
Db 6937 AGGACCATGTAATAATGTCAGCACAGTACATGATACATGGAATTAGGCCAGTGGTGC 6996
Qy 792 AACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATCTGAAA 851
Db 6997 AACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGGTGTAATTAGATCTGACAA 7056
Qy 852 TTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAAATTAATG 911
Db 7057 TTTTACGGACAATGCTTAAACCATTAATAGTACAGCTGAATGAATCTGTAAATAATTAATG 7116
Qy 912 TACAAGCCCAACACAAATACAGAGAGGTTATCTATAGGACAGGAGGAGCAATTTTA 971
Db 7117 TACAAGCCCAACACAAATACAGAGAGGTTATCTATAGGACAGGAGGAGCAATTTTA 7176
Qy 972 TGCAAGAGAAACATAATAGGAGATATAAGACACACATTTGAATAGTAGAGCAA 1031
Db 7177 TACAAGAGAAATAATAGGAGATATAAGACACACATTTGAATAGTAGAGCA 7236
Qy 1032 ATGGAATAACACTTTTCAACAGATAGTTTATAAATTAAGAGAAAAATTTAGGAATAAAAC 1091
Db 7237 ATGGAATAACACTTTTAAACAGATAGTTTGAATAATTAAGAGAAACAAATTTAATAAATAAC 7296
Qy 1092 AATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAAAATTTGAATGCAAGTTTAAATG 1151
Db 7297 AATAGCTTTTACTCTCCTCAGGAGGGATCCAGAAAAATTTGAATGCAAGTTTAAATG 7356
Qy 1152 TGGAGGGAAATTTCTTCTACTGTAATACAGACCACTGTTTAAATAGTACTTGGAAATGTAC 1211
Db 7357 TGGAGGGAAATTTTCTACTGTAATTAACACCACTGTTTAAATAGTACTTGGAAATGTAC 7416
Qy 1212 TGGAGGGCAAAATGGCACTGAGGAAATGACATAATCACTCCCAATCGAGAATAAAACA 1271
Db 7417 TGAAAAGTCAAGTGGCACTGAAGGAAATGACACCATCATCTCCCATGCAAGATAAAACA 7476

Qy 1272 AATTATAAATATGTGGCAGAAAGTAGAAAAGCAATGTATGCCCTCCCTCCATCAGAGACA 1331
Db 7477 AATTATAAACAATGTGGCAGAAAGTAGAAAAGCAATGTATGCTCTCTCCATTAAGAGACA 7536
Qy 1332 AATTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACAGAGATGGAGTAATAGTAC 1391
Db 7537 AATTAGATGTTTCATCAAAATATTACAGGCTGCTACTTAACAGAGATGGTGGTAA---AAA 7593
Qy 1392 TGACACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGCAATTTGGAGAAG 1451
Db 7594 TGAGAGTGAGATCGAGATCTTCAGACCTGGAGGAGGAGACATGAGGGAACAATTTGGAGAAG 7653
Qy 1452 TGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGAGTAGCACCACCACGAGGC 1511
Db 7654 TGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATAGAGTAGCACCACCACGAGGC 7713
Qy 1512 AAAGAGAAGACACTGCAAAAGAGAAAAAAGACCGGATCCAAAGAAG 1556
Db 7714 AAAGAGAAGAGTGGTGCAAGAGAAAAAAGAGCAGTGGGAATAGG 7758

RESULT 2

US-10-414-692-20
; Sequence 20, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-ceptor Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2612
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-414-692-20

Query Match 54.3%; Score 1199.2; DB 15; Length 2612;
Best Local Similarity 90.2%; Pred. No. 2.2e-266;
Matches 1347; Conservative 0; Mismatches 123; Indels 24; Gaps 5;

Qy 66 GAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTCTACAGAAAAATTTGTGGGTAC 125
Db 442 GGGCACCTTGCTCCTTGGGATATTAAATGATCTGTAGTCTGTAGAAAAAGTTGTGGGTAC 501
Qy 126 AGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTATTTGTGCATCAGA 185
Db 502 AGTCTATTATGGGTACCTGTGTGGAAAGAGCAACCACTCTATTATTTGTGCATCAGA 561
Qy 186 TGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGATCCAC 245
Db 562 TGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGATCCAC 621
Qy 246 AGACCCCAACCCACAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTAATCATGTGAA 305
Db 622 AGACCCCAACCCACAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTAATCATGTGAA 681
Qy 306 AAATAACATGTGTAGTACATGAGATATATCATGTTTAAATTTGGAATGAAAGCTAAA 365
Db 682 AAATAACATGTGTAGTACATGAGATATATCATGTTTAAATTTGGAATGAAAGCTAAA 741
Qy 366 GCCATGTCTAAAATTTAACCCCACTCTGTGTTTACTTTTAAATTTGCAATATCAC 425
Db 742 GCCATGTCTAAAATTTAACCCCACTCTGTGTTTACTTTTAAATTTGCAAGGATGT----- 792
Qy 426 TAAGAATACTACTAATCCCACTAGTACGCTGGGGAATGATGGAGAAAGGAAATAAA 485

Db 793 ---GAATGCTACTAATACCACTAATGATAGCGAGGGAACGATGGAGAGGGAATAATAA 849

Qy 486 AAATTGCTCTTTCTATATACCAAGCATAAAGAAATAGGTAAAGAAAGATATGCACT 545

Db 850 AAATGCTCTTTCAATATACCAAGCATAAAGATAGGTGCGAGAAAGATATGCTCT 909

Qy 546 TTTTAAATAGACTTGATAGTACCAATAGAAATACTAATACTAAGTATAGTTAAT 605

Db 910 TTTTATAAATCTTGATAGTACCAATAG---ATAATAATAATACCACTATAGTTGAT 966

Qy 606 AAGTGTAAACCTCAGTCATTACACAGCGCTGCTCAAAAGGTATCTTTAGCCCAATTC 665

Db 967 AAGTGTGACACCTCAGTCATTACACAGCGCTGCTCAAAAGATATCTTTAGCCCAATTC 1026

Qy 666 CATACATTATTGTGTCGCGCTGGTTCGCGATGCTAAAGTGTAAAGTGTAAAGACATTCAA 725

Db 1027 CATACATTATTGTGTCGCGCTGGTTCGCGATGCTAAAGTGTAAAGTGTAAAGACGTTCAA 1086

Qy 726 TGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCAGT 785

Db 1087 TGGAAAGGAGCCATGTAAAAATGTCAGCACAGTACAAATGTACACATGGAATTAGGCCAGT 1146

Qy 786 GGTGTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGATC 845

Db 1147 AGTATCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGAGGTAGTAATTAGATC 1206

Qy 846 TGAATAATTTACAGACAATGCTTAAACCATATAGTACAGCTTAAATGAATCTGTAGTAAT 905

Db 1207 TGACAATTTACAGACAATGCTTAAACCATATAGTACAGCTTAAAGATCTGTAGTAAT 1266

Qy 906 TAAATTGTACAGACCCACAAACATACAAAGAAAGTTATCTATAGACACGAGGAGAGC 965

Db 1267 TAAATTGTACAGACCCACAAACATACAAAGAAAGTTATACATATAGGACACGAGGAGAGC 1326

Qy 966 ATTTTATCAAGAAACATATAGGAGATATAGACAGCACATTTGTAACTAGTAG 1025

Db 1327 ATTTTATCAAGAGAAATATAGGAGATATAGACAGCACATTTGTAACTAGTAG 1386

Qy 1026 AGCAAAATGGAATAACACTTTTACACAGATAGTTTAAATTAAGAGAAATTTAGGAA 1085

Db 1387 AGCAAAATGGAATGACACTTTTAAACAGATAGTTTAAATTAAGAGAAATTTAGGAA 1446

Qy 1086 TAAACAATAGCTTTTAAATCAATCTCAGGAGGAGCCAGAAATTTGTAATGCAAGTTT 1145

Db 1447 TAAACAATAGCTTTTAAATCAATCTCAGGAGGAGCCAGAAATTTGTAATGCAAGTTT 1506

Qy 1146 TAAATTGCGAGGGAATTTCTTCTACTGTAATACACAGCACTGTTTAAATAGTACTTGG-- 1203

Db 1507 TAAATTGCGAGGGAATTTTCTCTGTAATTTCAACACAACTGTTTAAATAGTACTTGGAA 1566

Qy 1204 -AATGTTACTGGAGGACAAATGGCACTGAAGGAAATGACATAATCACTCCCAATGCAG 1262

Db 1567 TAAATAATCTGAAGGTCAAATAACACTGAAGNAAT---ACTATCACACTCCCATGCAG 1623

Qy 1263 AATAAAACAAATTAATAATATGTCGAGAAAGTAGGAAAGCAATGTATGCCCTCCCAT 1322

Db 1624 AATAAAACAAATTAATAATATGTCGAGAAAGTAGGAAAGCAATGTATGCCCTCCCAT 1683

Qy 1323 CACAGGACAAATTTAGATGTTCAATCAATATTTACAGGCTGCTACTTAAACAGAGATGGAGG 1382

Db 1684 CAGAGGACAAATTTAGATGTTCAATCAATATTTACAGGCTGCTACTTAAACAGAGATGGTGG 1743

Qy 1383 TAAATAGTACTGAGACTGAGATCTTTCAGACTCTGGAGGAGAGATATGAGGGACAA 1442

Db 1744 ---TATTATGNAATGGACCGAGATCTTCAGACTCTGGAGGAGAGATATGAGGGACAA 1800

Qy 1443 TTGGAGAGTGAATTAATAATATAAAGTATAGTAAGAAATTTGAAACAAATAGGATAGCACC 1502

Db 1801 TTGGAGAGTGAATTAATAATATAAAGTATAGTAAGAAATTTGAAACCAATAGGATAGCACC 1860

Qy 1503 CACAGGACCAAGAGAGAACAGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1556

Db 1861 CACCAAGGCAAGAGAGAGTGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1914

RESULT 3

US-09-759-841-3
; Sequence 3, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:

; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348PME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-759-841-3

Query Match 54.2%; Score 1197; DB 9; Length 1512;
Best Local Similarity 89.2%; Pred. No. 5.6e-266;
Matches 1316; Conservative 0; Mismatches 150; Indels 9; Gaps 2;

Qy 74 TGCTCTCTGGGATATGTATGATCTGTAGTCTACAGAAAAATTTGGGTACAGTCTATT 133

Db 38 TGCTGTGTGGAGCAGTCTTCGTTGGCTAGCGTAGAAAAATTTGTGGGTACAGTTATT 97

Qy 134 ATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAAAG 193

Db 98 ATGGGTACCTGTGTGGAAAGAGCAACCACTCTATTTTGTGCATCAGATGCTAAAG 157

Qy 194 CCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTACCACAGACCCCA 253

Db 158 CATATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTGCCACAGACCCCA 217

Qy 254 ACCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 313

Db 218 ACCCAAGAAAGTAGAATTTGAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACA 277

Qy 314 TGGTAGATCAGATGCGATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCCATGTG 373

Db 278 TGGTAGAACAGATGCGATGAGGATATAATCAGTTTATGGGATCAAAAGCCCTAAAGCCATGTG 337

Qy 374 TAAATTAACCCCTCTGTGTTACTTTTAAATTTGACATAATTTGA-----ATATCACATA 427

Db 338 TAAATTAACCTCCACTCTGTGTTACTTTTAAATTTGACATAATTTGAGGAATGCTACTAATG 397

Qy 428 AGAATFACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAGAAATAAAA 487

Db 398 GGAATGACACTAATACCACTAGTAGTAGCGGGAATGATGGGGGAGGAGAGAAATGAAA 457

Qy 488 ATTGCTCTTTCTATATACCAAGCATAGAAATAAGGTAAGAGAAAGATATGCACTTT 547

Db 458 ATTGCTCTTTCAAAATCAACCAAGAGGTAAAGTGTGAGAGAAAGATATGCACTTT 517

Qy 548 TTAATAGACTTTGATGTAGTACCAATAGAAAAATCTAATAATACTAAGTATAGTTAATAA 607

Db 518 TTTATGAACCTTGATATAGTACCAATAGATAATAATAGTAATAATAGATATAGTTGATAA 577

Qy 608 GTTGTAAACACCTCAGTCAATTACAGAGGCTGTCCAAAGGTATCTTTTCAGCCCAATTTCCA 667

Db 578 GTTGTAAACACCTCAGTCAATTACAGAGGCTGTCCAAAGATATCTTTTGAGCCCAATTTCCA 637

Qy 668 TACATTATTGTGTCGCCGCTGGTTTGGATGCTAAAGTGTAAACAAATTAAGACATTCAATG 727

```
|||||
638 TACATTATTGCCCCGCTGGTTTTCGATTCTAAAGTGTAAGAGATAAGAAAGTTCRAATG 697
QY
728 GATCAGGACCAATGCACAAATGTACAGCAGTACAAATGTACACATCGGAATTAGGCCAGTGG 787
Db
698 GAAAGGACCAATGTTCAAATGTCAGCAGTACAAATGTACACATCGGGATTAGGCCAGTAG 757
QY
788 TGTCAACTCAACTGCTGTTAAATGTCAGTGTAGCAGAGAGAGACATAGTAATTAGATCTG 847
Db
758 TATCAACTCAACTGCTGTTAAATGTCAGTGTAGCAGAGAGAGAGATAGTAATTAGATCCG 817
QY
848 AAAATTTTCCAGACCAATGCTAAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTA 907
Db
818 ABAATTTTCGCGACACATGCTAAAACCAATAATAGTACAGCTGAATGAATCTGTAGAAATTA 877
QY
908 ATTGTACAAGACCCCAACCAATCAAGAAAGAGTTATCTATAGGACCAAGGAGAGCAT 967
Db
878 ATTGTACAAGACCCCAACCAATCAAGAAAGAGTTATCATATAGGACCAAGGAGAGCAT 937
QY
968 TTTATGCAAGAGAAACATATAGGAGATATAAGACAAGCACATTTGTAAACATTTAGTAGAG 1027
Db
938 TATATACAACAGGAGAAATATAGGAGATATAAGACAAGCACATTTGTAAACCTTTAGTAGAG 997
QY
1028 CAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAATA 1087
Db
998 CAAAATGGAATGACACTTTTAAATAAGATAGTTATAAATTAAGAGAACAAATTTGGGAATA 1057
QY
1088 AAACAATAGCCTTTAATCAATCTCAGAGGGGCCCAAGAAATTTGTAATGCACAGTTTTTA 1147
Db
1058 AAACAATAGTCTTTAAGCATCTCCTCAGAGGGGCCCAAGAAATTTGTGACGACACAGTTTTTA 1117
QY
1148 ATTGTGGAGGGGAATTTCTTACTGTAATACAGACAACATGTTTAAATAGTACTTTGGAATG 1207
Db
1118 ATTGTGGAGGGGAATTTTCTACTGTAATCAACACAACATGTTTAAATAGTACTTTGGAATG 1177
QY
1208 TTACTGAGGAGCAAAATGGCACTGAAGGAAATGACATAATCACACTCCCAATGCAGAAATA 1267
Db
1178 TTACTGAGAGTCAAAATAACACTGTAGAAATAACACAATCACACTCCCATGCAGAAATA 1237
QY
1268 AACAAATTAATAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1327
Db
1238 AACAAATTAATAACATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1297
QY
1328 GACAAATAGATGTTTCATCAATATTACAGGCTCTACTAACAGAGATGGAGTAATA 1387
Db
1298 GACAAATAGATGTTTCATCAATATTACAGGCTCTATTACAGAGATGGTGTCCCG 1357
QY
1388 GTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGACCAATTTGA 1447
Db
1358 AGGCCAACA--AGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGACCAATTTGA 1414
QY
1448 GAAGTGAATTAATAATAAATAGTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1507
Db
1415 GAAGTGAATTAATAATAAATAGTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1474
QY
1508 GGGCAAGAGAGACAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1542
Db
1475 AGGCAAGAGAGAGAGTGGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1509
```

RESULT 4
US-10-728-195-7
; Sequence 7, Application US/10728195
; Publication No. US20040191269A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Shan
; APPLICANT: Pal, Ranajit
; APPLICANT: Kalyanaraman, V.S.
; APPLICANT: Whitney, Stephen Charles
; APPLICANT: Keen, Tim
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS
; FILE REFERENCE: 07917-269001

```
; CURRENT APPLICATION NUMBER: US/10/728,195  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: US 60/430, 732  
; PRIOR FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus  
US-10-728-195-7  
  
Query Match 53.4%; Score 1179.8; DB 18; Length 1422;  
Best Local Similarity 90.4%; Pred. No. 5.1e-262;  
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;  
  
QY 115 TTGTGGGTCAAGTCTATTATTTGGGTACCTGTGTGGAGAGAAAGCAACCCACACTCTATTT 174  
Db 1 TTGTGGGTCAAGTCTATTATTTGGGTACCTGTGTGGAAAGAAAGCAACCCACACTCTATTT 60  
  
QY 175 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATATATTTTGGGCCACACATGCC 234  
Db 61 TGTGCATCAGATGCTAAAGCATATGATACAGAGGTACATAATTTTGGGCCACACATGCC 120  
  
QY 235 TGTGTACCCACAGACCCCAACCCCAAGTAGTATTGGGAAATGTGCAGAGAAATTTT 294  
Db 121 TGTGTACCCACAGACCCCAACCCCAAGTAGTATTGGAAATGTGCAGAGAAATTTT 180  
  
QY 295 AACATGTGGAAAAATAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 354  
Db 181 AACATGTGGAAAAATAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
  
QY 355 GAAAGCCTAAAGCCATGTTAAATTAACCCCACTCTGTTTACTTTTAAATTTGCACTAAT 414  
Db 241 CAAGCCTAAAGCCATGTTAAATTAACCTCTGTTTACTTTTAAATTTGCACTGAT 300  
  
QY 415 TTGA-----ATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATG 468  
Db 301 TTGAGGAATGCTACTAATGGGAATGACACTAATACCCTAGTAGTAGCAGGGAATGATG 360  
  
QY 469 GAGAAAGAGAAAAATAAAAAATGCTCTTTTATATCACCACAGCATTAAGAAATAGGTA 528  
Db 361 GGGGAGAGAAAAATGAATAATTTGCTCTTTTAAAAATCACCAAAACATTAAGAGTAAAGTG 420  
  
QY 529 AAGAAGGAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAATAAT 588  
Db 421 CAGAAAGGAATATGCACTTTTATGAATGATATAGTACCAATAGAAATAGTAAAT 480  
  
QY 589 ACTAAGTATAGGTTAAATAAGTTGTAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTA 648  
Db 481 AATAGATATAGTTGATTAAGTTGTAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTA 540  
  
QY 649 TCCTTTACGCAATTTCCCATACATATTGTTGTCGGGCTGGGTTTGGCATGCTAAAGTGT 708  
Db 541 TCCTTTACGCAATTTCCCATACATATTGTTGTCGGGCTGGGTTTGGCATGCTAAAGTGT 600  
  
QY 709 AACAAATAGACATTTCAATGGATCAGGACCAATGTCACAAATGTACAGCAGTACAAATGTACA 768  
Db 601 AAAGATAAGAGTTTCAATGGAAAGGACCATGTTCAAAATGTACAGCAGTACAAATGTACA 660  
  
QY 769 CATGGAATTAGGCCAGTGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAA 828  
Db 661 CATGGATTAGGCCAGTGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAA 720  
  
QY 829 GACATAGTAATTAGATCTGAAAAATTTTACAGCAATGCTTAAACCATTAATAGTACAGTGA 888  
Db 721 GAGGTAGTAATTAGATCTGAAAAATTTTCCGCGACAAATGCTTAAACCATTAATAGTACAGTGT 780  
  
QY 889 AATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACCAATACAAAGAGAGAGTTATCT 948  
Db 781 AATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACCAATACAAAGAGAGATATACAT 840  
  
QY 949 ATAGGACCGGAGAGAGCATTTTATGCAAGAGAGAAACATAATAGGAGATATAAGACAAGCA 1008
```


Db 841 ATAGACCAAGGAGAGCAATATATACACAGGAGAAATATAGGAGATATATAGCAAGCA 900
Qy 1009 CATTGTAACTAGTAGACCAAAATGGAATACACCTTTTCAACAGATAGTATATAAATTA 1068
Db 901 CATTGTAACTAGTAGACCAAAATGGAATACACCTTTTAAATAGATAGTATATAAATTA 960
Qy 1069 AGAGAAAATTTAGGAATATAAACAATAGCCTTTTAAATCAATCTCAGGAGGAGCCAGAA 1128
Db 961 AGAGAAACAATTTGGGAATATAAACAATAGTCTTTTAAAGCATCTCAGGAGGAGCCAGAA 1020
Qy 1129 ATTGTAAATGCACAGTTTAAATTTGTGGGGAATCTTCTACTGTAAATACAGCAACTG 1188
Db 1021 ATTGTAAATGCACAGTTTAAATTTGTGGGGAATTTTCTACTGTAAATCAACAACATG 1080
Qy 1189 TTTAAATAGTACTTGAATCTTACTCGAGGACAAATGGCACTGAAGGAAATGACATAATC 1248
Db 1081 TTTAAATAGTACTTGAATCTTACTCGAGGACAAATGGAAGTCAATACACCAATC 1140
Qy 1249 ACACCTCAATGAGAAATATAAACAATTTAAATATGTGCGAGAAAGTAGGAAAGCAATG 1308
Db 1141 ACACCTCAATGAGAAATATAAACAATTTAAATATGTGCGAGAAAGTAGGAAAGCAATG 1200
Qy 1309 TATGCCCTCCCATCACAGGACAAATTAGATGTTTCAATATTTACAGGGCTGCTACTA 1368
Db 1201 TATGCCCTCCCATCACAGGACAAATTTAGATGTTTCAATATTTACAGGGCTGCTACTA 1260
Qy 1369 ACAAGAGATGAGAGGTAATAGTACTGAGACTGAGACTGAGACTCTCAGACCTCGAGGAGGA 1428
Db 1261 ACNAGAGATGAGGTCGAGGACGCAACA---AGACGAGGTCTTCAGACCTCGAGGAGGA 1317
Qy 1429 GATATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAATAGTAGTAAGAAATGAACCA 1488
Db 1318 GATATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAATAGTAGTAAGAAATGAACCA 1377
Qy 1489 ATAGAGTAGACCCACCGGCAAGGCAAGAGAGCAAGTGCA 1529
Db 1378 TTAGGAGTAGCACCCACCAAGGCAAGAGAGAGTGGTGA 1418

RESULT 5
US-10-441-788-78/c
; Sequence 78, Application US/10441788
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/10/441,788
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/136,159A
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-10-441-788-78
Query Match 53.2%; Score 1174.2; DB 15; Length 3807;
Best Local Similarity 88.1%; Pred. No. 1.6e-260;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;
Qy 52 TGGATCTCGGCTTCGAGATCCATGCTCTCTGGGATATTTGATGATCTGTAGTCTCAGAA 111
Db 1668 TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTCTCAGAA 1609
Qy 112 AAATTGTGGGTACACAGTCTATTATGGGTACTCTGTGAGAGAGAGCAACACCACTCTA 171
Db 1608 AAATTGTGGGTACACAGTCTATTATGGGTACTCTGTGAGAGAGAGCAACACCACTCTA 1549
Qy 172 TTTTGTGATCAGATGCTTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 231
Db 1548 TTTTGTGATCAGATGCTTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACAT 1489
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTTGGGAAATGTGACAGAAAT 291
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTTGGTAAATGTGACAGAAAT 1429
Qy 292 TTTAACATGTGGAAAAATAACATGCTAGATCAGATGATGAGGATATATCAAGTTTATGG 351
Db 1428 TTTAACATGTGGAAAAATAACATGCTAGATGATGAGGATATATCAAGTTTATGG 1369
Qy 352 GATGAAAGCCCTAAAGCCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACT 411
Db 1368 GATGAAAGCCCTAAAGCCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACT 1309
Qy 412 AATTGT-----AATATCACTAAGAAATACTATAATCCCACTAGTAGAGCTGG 459
Db 1308 GATTGTGAGGAATACTACTAATACCAATATAGTACTGTCTAATAACAATAGTAATAGCGAG 1249
Qy 460 GGAATGTGGAGAGAGGAGAAATAAATAATTTGCTCTTTCTATATCACCACAGCATAGA 519
Db 1248 GGAACAATAAAGGGAGGAGAAATGAAAACTGCTCTTTCAATATCACCACAGCATAGA 1189
Qy 520 AATAAGGTAAAGAGAAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAT 579
Db 1188 GATAAGATGCAGAAAGATATGCACCTCTTTATAAATTTGATATAGTATCAAT---AAT 1132
Qy 580 ACTAATAATCTAAGTATAGGTTAATAAGTTTAAAGTTGTAAACCTCAGTCATTTACAGGCTGT 639
Db 1131 AATGATAGTACGAGCTATAGGTTGATAAGTTGTAAATAGTCTCAGTCATTTACAGGCTGT 1072
Qy 640 CCAAGGTATCTTTTCAGCCCAATCCCATACATTTTGTGTCCTCCCGCTGGGTTTCGGATG 699
Db 1071 CCAAGATATCTTTTTCAGCCCAATCCCATACATTTTGTGTCCTCCCGCTGGGTTTCGGAT 1012
Qy 700 CTAAGGTGTAACAATAAGACATTTCAATGGATCAGGACCATGCAACAATGTTCAGACAGTA 759
Db 1011 CTAAGGTGTAACAATAAGATTTCAATGGAAAGGATCATGTAAATAATGTTCAGACAGTA 952
Qy 760 CAATGTACATGGAATTTAGGCCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTA 819
Db 951 CAATGTACATGGAATTTAGGCCAGTGGTGTCAACTCAACTGCTTTAAATGGCAGTCTA 892
Qy 820 GCAGAGAGACATAGTAAATTTAGATCTGAAATTTTCAGACCAATGCTTAAACCATATA 879
Db 891 GCAGAGAGAGAGGTAGTAAATTTAGATCTGAGAAATTTCAATGATTAATGCTTAAACCATATA 832
Qy 880 GTACAGCTAAATGATCTGTAGTAAATTTTGTACAGAGCCCAACAACAACTACAGAGAA 939
Db 831 GTACATCTGAATGATCTGTACAAATTTAATTTGTACAGAGCCCAACAACAACTACAGAGAA 772
Qy 940 AGGTTATCTATAGGACCGAGGAGAGCAATTTTATGCAAGAGAAACATATAATAGGAGATATA 999

Db 771 AGGATACATATAGGACCGGAGGACATTTTATACAACAAAAATATATAGGAACATATA 712
Qy 1000 AGACAAGACACATTGTAACATTAGTAGAGCAAAATGAATACACCTTTTACACAGATAGTT 1059
Db 711 AGACAAGACACATTGTAACATTAGTAGAGCAAAATGAATACACCTTTTAAAGACAGATAGTT 652
Qy 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAAATCAATCCTCAGGAGGG 1119
Db 651 AGCAAAATTAAGAACAATTTAAGAAATAAACAATAGTCTTTTAAATCAATCCTCAGGAGGG 592
Qy 1120 GACCAGAAAATGTAATACACAGTTTTTAAATGTGGAGGGAAATCTTCTACTGTAAATACA 1179
Db 591 GACCAGAAAATGTAATACACAGTTTTTAAATGTGGAGGGAAATCTTCTACTGTAAATACA 532
Qy 1180 GCACAACCTGTTTAAATAGTACTTGGAAATGTTACTTGGAGGACAAATGGCAGCTGAAGG---A 1236
Db 531 TCACCACCTGTTTAAATAGTACTTGGAAATGTTAAATACTTGGAAATTAATCTACAGGGTCA 472
Qy 1237 AATGACATAATCACACTCCAAATGCAGATAAAACAATTTATAAATATGTGGCAGAAAGTA 1296
Db 471 AATAACAATATCACACTTCATTCGCAAAATATAAACAATTTATAAATATGTGGCAGAAAGTA 412
Qy 1297 GGAAGAAGCAATGTATGCCCTCCCATCACAGGACAAAATTAGATGTTTCATCAAAATATTACA 1356
Db 411 GGAAGAAGCAATATATGCCCTCCCATTCGAAGGACAAAATTAGATGTTTCATCAAAATATTACA 352
Qy 1357 GGGCTGCTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTTC 1413
Db 351 GGGCTACTATTAAACAAGAGATGGTGGTAAGGACACGGACACGAAACGACACCGAGATCTTC 292
Qy 1414 AGACCTGGAGGAGGAGATATGAGGACAAATGGAGAAGTGAATTTATATAAATATAAAGTA 1473
Db 291 AGACCTGGAGGAGGAGATATGAGGACAAATGGAGAAGTGAATTTATATAAATATAAAGTA 232
Qy 1474 GTAAGAATTTGAACCAATAGGAGTAGCACCACCGGCAAAAGAGAGAACAGTGC AAAAGA 1533
Db 231 GTAACAATTTGAACCAATAGGAGTAGCACCACCGGCAAAAGAGAGTGGTGCAGAGA 172
Qy 1534 GAAAAAAGA 1542
Db 171 GAAAAAAGA 163

RESULT 6

US-09-966-931-27
; Sequence 27, Application US/09966931
; Publication No. US20030064361A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: 2000-01-27
; ATTORNEY/AGENT INFORMATION:

NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 2552 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2552
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-966-931-27
Query Match 53.1%; Score 1173; DB 10; Length 2552;
Best Local Similarity 88.8%; Pred. No. 2.5e-260;
Matches 1337; Conservative 0; Mismatches 135; Indels 33; Gaps 5;
Qy 64 TCGAGATCCATGCTCCTTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGGTG 123
Db 46 TGGGGCACCATGCTCCTTTGGGATGTTGATGATCTGTAGTGTACAGAAAAATTTGGGTG 105
Qy 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTATTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGAAAGCAACCACTCTATTATTGTGCATCA 165
Qy 184 GATCTAAAGCCTATGATACAGAGGTACATATGTTTGGGCCACACATGCTGCTGTACCC 243
Db 166 GATCTAAAGCATATGATACAGAGGTACATATGTTTGGGCCACACATGCTGCTGTACCC 225
Qy 244 ACAGACCCCAACCCACAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGG 303
Db 226 ACAGACCCCAACCCACAGAAATAGGATTGGAAATGTAAACAGAAAAATTTAAACATGTGG 285
Qy 304 AAAAATAACATGGTAGATCAGATGATGAGATATATCAGTTTATGGATGAAGCCCTA 363
Db 286 AAAAATAACATGGTAGAACAGATGATGAGATATATCAGTTTATGGATGAAGCCCTA 345
Qy 364 AAGCCATGTGTAATAATTAACCCCTCTGTTTACTTTTAAATTTGACATAATATC 423
Db 346 AAGCCATGTGTAATAATTAACCCCTCTGTTTACTTTTAAATTTGACATAATATC 399
Qy 424 ACTAAGAACTACTTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAGGAGAAATA 483
Db 400 ---AAAAATGCTACTTAATACCCTAGTAGCAGCTGGGAAAGATGGAGAGGAGAAATA 456
Qy 484 AAAAATGCTCTTTCTATATCACCACAGCATAGAATAAGTTAAAGAAAGAAATATGCA 543
Db 457 AAAAATGCTCTTTCTATATGTCACCAAGTATAAGAGATAGAAGAAAGAAATATGCA 516
Qy 544 CTTTTTAATAGACTTTGATGTAGTACCAATAGAAAATCTAATACTAAGTATAGGTATA 603
Db 517 CTTTTTAATAAATGATGTAGTACCAATAG---ATAATGATATACTAGCTATAGGTG 573
Qy 604 ATAAGTTGTAACACCTCAGTCAATACACAGGCCTGTCCAAAGGATATCCTTTTCAGCAATT 663
Db 574 ATAAGTTGTAACACCTCAGTCAATACACAGGCCTGTCCAAAGGATATCCTTTTCAGCAATT 633
Qy 664 CCCATACATTTATGTGTCCTGGGTTTGGGATGCTAAAGTGTAAACAATAGCAATTC 723
Db 634 CCCATACATTTATGTGTCCTGGGTTTGGGATGCTAAAGTGTAAACAATAGCAATTC 693
Qy 724 AATGGATCAGGACCAATGCACAAATCTCAGCAGTACATGATGATACATGGAATTAGGCCA 783
Db 694 AACGACACAGGACCAATGCACAAATCTCAGCAGTACATGATGATACATGGAATTAGGCCA 753
Qy 784 GTGGTGTCAACTCAACTCTCTGTTAAATGGCAGTCTTAGCAGAGAGACATAGTAATTAGA 843


```
Db 757 ACACATGGATTAGGCCAGTAGTATCACTCACTGCTGTTAAATGGCAGTCTACAGAA 816
Qy 826 GAAGACATAGTAATAGATCTGAAATTTCAAGCAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATAGATCTGAGAATTTCACTGATATGCTTAAACCATATAGTACAT 876
Qy 886 CTAAATGATCTGTAGTAAATTTGTCAAGACCCCAACAACATACAGAGAGGTGA 945
Db 877 CTGAATGATCTGTCAAAATTAATTTGTCAAGACCCCACTCAATTAAGAAAAAGGATA 936
Qy 946 TCTATAGGACCGGAGAGCATTATTATGCAAGAAACATATAGGAGATATAAGACAA 1005
Db 937 CATATAGGCCAGGAGAGCATTATTATACAAACAAAATATATATAGGAACTATAGACAA 996
Qy 1006 GCACATTTGAACATTAGTAGACAAATGGAATAACATTTTACACAGATAGTTATATAA 1065
Db 997 GCACATTTGAACATTAGTAGACAAATGGAATGACACTTTTAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAATTTAGGATATAACATAGCTTTTAAATCCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAACATTTAAGAAATAAACAATAGTCTTTAATCAATCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGCACAGTTTAAATTTGTGAGGGGAATTTCTTACTGTAAATACACAAA 1185
Db 1117 GAAATTTGTAATGCACAGTTTAAATTTGTGAGGGGAATTTTCTACTGTAAATACACCA 1176
Qy 1186 CTGTTTAATAGTACTTGGAGT---TTACTGGAGGGACAAATGGCACTGAAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGGAGTAAATTAATCTTGGAAATAATCTACACAGGGTCAAATAAC 1236
Qy 1243 ATAATCACACTCCATGACAGATATAACAAATTAATATATGTCAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCAATGCAAAATAAACAATTAATAACATGTGCGCAAGGATAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGACAAATTTAGATGTTCAATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATGGAAGACAAATTAATGTTCAATCAAAATATTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGACACGGACACGACGACACCGAGATCTTCAGACCT 1416
Qy 1420 CGAGAGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATATAAGTAGTAGA 1479
Db 1417 CGAGAGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATATAAGTAGTAGA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCCACCGAGGCAAGAGAGAAAGTGCAGAGAGAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCCACCGAGGCAAGAGAGAGAGTGGTGCAGAGAGAAA 1536
Qy 1540 AGACCGGATCCAAGA 1554
Db 1537 AGAGCAGCGATAGGA 1551
```

RESULT 9

US-10-077-294-3
; Sequence 3, Application US/10077294
; Publication No. US20020159979A1

GENERAL INFORMATION:

; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,294

; FILING DATE: 15-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/691,604

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: No. US20020159979A1and, Greta E.

; REGISTRATION NUMBER: 31975

; REFERENCE/DOCKET NUMBER: 31975

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2571 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-077-294-3

Query Match 53.1%; Score 1172.2; DB 13; Length 2571;

Best Local Similarity 87.9%; Pred. No. 3.8e-260;

Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG 117

Db 40 TGGGGATGGGCGACGATGCTCCTTGGGTTATTAATGATCTGTAGTGTCTACAGAAAAATTG 99

Qy 118 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACACCACTCTATTTTGT 177

Db 100 TGGGTCAAGTCTATTATGGGGTACCTGTGTGGAGAGAGCAACACCACTCTATTTTGT 159

Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGTACATATGTTGGGCCACACATGCTCTGT 237

Db 160 GCATCAGATGCTAAAGCCTATGATACAGAGTACATATGTTGGGCCACACATGCTCTGT 219

Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAAC 297

Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGTAAATGTGACAGAAAAATTTTAAAC 279

Qy 298 ATGTGGAAAAATAACATGCTGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357

Db 280 ATGTGGAAAAATAACATGCTGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 339

Qy 358 AGCCTAAAGCCATGTGTAAATAATTAACCCCTCTGTGTACTTTTAAATTTGCACTAAATTTG 417

Db 340 AGCCTAAAGCCATGTGTAAATAATTAACCCCTCTGTGTACTTTTAAATTTGCACTAAATTTG 399

Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465

Db 400 AGGAATACTACTAATAACCAATAATAGTACTCTAATAACATAAGTAGTAGCGGGAACA 459

Qy 466 ATGAGAGAGAGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCATTAAGAAATAG 525

Db 460 ATAAAGGAGAGAGAAATGAAAAACTGCTCTTTCAATATCACCACAGCATTAAGAGATAG 519

Qy 526 GTAAGAGAGAGATGCACTTTTAAATAGACTTGTAGTACCAATAGAGAAATACTAAT 585

Db 520 ATGAGAGAGAGATGCACTTTTAAATAGACTTGTAGTACCAATAGAGAAATACTAAT 576

Qy 586 AATACTAAGTATAGTTTAAATAGTTTGAACACCTCAGTCATTACACAGGCTGTCCAAAG 645

Db 577 AGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAGCTGTGCCAAG 636

Qy 646 GTATCTCTTTCAGCAATTTCCCATACATATTGTGTGCCGCTGGGTTTGGCATGCTAAAG 705

Db 340 AGCCTAAGCCATGTGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTCACCTGATTTG 399
Qy 418 -----AATATCACTAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTAGTCTCTAATAACAAATAGTAATAGCGAGGAACA 459
Qy 466 ATGGGAAGAGGAATAAATAATGCTCTTCTATATACCAACAGCATAGAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAAAACCTGCTCTTCAATATCACCACCAAGCATAGAATAAG 519
Qy 526 GTAAAGAAAGAAATATGCATCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAGAAATATGCATCTTTTATAAACTTGATATAGTATCAATAG---ATAATGAT 576
Qy 586 AATACTAAGTATAGTTAATAGTTGTAACCTCAGTCATATACAGGCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATATACACAGCTTGTCCAAAG 636
Qy 646 GTATCCTTTAGCCCAATTCCCATACATTAATGTGTCCCGCTGGTTTGCATGCTAAAG 705
Db 637 ATATCCTTTAGCCCAATTCCCATACACTATTTGTGCCCGCTGGTTTGCATGCTTAAAA 696
Qy 706 TGTAACTAATAAGACATTCATAGGATCAGGACCATGCACAAATGTTCAGCACAGTACAATGT 765
Db 697 TGTAACTAATAAGTTCAGTGGAAAGGATCATGTAAATGTTCAGCACAGTACAATGT 756
Qy 766 ACACATGGAATTAGCCAGTGGTGTCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGCCAGTGGTGTCAACTCAACTGTCTTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTAGATCTGAAATTTTCAGACATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTTCTAGTAATGTCTTAAACCATATAGTACAT 876
Qy 886 CTAAATGAATCTGTAGTAATTAATGTACAAAGCCCAACAAATACAAAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTAATGTACAGACCCCACTACATTAAGAAAGGATA 936
Qy 946 TCTATAGGACAGGAGAGCACTTTTATGCAAGAGAAACATAATAGGAGATATAGACAA 1005
Db 937 CATATAGGACAGGAGAGCACTTTTATACAAACAAAATAATATAGGAACATATAGACAA 996
Qy 1006 GCACATTTCACTATAGTAGCAAAATGGATACACTTTTACACACATAGTTATATAAA 1065
Db 997 GCACATTTCACTATAGTAGCAAAATGGATACACTTTTAAAGACATAGTTAGCAAA 1056
Qy 1066 TTAAGAGAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAAATTTAGANATAAAACAATAGTCTTTAATCAATCCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGATGACACAGTTTTAATTTGGAGGGGAATTTCTTCTACTGTAATACAGACAA 1185
Db 1117 GAAATTTGATGACACAGTTTTAATTTGGAGGGGAATTTTCTACTGTAATACATACCA 1176
Qy 1186 CTGTTTAAATAGTACTTGAATG---TTACTGGAGGACAAATGGCACTGAAGGAATCAC 1242
Db 1177 CTGTTTAAATAGTACTTGAATGGAATTAATAATCTTGGAAATAATCTACAGGGTCAATAAC 1236
Qy 1243 ATAATCACACTCCAATGACAGATAAAACAAATTTATAAATATGTGCGAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCCAATGACAGATAAAACAAATTTATAAATGTCGACGAGNAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATAAATATTACAGGGTGT 1362
Db 1297 GCAATGTATGCCCTCCCATGAGGACAAATTAGATGTTCAATAAATATTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACT 1419
Db 1357 CTATTTAAACAGAGATGGTGGTAAGGACACGGACACGAACGACACCGAGATCTTCAGACT 1416
Qy 1420 GGAGGAGGAGATATAGGGGACAAATTTGGAGAGTGAATTAATAAATAAAGTAGTAAGA 1479

Db 1417 GGAGGAGGAGATATGAGGAGCAATTTGGAGAAGTGAATTTATATAATAAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCCACCAGGCGCAAGAGAGAACAGTGCACAGAGAAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCCACCAGGCGCAAGAGAGAGAGTGGTGACAGAGAAAAA 1536
Qy 1540 AGACCGGATCCAAG 1554
Db 1537 AGACGAGGATAGGA 1551
RESULT 12
US-10-375-777-3
; Sequence 3, Application US/10375777
; Publication No. US20030147912A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,777
; FILING DATE: 26-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030147912A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-375-777-3
Query Match 53.1%; Score 1172.2; DB 15; Length 2571;
Best Local Similarity 87.9%; Pred. No. 3.8e-260;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCACTGCTCTGGGATATGATGCTGTAGTGCTACAGAAAATTG 117
Db 40 TGGGATGGGCGACGATGCTCTTGGGTATTAATGATCTGTAGTGCTACAGAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGCAACCAACCACTCTATTATTG 177
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGCAACCAACCACTCTATTATTG 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCGACACATCCCTGT 237

Db 160 GCATCAGATCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACAGCCTGT 219
Qy 238 GTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCAAGAGTAGAATTGGTAAATGTGACAGAAAATTTTAAAC 279
Qy 298 ATGTGGAAAATAACATGTTAGATCAGATGCATGAGGATATATATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAATAACATGTTAGATGCATGAGGATATATATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACCTTTAAATTTGCACTAATTTG 417
Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACCTTTAAATTTGCACTAATTTG 399
Qy 418 -----AATATCACTAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAAATAGCGAGGGAACA 459
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACCAAGCATAGAAATAAG 525
Db 460 ATAAAGGGAGGAGAAATGAAAACCTGCTCTTTCAATATACCAACCAAGCATAGAGATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTAGTACCAATAGAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCACCTTTTAAATAGACTTGTAGTACCAATAGAAAATACTAAT 576
Qy 586 AATACTAAGTATAGTTAATAAGTTGTAAACCTCAGTCATTACACAGCCCTGTCCAAG 645
Db 577 AGTACCAGCTATAGTTGATAAGTTGTAAATACCTCAGTCATTACACAGCTTGTCCAAG 636
Qy 646 GTATCCTTTTACCCCAATCAATATTTGTGTCCCGCTGGGTTCGCGATGCTAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACACTATTTGTGCCCGCTGGTTTTCGCAATTTAANA 696
Qy 706 TGTAAACATAAGACATTTCAATGGATCAGGACCATGCACAAATGTGACACAGCTACAATGT 765
Db 697 TGTAAACATAAGATTTGAGTGGAAAGGATCATGTAAATATGTGACACAGCTACAATGT 756
Qy 766 ACACATGGAATTTAGCCAGTGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTTAGCCAGTGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAAATTTACAGACAAATGCTTAAACCAATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAGAATTTTCACTGATAATGCTTAAACCAATCATAGTACAT 876
Qy 886 CTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAAAGAGAGGTTA 945
Db 877 CTGAATGAATCTGTACAATTAATTTGTACAGACCCCAACTCAATTAAGAAAAGGATA 936
Qy 946 TCTATAGGACCGAGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCGAGGAGAGCATTTTATACAAAAAATATATATAGGAACATATAAGACAA 996
Qy 1006 GCACATTTGTAATTTAGTAGACAAAATGGAATAACATTTTACACAGATAGTTTATAAA 1065
Db 997 GCACATTTGTAATTTAGTAGACAAAATGGAATAACATTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAACAGAAAATTTTAGGAATAAACAATAGCCTTTTAAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAAAACAAATTTAAGAAATAAACAATAGTCTTTTAAATCAATCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGCACAGATTTTAAATTTGAGGGGAATTTCTTACTGTAATAACAGACAA 1185
Db 1117 GAAATTTGTAATGCACAGATTTTAAATTTGAGGGGAATTTTCTACTGTAATAACATACCA 1176
Qy 1186 CTGTTTAAATAGTACCTGGAATG---TTACTGAGGAGCAAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACCTGGAATGGAATAATACTTTGGAATAATACTACAGGGTCAATAAC 1236
Qy 1243 ATAATCACACTCCAATGCAGATAAACAATAATTAATATATGTGCGACAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCCAATGCAGATAAACAATAATTAATAACATGTGCGAGGAAGTAGGAAA 1296

Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCAATAATTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCAATAATTTACAGGGCTA 1356
Qy 1363 CTACTAAACAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAAGGACACGACACGACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATAATAAGTAGTAAGA 1479
Db 1417 GGAGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATAATAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGAGTAGACCCACAGGGGCAAGAGAGAAACAGTGCAGAAAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGACCCACCAAGGCAAGAGAGAGTGTGTCAGAGAGAAAA 1536
Qy 1540 AGACCGGATCCNAGA 1554
Db 1537 AGACGCGATAGGA 1551

RESULT 13
US-10-351-938-3
; Sequence 3, Application US/10351938
; Publication No. US20040009603A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/10/351,938
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US/09/552,950
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-351-938-3

Query Match 53.1%; Score 1172.2; DB 16; Length 2571;
Best Local Similarity 87.9%; Pred. No. 3.8e-260;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATG 117
Db 40 TGGGATGGGCGACGATGCTCCTGGGTATTAATGATCTGTAGTGCTACAGAAAAATG 99
Qy 118 TGGGTCAAGTCTATTATGGGTACCTGTGGAGAGAACCAACCACTCTATTTGT 177
Db 100 TGGGTCAAGTCTATTATGGGTACCTGTGGAGAGAACCAACCACTCTATTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTGTATTGGGAAATGTGACAGAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTGTATTGGTAAATGTGACAGAAAATTTTAAAC 279
Qy 298 ATGTGGAAAAATAACATGTTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGTTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTG 417
Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTG 399
Qy 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAAATAGCGAGGGAACA 459

```
QY 466 ATGGAAGAGGAGAAATAAAAAATTGCTCTTTCTATATACACCAAGCATTAAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAAAACCTGCTCTTCAATATACACCAAGCATTAAGATAAG 519
QY 526 GTAAAGAAAGATATGCATCTTTTAAATAGACTGTAGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGATATGCATCTTTTAAATAGACTGTAGTAGTACCAATAG---ATAATGAT 576
QY 586 AATACATAGTATAGTTAATAGTTGTAAACACCTCAGTCATTACACAGGCGCTGTCCAAG 645
Db 577 AGTACCAGCTATAGTTGTAATAGTTGTAAATACCTCAGTCATTACACAAGCTTGTCCAAG 636
QY 646 GTATCCTTTTACGCCAATTTCCCATACATTATGTGTCGGCTGGGTTTGGCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAATTTCCCATACATTATGTGTCGGCTGGGTTTGGCGATGCTAAAG 696
QY 706 TGTAAACAATAGACATTCAAATGGATCAGGACCATGCACAAATGTGCAGCACAGTACAATGT 765
Db 697 TGTACGATAAAAAGTTCAGTGGAAAAGGATCATGTAAAAATGTGCAGCACAGTACAATGT 756
QY 766 ACACATGGAATTAGGCCAGTGTGTCAACTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGTGTCAACTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGACATAGTAATAGATCTGAAAATTTTACAGACAATGCTTAAACCATTAATAGTACAG 885
Db 817 GAAGAGGTAGTAATAGATCTGAAAATTTTACAGACAATGCTTAAACCATTAATAGTACAT 876
QY 886 CTTAAATGAATCTGTAGTAAATTAATTTGTACAAGACCCCAACAATACAAAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAATTAATTTGTACAAGACCCCAACAATACAAAGAAAGGATA 936
QY 946 TCTATAGACCGAGGAGAGCATTTTATGCAAGAAGAAACATTAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCGAGGAGAGCATTTTATACAAACAAAAATATAATAGGAACTATAAGACAA 996
QY 1006 GCACATTTGAACATTTAGTAGCAAAAATGGAATAACCTTTTACACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGAACATTTAGTAGCAAAAATGGAATAACCTTTTACACACAGATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCTTTTAAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAACAAATTTAAGAAATAAAAACAATAGCTTTTAAATCAATCTCAGGAGGGACCCA 1116
QY 1126 GAAATTTGTAATGCACAGTTTAAATTTGTGAGGGGAATCTTCTACTGTAAATACACACAA 1185
Db 1117 GAAATTTGTAATGCACAGTTTAAATTTGTGAGGGGAATTTTCTACTGTAAATACATCACA 1176
QY 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGGACAAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGTTAAATATACCTTGGAAATATACCTAGGAGGTCAATATAC 1236
QY 1243 ATAATCACACTCCAATGCAGATAAAAACAAAATATAAAATATATGTCGAGAAAGTAGGAAA 1302
Db 1237 ATATACACACTTCAATGCAAAATAAAAACAAAATATAAAACATGTGCGAGGAAGTAGGAAA 1296
QY 1303 GCAATGTATGCCCTCCCATACAGGAACAAATTTAGATGTTCAATCAAAATATACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAAATTTAGATGTTCAATCAAAATATACAGGGCTA 1356
QY 1363 CTACTAAACAAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAAGATGGTGGTAAGGACACGGACACGACGACACCGAGATCTTCAGACCT 1416
QY 1420 GGAGGAGGAGATATAGGGGACAAATTTGGGAAGTGAATTAATAATAATAAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATAGGGGACAAATTTGGGAAGTGAATTAATAATAATAAAGTAGTAACA 1476
QY 1480 ATTGAACCAATAGGAGTAGCACCCACCGGCAAGAGAGAACAGTGCAGAAAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGCACCCACCGGCAAGAGAGAACAGTGCAGAGAGAAAA 1536
```

```
QY 1540 AGACCGGATCCAAGA 1554
Db 1537 AGAGCAGGATAGGA 1551

RESULT 14
US-09-966-931-29
; Sequence 29, Application US/09966931
; Publication No. US20030064361A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: 2000-01-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2573
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-966-931-29

Query Match 53.0%; Score 1169.8; DB 10; Length 2573;
Best Local Similarity 87.9%; Pred. No. 1.4e-259;
Matches 1334; Conservative 0; Mismatches 147; Indels 36; Gaps 4;

QY 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGGGTC 123
Db 46 TGGGCGACCATGCTCCTTGGGATATTGATGATCTGTAGTGTGCGAGGAAATTGGGGTC 105
QY 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACACCACTCTATTTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACACCACTCTATTTTGTGCATCA 165
QY 184 GATGCTAAAGCCCTATGATACAGAGGTACATATGTTTGGGCCACACATGCTGTGTACCC 243
Db 166 GATGCTAAAGCATATGATACAGAGATACATAATGTTTGGGCCACACATGCTGTGTACCC 225
QY 244 ACAGACCCCAACCCCAAGAGTAGTATTGGAAATGTGACAGAAAAATTAAACATGTGG 303
Db 226 ACAGACCCCAACCCCAAGAGTAGTATTGGAAATGTGACAGAAAAATTAAACATGTGG 285
```

304 AAAAAATACATGGTAGATCAGATGCATGAGGATATAAATCAGTTTATGGATGAAGACCTA 363
Db AAAAAATACATGGTAGATCAGATGCATGAGGATATAAATCAGTTTATGGATGAAGACCTA 345
364 AAGCCATGTTAAATTAACCCACTCTGTGTTACTTTAAATTTGACATTAATTTGATATC 423
Db AAGCCATGTTAAATTAACCCACTCTGTGTTACTTTAAATTTGACATTAATTTGATATC 396
424 ACTAAGAATATCTACTTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATA 483
Db GCGGGGATATCTACTTAATACCAATAGTAGTAGCAGGGAAGAGCTGGAGAAAGGAGAAATA 456
484 AAAAAATGCTCTTTCTATATACCAACCAAGCATAAAGGTAAGGTAAGGTAAGGTAAGGTA 543
Db AAAAAATGCTCTTTCTATATACCAACCAAGCATAAAGGTAAGGTAAGGTAAGGTAAGGTA 516
544 CTTTTTAATAGACTTGTAGTAGTACCAATAGAAA-----TACTAAT 585
Db CTTTTTAATAGACTTGTAGTAGTACCAATAGAAA-----TACTAAT 576
586 AATACTAGTATAGTGTAAATAGTTGTAAACACCTCAGTCATTACACAGCCCTGTCCAAAG 645
Db AGTACTACTATAGTGTAAATAGTTGTAAACACCTCAGTCATTACACAGCCCTGTCCAAAG 636
646 GTATCCTTTACGCCAATTTCCCATACATTAATTTGTGTCGGGCTGGTTTGGCATGTAAAG 705
Db GTATCCTTTACGCCAATTTCCCATACATTAATTTGTGTCGGGCTGGTTTGGCATGTAAAG 696
706 TGTAAATATAGACATTTCAATGGATCAGGACCATGCACAAATGTCTAGCAGCAGTACAATGT 765
Db TGTAAATATAGACATTTCAATGGATCAGGACCATGCACAAATGTCTAGCAGCAGTACAATGT 756
766 ACACATGAAATTAGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTACAGAA 825
Db ACACATGAAATTAGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTACAGAA 816
826 GAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATATAGTACAG 885
Db GAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATATAGTACAG 876
886 CTAATGATCTGTAGTAAATTTATGTAACAGCCCAACCAATACAGAGAGGTTA 945
Db CTAATGATCTGTAGTAAATTTATGTAACAGCCCAACCAATACAGAGAGGTTA 936
946 TCTATAGCACAGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 1005
Db TCTATAGCACAGGAGAGCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAA 996
1006 GCACATTTGAATTTAGTAGACCAAAATGGGAATAACATTTTACACACAGATAGTTTAAAA 1065
Db GCACATTTGAATTTAGTAGACCAAAATGGGAATAACATTTTACACACAGATAGTTTAAAA 1056
1066 TTAAGAGAAATTTAGGAATAAACAATAGCTTTTATCACTCTCAGGAGGGACCCA 1125
Db TTAAGAGAAATTTAGGAATAAACAATAGCTTTTATCACTCTCAGGAGGGACCCA 1116
1126 GAAATTTGAATGACAGTTTAAATTTGAGGGGAAATTTCTTACTGTAAATACACACAA 1185
Db GAAATTTGAATGACAGTTTAAATTTGAGGGGAAATTTCTTACTGTAAATACACACAA 1176
1186 CTGTTTAATAGTACTTGAATTTTACTGGAGGACAAATG-----GCACATGAAGGAAAT 1239
Db CTGTTTAATAGTACTTGAATTTTACTGGAGGACAAATG-----GCACATGAAGGAAAT 1236
1240 GACATAATCACCTCAATGCAAGTAATAAACHAATTAATATATGTCGAGAAAGTAGGA 1299
Db GACATAATCACCTCAATGCAAGTAATAAACHAATTAATATATGTCGAGAAAGTAGGA 1296
1297 AAGCAATGATGCCCCCTCCCATCAGAGACAAATTTAGATGTTCAATCAAAATTTACAGGG 1359
Db AAGCAATGATGCCCCCTCCCATCAGAGACAAATTTAGATGTTCAATCAAAATTTACAGGG 1356

1360 CTGCTACTAACAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTCTTCAGACCT 1419
Db TTGCTATTAAACAAGAGATGGAGG---TAGTAACAACAGCATGAATGAGACCTTCAGACCT 1413
1420 GGAGGAGAGATATGAGGGCAAAATTTGGGAGAGTGAATTTATATAAATATATAAGTAGTAAGA 1479
Db GGAGGAGAGATATGAGGGCAAAATTTGGGAGAGTGAATTTATATAAATATATAAGTAGTAAGA 1473
1480 ATTGAACCAATAGGAGTAGCACCACAGGCAAGAGAGAAACAGTGCAGAGAGAAAA 1539
Db ATTGAACCAATAGGAGTAGCACCACAGGCAAGAGAGAAACAGTGCAGAGAGAAAA 1533
1540 AGACCGGATCCCAAG 1556
Db AGACCGGATCCCAAG 1550
1534 AGACGAGTGGGAATAGG 1550

RESULT 15
US-10-459-121-29
; Sequence 29, Application US/10459121
; Publication No. US20040121317A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; ; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10-459,121
; FILING DATE: 10-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/448,603
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2573
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-459-121-29

Query Match 53.0%; Score 1169.8; DB 17; Length 2573;
Best Local Similarity 87.9%; Pred. No. 1.4e-259;
Matches 1334; Conservative 0; Mismatches 147; Indels 36; Gaps 4;
64 TCGAGATCCATGCTCTTGGGATATGATGATGCTGTAGTGTACAGAAAAATTTGGGTC 123

[illegible]

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	641.2	29.0	786	9	AY416061 Homo sapi
	2	641.2	29.0	786	9	AY416062 Pan trogl
	3	570	25.8	767	6	CD638712 AGENCOURT
	4	505	22.9	806	6	CD521613 AGENCOURT
	5	450.8	20.4	783	9	AY416063 Mus muscu
	6	399.4	18.1	702	6	CD640741 AGENCOURT
	7	395.2	17.9	690	6	CD642064 AGENCOURT
	8	389	17.6	796	6	CD520208 AGENCOURT
	9	286.4	13.0	571	7	CN794193 B
	10	246.4	11.2	740	7	CK834247 4058618 B
C	11	244.4	11.1	492	2	BF599437 2633218 MA
	12	240	10.9	628	7	CN786611 4120632 B
	13	176.4	8.0	527	8	BH886550 LB00861a.
	14	169	7.7	398	2	AW486605 75217 MAR
	15	137.4	6.2	636	7	CO702364 DG32-2280
	16	94.2	4.9	847	7	CK777858 965004 MA
	17	94.2	4.3	1376	9	CG747831 P041-3-B0
	18	93.4	4.2	1811	9	CG753732 P048-4-G0
	19	91.4	4.1	1641	9	CL078595 CH216-151
	20	90.6	4.1	1256	9	CL119201 ISB1-76J1
C	21	90	4.1	1459	9	CL040025 CH216-49A
	22	89.6	4.1	1917	9	CL036131 CH216-40P
	23	89.4	4.0	1843	9	AG435185 Mus muscu
	24	89.2	4.0	1279	9	CL078951 CH216-154

Db 138 TCATAGAGGCTGGCAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGATTTCAT 197

Qy 1608 GAAACGATACAGAGATCAACACAGGAGAAGATCCTTATCTTACTGAAGTGTGAGGA 1667

Db 198 GAAACGATACAGAGATCAACACAGGAGAAGATCCTTATCTTACTGAAGTGTGAGGA 257

Qy 1668 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1727

Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317

Qy 1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 1787

Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 377

Qy 1788 CATAGTGAAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 1847

Db 378 CATAGTGAAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437

Qy 1848 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 1907

Db 438 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 497

Qy 1908 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 1967

Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 557

Qy 1968 AGCTCCATTATAGCAGCCTTGCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 2027

Db 558 AGCTCCATTATAGCAGCCTTGCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 617

Qy 2028 CAGAGCTCAAAATACCCAGTTCGCGCAAACTTTCGGGCAACAACTTCAATTCACCTTGGG 2087

Db 618 CAGAGCTCAAAATACCCAGTTCGCGCAAACTTTCGGGCAACAACTTCAATTCACCTTGGG 677

Qy 2088 AGGAGTATTGAAATGCAACCAAGTGTTCGAGTGTTCGATGACTGATCCTCAAGCCA 2147

Db 678 AGGAGTATTGAAATGCAACCAAGTGTTCGAGTGTTCGATGACTGATCCTCAAGCCA 737

Qy 2148 AGTGAGCCATGGCAGTTCGCTTACGCTCTTGGCTTACTCAAACTC 2193

Db 738 AGTGAGCCATGGCAGTTCGCTTACGCTCTTGGCTTACTCAAACTC 783

RESULT 2

AY416062

LOCUS

DEFINITION

AY416062

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

them based on alignment.

Location/Qualifiers

1. .786

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1. .>786

/gene="TNFSP5"

/locus_tag="HCM5765"

ORIGIN

Query Match 29.0%; Score 641.2; DB 9; Length 786;

Best Local Similarity 99.5%; Pred. No. 1.5e-146;

Matches 643; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1548 TCCAAAGAGGTTTGACAAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGATTTCAT 1607

Db 138 TCATAGAGGTTTGACAAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGATTTCAT 197

Qy 1608 GAAACGATACAGAGATCAACACAGGAGAAGATCCTTATCTTACTGAAGTGTGAGGA 1667

Db 198 GAAACGATACAGAGATCAACACAGGAGAAGATCCTTATCTTACTGAAGTGTGAGGA 257

Qy 1668 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 1727

Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA 317

Qy 1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 1787

Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 377

Qy 1788 CATAGTGAAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 1847

Db 378 CATAGTGAAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437

Qy 1848 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 1907

Db 438 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 497

Qy 1908 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 1967

Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 557

Qy 1968 AGCTCCATTATAGCAGCCTTGCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 2027

Db 558 AGCTCCATTATAGCAGCCTTGCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 617

Qy 2028 CAGAGCTCAAAATACCCAGTTCGCGCAAACTTTCGGGCAACAACTTCAATTCACCTTGGG 2087

Db 618 CAGAGCTCAAAATACCCAGTTCGCGCAAACTTTCGGGCAACAACTTCAATTCACCTTGGG 677

Qy 2088 AGGAGTATTGAAATGCAACCAAGTGTTCGAGTGTTCGATGACTGATCCTCAAGCCA 2147

Db 678 AGGAGTATTGAAATGCAACCAAGTGTTCGAGTGTTCGATGACTGATCCTCAAGCCA 737

Qy 2148 AGTGAGCCATGGCAGTTCGCTTACGCTCTTGGCTTACTCAAACTC 2193

Db 738 AGTGAGCCATGGCAGTTCGCTTACGCTCTTGGCTTACTCAAACTC 783

RESULT 3

CD638712

LOCUS

DEFINITION

IMAGE:30416146 5', mRNA sequence.

CD638712

VERSION

CD638712.1

GI:31804800

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM215 row: h column: 11
 High quality sequence stop: 564.
 Location/Qualifiers

FEATURES

source
 1..767
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30416146"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.8%; Score 570; DB 6; Length 767;
 Best Local Similarity 97.8%; Pred. No. 5e-129;
 Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1548 TCCAGAGAGTTGGCAAGATAGAGATCAAGGAATCTTCATGAAGATTTGTATTTCAT 1607
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1608 GAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCTCTTACTGAACTGTGAGGA 1667
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1668 GATTAAGCCGTTTGAAGCGTTTGAAGGATATATGTATTAACAAGAGGAGACGAA 1727
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 147 GATTAAGCCGTTTGAAGCGTTTGTGAAGGATATATGTATTAACAAGAGGAGACGAA 206
 Qy 1728 GAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCTCTTACTGAACTGTGAGGA 1787
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 207 GAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCTCTTACTGAACTGTGAGGA 266
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1788 CATAGTGAAGCCGATCAACACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 1847
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 267 CATAGTGAAGCCGATCAACACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 326
 Qy 1848 CACCATGAGCAACACTTGGTAACTGGAAATCGGAAACAGCTGACCGTTAAAGACA 1907
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 327 CACCATGAGCAACACTTGGTAACTGGAAATCGGAAACAGCTGACCGTTAAAGACA 386
 Qy 1908 AGGACTCTATTATCTATGCGCAAGTCACCTTCGTTCCAAATCGGAGCTTCGAGTCA 1967
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 387 AGGACTCTATTATCTATGCGCAAGTCACCTTCGTTCCAAATCGGAGCTTCGAGTCA 446

Qy 1968 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 2027
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 447 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 506
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 2028 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 2087
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 507 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 566
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 2088 AGGAGTATTTGAATTTGCAACAGTTCGGTTCGTTGTGTCATGTGACTGATCCAAAGCA 2147
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 567 AGGAGTATTTGAATTTGCAACAGTTCGGTTCGTTGTGTC-ATGTGACTGATCCNAGCA 625

RESULT 4
 CD521613
 LOCUS
 DEFINITION CD521613 806 bp mRNA linear EST 06-JUN-2003
 IMAGE:30413128 5', mRNA sequence.
 CD521613
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (Bases 1 to 806)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM207 row: j column: 17
 High quality sequence stop: 466.
 Location/Qualifiers

1..806
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30413128"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

FEATURES

source

1..806

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30413128"

/tissue_type="Pooled"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_191"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 22.9%; Score 505; DB 6; Length 806;
 Best Local Similarity 96.7%; Pred. No. 5e-113;
 Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 1548 TCCAGAGAGTTGGCAAGATAGAGATCAAGGAATCTTCATGAAGATTTGTATTTCAT 1607

Db 232 TCATAGAAGGTTGGACAAGATAGAAAGTAAAGGAATCTTCATGAAGATTTTGTATTTCAT 291

Qy 1608 GAAACGATACAGAGATCGACACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 1667

Db 292 GAAACGATACAGAGATCGACACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 351

Qy 1668 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 1727

Db 352 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 411

Qy 1728 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 1787

Db 412 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 471

Qy 1788 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 1847

Db 472 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 531

Qy 1848 CACCATGAGCAACACTTTGGTAACCCCTGGAAAATGGGAAACAGCTGCACGTTTAAAGACA 1907

Db 532 CACCATGAGCAACACTTTGGTAACCCCTGGAAAATGGGAAACAGCTGCACGTTTAAAGACA 591

Qy 1908 AGGACTCTATTATATCTAATGCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 1967

Db 592 AAGACTCTATTATATCTAATGCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 651

Qy 1968 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 2027

Db 652 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 711

Qy 2028 CAGAGCTGCAATACCCACAGTTCGCGCAAAAGCTT-GCGGGCAACAAATCCCAATTCCTTGG 2086

Db 712 CAGAGCTGCAATACCCACAGTTCGCGCAAAAGCTT-GCGGGCAACAAATTCCTTGG 771

Qy 2087 GAG 2089

Db 772 GGG 774

RESULT 5

AY416063

LOCUS

DEFINITION Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY416063

VERSION AY416063.1 GI:39772023

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 783)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 783)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

1..783

source /organism="Mus musculus"

gene

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>783

/gene="TNFSF5"

/locus_tag="HCMS765"

ORIGIN

Query Match 20.4%; Score 450.8; DB 9; Length 783;

Best Local Similarity 82.2%; Pred. No. 1.1e-99;

Matches 531; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

Qy 1548 TCCAAGAGGTTGGACAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 1607

Db 138 TCATAGAAGATTGTAAGGTCGAAGGAAAGTAACCTTCATGAAGATTTTGTATTTCAT 197

Qy 1608 GAAACGATACAGAGATCGACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 1667

Db 198 AAAAAGCTAAAGAGATGCAACAAAGGAGAAAGGATCTTTATCTTGTCTGAACTGTGAGGA 257

Qy 1668 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 1727

Db 258 GATGAAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAGA---GAA 314

Qy 1728 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 1787

Db 315 AAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGGATCCTCAAAATTCGAGCACACGT 374

Qy 1788 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 1847

Db 375 TGTAAAGCAAGCCCAACAGTAATGCAGCATCCGTTTCTACAGTGGGCAAGAAAGGATATTA 434

Qy 1848 CACCATGAGCAACACTTTGGTAACCCCTGGAAAATGGGAAACAGCTGCACGTTTAAAGACA 1907

Db 435 TACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCTGCACGTTTAAAGAGA 494

Qy 1908 AGGACTCTATTATATCTAATGCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 1967

Db 495 AGGACTCTATTATATCTAATGCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 554

Qy 1968 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 2027

Db 555 ACGCCCATTCATCTGTCGGCCTCTGCTGAAAGCCAGCAGTGGATCTGAGAGAACTTTACT 614

Qy 2028 CAGAGCTGCAATACCCACAGTTCGCGCAAAAGCTTTCGGGGCAACAAATCCATTCCTTGGG 2087

Db 615 CAAGCGCAATATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCCTTGGG 674

Qy 2088 AGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCATGTTCATGTGACTGATCCAGGCA 2147

Db 675 CGGAGTGTTCGAATTTACAAGCTGGTGTCTCTGTGTTTGTCAACGCTGACTGAAGCAAGCCA 734

Qy 2148 AGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 2193

Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780

RESULT 6

CD640741

LOCUS

DEFINITION CD640741

IMAGE:30414715 5', mRNA sequence.

ACCESSION CD640741

VERSION CD640741.1 GI:31808911

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 702)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM211 row: 1 column: 20
High quality sequence stop: 571.
Location/Qualifiers
1. 702
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30414715"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBM - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES

source
Location/Qualifiers
1. 702
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30414715"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBM - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 18.1%; Score 399.4; DB 6; Length 702;
Best Local Similarity 95.9%; Pred. No. 4.7e-87;
Matches 421; Conservative 0; Mismatches 16; Indels 2; Gaps 1;
QY 1548 TCCAAGAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTGTATTTCAT 1607
DB 208 TCATAGAAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTGTATTTCAT 267
QY 1608 GAAACAGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGTGAGGA 1667
DB 268 GAAACAGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGTGAGGA 327
QY 1668 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 1727
DB 328 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 387
QY 1728 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 1787
DB 388 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 447
QY 1788 CATAGTCAGGCCAGCTTAAACACATCTGTGTACAGTGGGCTGAAAAGGATACCTA 1847
DB 448 CATAGTCAGGCCAGCTTAAACACATCTGTGTACAGTGGGCTGAAAAGGATACCTA 507
QY 1848 CACCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 1907
DB 508 CACCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 567
QY 1908 AGGACTCTATTATATCTATGCGCAAGTCACTTCTGTGTTCCAAATCGGGAAGCTTCAGTCA 1967
DB 568 AGGACTCTATTATATCTATGCGCAAGTCACTTCTGTGTTCCAAATCGGGAAGCTTCAGTCA 627
QY 1968 AGCTCCATTATAGCCAGC 1986
DB 628 --GCTCATTTATAGCCAGC 644

RESULT 7

CD642064
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD642064 690 bp mRNA linear EST 17-JUN-2003
AGNCOURT 14538852 NIH MGC 191 Homo sapiens cDNA clone
IMAGE:30418744 5', mRNA sequence.

CD642064
CD642064.1 GI:31811566
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 690)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: NDCM222 row: d column: 17
High quality sequence stop: 536.
Location/Qualifiers
1. 690
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30418744"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBM - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES

source

Location/Qualifiers

1. 690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30418744"

/tissue_type="Pooled"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 191"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBM - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.9%; Score 395.2; DB 6; Length 690;
Best Local Similarity 99.0%; Pred. No. 5e-86;
Matches 397; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1548 TCCAAGAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTGTATTTCAT 1607
DB 213 TCATAGAAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTGTATTTCAT 272
QY 1608 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGTGAGGA 1667
DB 273 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACGTGTGAGGA 332
QY 1668 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 1727
DB 333 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 392
QY 1728 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAATGT 1787

Db 393 GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGGCGCACATGT 452
 Qy 1788 CATTAAGTCAGCCAGCAGTAACACACATCTGTGTTACAGTGGCTGAAAGGATACTA 1847
 Db 453 CATTAAGTCAGCCAGCAGTAACACACATCTGTGTTACAGTGGCTGAAAGGATACTA 512
 Qy 1848 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 1907
 Db 513 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 572
 Qy 1908 AGGACTCTATTATATATCTAGTGGCCAGTCACTCTCTGTTCCA 1948
 Db 573 AGGACTCTATTATATCTAGTGGCCAGTCACTCTCTGTTCCA 613

RESULT 8
 CD520208 796 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT_14355767 NIH_MGC_191 Homo sapiens cDNA clone
 DEFINITION IMAGE:30412573 5', mRNA sequence.

ACCESSION CD520208
 VERSION CD520208.1 GI:31451926
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 796)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDCM206 row: c column: 14
 High quality sequence stop: 541.

FEATURES
 source

1..796
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30412573"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgtctgcgc); Library is oligo-dT primed
 and directionally cloned. PMBC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCCATTTAGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGCGCGGCAGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 Kb (range 0.70-5.0 Kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.6%; Score 389; DB 6; Length 796;
 Best Local Similarity 98.3%; Pred. No. 1.7e-84;
 Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1548 TCCAAAGAGGTTGGCAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 1607
 Db 205 TCATAGAAGGTTTGACAAAGATAGAAGGAATCTTCATGAAGATTTTGTATTCAAT 264
 Qy 1608 GAAACAGATACAGAGATGCAACACAGGAGAAGATCCTTATCCTTACTGAACCTGTGAGGA 1667
 Db 265 GAAACAGATACAGAGATGCAACACAGGAGAAGATCCTTATCCTTACTGAACCTGTGAGGA 324
 Qy 1668 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 1727
 Db 325 GATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 384
 Qy 1728 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAATGT 1787
 Db 385 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAATTCGGGCAATGT 444
 Qy 1788 CATTAAGTCAGCCAGCAGTAACACACATCTGTGTTACAGTGGCTGAAAGGATACTA 1847
 Db 445 CATTAAGTCAGCCAGCAGTAACACACATCTGTGTTACAGTGGCTGAAAGGATACTA 504
 Qy 1848 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 1907
 Db 505 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 564
 Qy 1908 AGGACTCTATTATATCTATATGCCCAAGTCA-CCTTCTGTTCCTCAATTCGGGAA 1956
 Db 565 AGGACTCTATTATATCTATATGCCCAAGTCACTCTCTGTTCCTCAATTCGGGAA 614

RESULT 9
 CN794193

LOCUS CN794193
 DEFINITION CN794193 BARC 8BOV Bos taurus cDNA clone 8BOV_50H03 5', mRNA
 sequence.

ACCESSION CN794193
 VERSION CN794193.1 GI:47690173

KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 571)
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
 Matukumalli,L.K.

TITLE Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)
 COMMENT Contact: Richard G. Baumann

Bovine Functional Genomics Lab
 ANRI
 BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.00925 using options -trim alt '' -trim fasta. Vector identified
 by cross_match using options -minmatch 12 -minscore 18

Plate: 50 row: H column: 03
 Seq primer: CCTATTAGGTGACACTATAGAAC
 High quality sequence stop: 571.

FEATURES
 source

1..571
 /location/Qualifiers
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_50H03"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B Tona"
 /clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
 NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
 library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
 Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 13.0%; Score 286.4; DB 7; Length 571;
 Best Local Similarity 89.5%; Pred. No. 2.8e-59;
 Matches 308; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1850 CCATGAGCAACACTGTGTAACTCCCTGGAAAATGGAAAACAGCTGACCTTTAAAGACAAG 1909
 Db 1 CCCTAAGCAACAACTGTGTAACTCCCTGGAAAACGGGAAAACAGCTGCGCCGTGAAAAGACAAG 60
 QY 1910 GACTCTATTATATCTATGCCCAAGTCACCTCTCTCTCTCAATCGGGAAGCTTCGAGTCAAG 1969
 Db 61 GATTCTATCATCATCTACCAAGTCACCTCTCTCTCTCAATCGGGAAGCTTCGAGTCAAG 120
 QY 1970 CTCCATTATAGCAGCCTCTGCTCTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 2029
 Db 121 CTCCATTATAGCAGCCTCTGCTCTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 180
 QY 2030 GAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAACAATCCATTCACCTGGGAG 2089
 Db 181 GAGCTGCAAAACACCCACAGTTCCTTCCAAACCACTGCGGCGAGCAATCCATTCACCTAGGAG 240
 QY 2090 GAGTATTGTAATGCAACAGTCTCGGTGTTGTCGAATGCTGACTGATCCAGGCCAAG 2149
 Db 241 GAGCTTTGTAATGCAATCGGGTGTCTCGGTGTTGTCGAATGCTGACTGATCCAAAGTCAAG 300
 QY 2150 TGAGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAACTC 2193
 Db 301 TGAGCCAGGAGCGGCTTCACATCATTTGGCTTACTCAAACTC 344

RESULT 10
 CK834247 740 bp mRNA linear EST 04-MAR-2004
 LOCUS 4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA
 DEFINITION sequence.

ACCESSION CK834247
 VERSION CK834247.1 GI:45064536
 KEYWORDS EST.

SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 740)
 AUTHORS Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
 TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Richard G. Baumann
 Bovine Functional Genomics Lab

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744
 Email: rbaumann@nri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.00925 using options -trim_alt -trim_fasta. Vector identified

by cross_match using options -minmatch 12 -minscore 12

Plate: 2 row: M column: 16

Seq primer: CCTATTAGGTGACATATAGAAC

High quality sequence stop: 740.

Location/Qualifiers

1..740

/organism="Bos taurus"

FEATURES

source

/mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_2M16"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stages="Lactating, Neonatal"
 /lab_host="DHI08 Tona"
 /clone_lib="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
 NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
 library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
 Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 11.2%; Score 246.4; DB 7; Length 740;
 Best Local Similarity 86.9%; Pred. No. 2.1e-49;
 Matches 271; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 QY 1548 TCCAAAGAGGTTGCACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 1607
 Db 429 TCACAGAGATTGCACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 488
 QY 1608 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCTCTTACTGAACTGTGAGGA 1667
 Db 489 GAAACAGATACAGAGATGCAATAAAGGAGAGGGTCCCTTATCTTACTGAACTGTGAGGA 548
 QY 1668 GATTAAAGCCAGTTTGAGGCTTTGCAAGATATATATGTTAAACAAGAGGAGACGNA 1727
 Db 549 AATTAGAGCCGGTTTGAAGACTTTGGTCAAGGATATATATGCAAAACAAGAGATGAAGAA 608
 QY 1728 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCTCAATTCGGGCACTGT 1787
 Db 609 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGGAGCTTCAGATAGCGGCACATGT 668
 QY 1788 CATAAGTGAGCCAGCAGCTAAACAACATCTGTGTACAGTGGGCTGAAAAGAGTACTTA 1847
 Db 669 CATCAGTGAGCCAGTAGTAAACAACCTCTGTTCTCCAGTGGGCCCCCAAGGATACTTA 728
 QY 1848 CACCATGAGCAA 1859
 Db 729 CACCCTAAGCAA 740

RESULT 11

BF599437 492 bp mRNA linear EST 25-APR-2001
 LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION

ACCESSION BF599437

VERSION BF599437.1 GI:11695919

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos

1 (bases 1 to 492)

Smith, T.P.L., Grossee, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
 Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

PUBMED

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGAG
Plate: 33 row: N column: 5
Seq primer: ATTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
1..492
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN

Query Match 11.1%; Score 244.4; DB 2; Length 492;
Best Local Similarity 86.8%; Pred. No. 5.9e-49;
Matches 269; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1548 TCCAGAAAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 1607
Db 183 TCACAGAAGATTGACACAGATAGAGAGAAAGAACTTCATGAAGATTTGTGTTCAT 242

Qy 1608 GAAACAGATCAGAGATCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 1667
Db 243 GAAACAGATCAGAGATCAATAAAGGAGAGGGGTCTTATCCTTACTGAACTGTGAGGA 302

Qy 1668 GATTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTAAACAAGAGGAGAGCGAA 1727
Db 303 AATTAGAAGCCGGTTTGAAGACTTGGTCAAGGATATATGCAAAACAAGAAAGTAAAGAA 362

Qy 1728 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAATTTGGGGCACATGT 1787
Db 363 GAAGAAACAACTTTGAAATGCAAAAGGTGATCAGAGGCTCAGATAGCGGCACATGT 422

Qy 1788 CATAGTCAGCCAGCAGCTAAACAAACATCTGTGTGTTACAGTGGGCTGAAAAGGATCTA 1847
Db 423 CATAGTCAGCCAGCTAGTAAACAAACCTCTGTTCTCCAGTGGGCCCCCAAGGATACTA 482

Qy 1848 CACCATGAGC 1857
Db 483 CACCCTAAGC 492

RESULT 12

LOCUS CN786611 628 bp mRNA linear EST 26-MAY-2004
DEFINITION 4120632 BARC 8BOV Bos taurus cDNA clone 8BOV_29K22 5', mRNA
sequence.

ACCESSION CN786611
VERSION CN786611.1 GI:47682100
KEYWORDS EST.

SOURCE

Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 628)
Baumann, R.G.; Baldwin, R.L.; Sonstegard, T.S.; Van Tassell, C.P. and
Matukumalli, L.L.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)

COMMENT

Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt -trim fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18
Plate: 29 row: K column: 22
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 628.

FEATURES

source

Location/Qualifiers
1..628
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_29K22"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 10.9%; Score 240; DB 7; Length 628;
Best Local Similarity 89.7%; Pred. No. 7.5e-48;
Matches 280; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

Qy 1882 GGGAAACAGCTGACCGTTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACTTC 1941
Db 11 GGGAAACAGCTGCGCGTGGTAAAGAC-AGGATCTATTACATCTACCCAGTCACTTC 69

Qy 1942 TGTTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCC 2001
Db 70 TGTTC-ATCGGGAAGCTTTGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTGAAGTCC 128

Qy 2002 CCCGGTAGTTCGAGAGATCTTACTAGAGCTGCAAAATACCCAGTTCGCCCAAACT 2061
Db 129 CCAAGTGGATCAGAGAGAACTTCTACTGAGAGCTGCAAAACACCCACAGTCTTCCAAACCA 188

Qy 2062 TCGGGGCAACATCCATTCACCTTGGGAGAGTATTGAATTGCACACAGGTGCTTCGGTG 2121
Db 189 TCGGGGCGAGCAATCCATTCACCTTAGGAGAGTCTTTGAATTGCATCGGGTCTTCGGTG 248

Qy 2122 TTTGTCAATGTGACTGATCCAAAGCAAGTGCACCTGCTTCACTGCTTCACTTGGC 2181
Db 249 TTTGTCAATGTGACTGATCCAAAGTCAAGTGCACCGGCGGCTTCCATCATCTTGGC 308

Qy 2182 TTACTCAAACTC 2193
Db 309 TTACTCAAACTC 320

RESULT 13

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BH86550
LB00861a.d SP6.1 Leishmania major
major genomic clone LB00861a, genomic survey sequence.
BH86550
BH86550.1 GI:22130945
GSS.
Leishmania major
Leishmania major

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

REFERENCE

1 (bases 1 to 527)
Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E., Stuart,K. and Ragland,M.
Leishmania major Friedlin BAC End Sequences

TITLE

Unpublished (2002)
Other GSSs: LB00861a.d.T7.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: Sp6
Class: BAC ends.

FEATURES

Location/Qualifiers
1..527
/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="LB00861a"
/lab_host="E. coli GeneHogs + TrfA"
/clone_lib="Leishmania major Friedlin BAC Library"
/note="Vector: pCG270; Site 1: HindIII; Genomic DNA from Leishmania major Friedlin in agarose blocks was partially digested with HindIII, size selected, and ligated with HindIII-digested pCG270 vector DNA. 10368 clones were picked and arrayed in 384- and 96-well plates. Library construction and arraying was carried out by ResGen Corporation and clones and filters are available from them"

ORIGIN

Query Match 8.0%; Score 176.4; DB 8; Length 527;
Best Local Similarity 88.3%; Pred. No. 3.2e-32;
Matches 203; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
Qy 52 TGGATCTCGGCTTCAGATCCATGCTCTCGGATATTGATGATCTGAGTGCT-ACAGA 110
Db |||||
Qy 230 TGGGGTGGAGATGGGCACCATGCTCTCTGGATGTTGATGATCTGAGTGCTCACAGA 171
Db |||||
Qy 111 AAAATTGTGGGTTCACAGTCTATTATGGGGTACCTGTGTGGAGAACCAACCACTCT 170
Db |||||
Qy 170 AAAATTGTGGGTTCACAGTCTATTATGGGGTACCTGTGTGGAGAACCAACCACTCT 111
Db |||||
Qy 171 ATTTTGTGCATCAGATGCTAAAGCCATGATACAGAGGTACATATGTTTGGGCCACACA 230
Db |||||
Qy 110 ATTTTGTGCATCAGATGCTAAAGCATATGAACACAGAGGCACATATGTTTGGGCCACACA 51
Db |||||
Qy 231 TGCCTGTGTACCCACAGACCCCAACCCACAGAGTACTATTGGGAATG 280
Db |||||
Qy 50 TGCCTGTGTACCCACAGCCCGCAATCCCAAGAGTTATTTTGAAGAAG 1
Db |||||

RESULT 14
AW486605
LOCUS AW486605 398 bp mRNA linear EST 25-APR-2001
DEFINITION 75217 MARC 180V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW486605
VERSION AW486605.1 GI:7056711
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
1 (bases 1 to 398)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bioscience AG

TITLE

JOURNAL MEDLINE
PUBMED 21180013
11282378

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGAG
Plate: 34 row: F column: 23
Seq primer: ATTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
1..398
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 180V"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: Sall;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN

Query Match 7.7%; Score 169; DB 2; Length 398;
Best Local Similarity 88.0%; Pred. No. 2e-30;
Matches 184; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1548 TCCAAGAGGTTGGCAGATAGAGATGAAAGGAATCTTCATGAAGATTTGTATTCAT 1607
Db |||||
Qy 190 TCACAGAAGATTGGACAGATAGAGACGAAGGAATCTTCATGAAGATTTGTGTTTCA 249
Db |||||
Qy 1608 GAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCTTACTGACTGTGAGGA 1667
Db |||||
Qy 250 GAAACGATACAGAGATGCAATAAAGGAGAGGGTCTTATCTTACTGAACTGTGAGGA 309
Db |||||
Qy 1668 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAGAGGACGAA 1727
Db |||||
Qy 310 AATTGAAGCCGGTTTGAAGACTTTGGTCAAGATATATATGCAAAACAAGTAAGAA 369
Db |||||
Qy 1728 GAAAGAAACACAGCTTTGAAATGCAAAAAG 1756
Db |||||
Qy 370 GAAAGAAACACCTTTGAAATGCAAAAAG 398
Db |||||

RESULT 15
CO702364/c
LOCUS CO702364 636 bp mRNA linear EST 26-JUL-2004
DEFINITION DG32-22804 DG32-liver Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO702364
VERSION CO702364.1 GI:50651032
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 636)
Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
Henrich,J. and Loebbert,R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bioscience AG

Chitko-McKown,C.G., Perteu,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 5828.61 Seconds
(without alignments)
16453.933 Million cell updates/sec

Title: US-09-687-864A-15
Perfect score: 2028
Sequence: 1 aagttgcgcgcgtgta.....aactcagtgataatctaga 2028

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.pa.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1471	72.5	10000	14 AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome.
2	1453.4	71.7	2046	6 CQ753319	Simian-Human immunodeficiency virus
3	1453.4	71.7	2610	6 CQ753321	Simian-Human immunodeficiency virus
4	1453.4	71.7	9860	14 AF217181	Simian-Human immunodeficiency virus
5	1453.4	71.7	9860	14 SIU89134	Simian-Human immunodeficiency virus
6	1453.4	71.7	10501	6 BD161892	Simian-Human immunodeficiency virus
7	1447.6	71.4	9713	14 HIV1039362	Simian-Human immunodeficiency virus
8	1339.4	66.0	2010	6 CQ753323	Simian-Human immunodeficiency virus
9	1339.4	66.0	2574	6 CQ753325	Simian-Human immunodeficiency virus
10	1262.8	62.3	2553	14 AY247221	Simian-Human immunodeficiency virus
11	1242.2	61.3	2568	14 AY426111	Simian-Human immunodeficiency virus
12	1240.6	61.2	2568	14 AY426112	Simian-Human immunodeficiency virus
13	1239	61.1	2568	14 AY426118	Simian-Human immunodeficiency virus
14	1237.4	61.0	2568	14 AY426110	Simian-Human immunodeficiency virus
15	1237.4	61.0	2568	14 AY426113	Simian-Human immunodeficiency virus
16	1237.4	61.0	2568	14 AY426115	Simian-Human immunodeficiency virus
17	1237.4	61.0	2568	14 AY426117	Simian-Human immunodeficiency virus
18	1235.8	60.9	2568	14 AY426114	Simian-Human immunodeficiency virus
19	1235.8	60.9	2568	14 AY426116	Simian-Human immunodeficiency virus

20	1227	60.5	3061	14 HIVENBAA1A	M63929 Human immun
21	1225.4	60.4	3807	6 AR034235	AR034235 Sequence
22	1225.4	60.4	3807	6 I12144	I12144 Sequence 5
23	1225.4	60.4	3807	6 I28919	I28919 Sequence 5
24	1225.4	60.4	3808	14 HIVBAL1A	M68893 Human immun
25	1224.2	60.4	2559	14 AY669732	AY669732 HIV-1 iso
26	1223.4	60.3	2547	14 AY426125	AY426125 HIV-1 iso
27	1223.4	60.3	2547	14 AY426127	AY426127 HIV-1 clo
28	1221.8	60.2	2544	14 AY669726	AY669726 HIV-1 iso
29	1221.8	60.2	2547	14 AY426126	AY426126 HIV-1 clo
30	1221.8	60.2	9540	14 HIVJRCFS	M38429 Human immun
31	1220.8	60.2	2568	14 AY247225	AY247225 HIV-1 iso
32	1218.6	60.1	3211	14 HIVU45960	U45960 Human immun
33	1209	59.6	2552	6 I05789	I05789 Sequence 8
34	1208.2	59.6	2559	14 AF025750	AF025750 HIV-1 iso
35	1206.8	59.5	2577	14 AF025763	AF025763 HIV-1 iso
36	1201.2	59.2	3600	14 HIVBRVA	M21098 Human immun
37	1198.8	59.1	8896	14 HIVU63632	U63632 HIV-1 isola
38	1197	59.0	1512	6 AX153805	AX153805 Sequence
39	1197	59.0	1512	6 BD017695	BD017695 A88ay met
40	1196	59.0	2565	14 AF025754	AF025754 HIV-1 iso
41	1195.4	58.9	2571	14 HIVENVVB	L08656 Human immun
42	1195.4	58.9	9074	14 HIVU43096	U43096 Human immun
43	1195.2	58.9	2553	14 HIVIMB314	Y13719 Human immun
44	1195.2	58.9	2559	14 HIVU36877	U36877 Human immun
45	1194.6	58.9	2559	14 AY247220	AY247220 HIV-1 iso

ALIGNMENTS

RESULT 1	AF038398	Simian-Human immunodeficiency virus strain SHIV-89.6, complete genome.	10000 bp	DNA	linear	VRL 02-FEB-1998
LOCUS	AF038398					
DEFINITION	AF038398.1	GI:2828036				
ACCESSION	AF038398					
VERSION	AF038398.1					
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						

gene	536. .2068	/product="vpr"	/protein_id="AAB99962.1"	/db_xref="GI:2828041"	/translation="MEERPENEGQREPWDEWVVELEELKEALKHFDPRLLTALG NHIYNRHGDTLLEGAGELIRILQALFMHFRGGCIHSRIGQPGGNPLSAIPPSRML"
	CDS	/gene="gag"	/db_xref="GI:2828041"	5948. .8761	5948. .8761
gene		/product="gag"	/protein_id="AAB99958.1"	/db_xref="GI:2828037"	/translation="MGRVNSVLGKKKADELEKIRLPNGKKKYMLKHVWAANELDRP GLAELLNKGCCILISVLAPLPTGSENLSKSYNTVCVWCIHABEKVKHTEAQ IVQRLHVEVETTTMTKTSRTPAPSGRGNGYVQIGGYVHLPISPRTLNAWVKL IEEKFAGVPGFALSSEGTPTDINQMLNCVGHQAAMQIIRDIINEEAADWLOH POPAQOQLREPSGSDIAGTTSVDEQIOMYRQONPIPVGNIYRWIOLGLOKQVR MYNPTNLDVKGKPEQSVVDYFYKSLRAEOTDAAKVNMWTTOTLIIQANPDCKLV LKGCVNPTLEMLTACQGVGPGQKARLMAELKAALPVPIPPAAAQGRPKPIK CWNCGKBGSAQCRAPRPGGCKGMDHMAKCPDQAGFLGLGPGWGRKPRFMA QVHQGLMPTAPPDPAVDLLKNYNQLGKQKQREKREKPEVTEDDLHNSLFGG DQ"
	CDS	<1714. .4893	/gene="pol"	/db_xref="GI:2828038"	<1714. .4893
gene		/product="pol"	/protein_id="AAB99959.1"	/db_xref="GI:2828039"	/translation="LELWERTGLCKAMQSPKKTGMLEWKNKGPCYGMQPTGGFFRP WSMGKEAPQFPHGSSAGDANCSPRGSCGSAKELHAGQAERKAERKOREALQGG DRFPAAPQFSLWRPVPVTAHIEGQVEVLLDGDADSIVTGIELGPHYTPKIVGGIGG FINTKYKNVBI EVLGKRIKGTIMGTPTINIFGRNLTALGMSLNPPIAKVEPVKA LPGKDQPKLQWPLSKIEKIVALREICEKMEKQGLEAAPTPYNTPTPAIKKDKN KRWMLIDPRELNRVTQDFTEVLQGI PHPAGLAKKRI TVLDIGDAYFSI PLDEEFQY TAFILPSVNNAPGKRIYIKVLPQMGKSPAIQTIMRWLEPPFRKANPDVLVQYMD DILASDRDTHEDRVLQSKELLNSIGFSPBEKFOKPPQFMGYELMWTKWLQK IELQRETWTVDNIQKLVGLNAAQIYPGIIKTKHLCRLIRGKMTL EEVQWTEMAEA EYBENKI LSQEQGYYQEGKPLEATVIKSDQNSWKIHOEDKILKVGKFAKINT HTNGVRLAHVIOIKGEAIVIGQVPKFLPVEKDVWQWMTDYQVWTIPEWDFIS TPPLVRLVNLKQDPIEGEETYYTDGSCNKQSKGAGYITDRGDKVUKLEOJTNQO AELAFALMALDGSFKNANIVDSQYVMGIIITGPTESERLNVQIIEEMIKKSIYVA WVPAHKGIGNQSDIHLVSQIRQVLFLEKI EPOAEHDKYHSNVKELVPFGPLPRIV ARQIVTCDKCHQGEAIHQANSDLGTWQMDCTHLEGKIIIVAVHVASGFIEAEVLP QETGRQTLAKLAGRWPI THLTDNGANFASQVKVMAWAGIETFGVYPNPQSQ GVRAMNHHLNQIDIRIQANSVETI VLMAVHCMNFKRGGIGDMTPAERLINMITT EQEIQFQOSKSKFNFRVYREGRDOLWKGPGELLWKGEAGVILKVGTDIKVYPRRK AKIINDFGGKEVDSSSHMEDTGEAREVA"
	CDS	4823. .5467	/gene="vif"	/db_xref="GI:2828039"	4823. .5467
gene		/product="vif"	/protein_id="AAB99960.1"	/db_xref="GI:2828039"	/translation="MEERKRWIAYPTWRI PERLWRHSLIKYLYKTKDLQKVCYVPH FKVGAWMTCSRVIFPLQEGSHLEVQGWHLTPBKGMSTYAVRI TWYKNFTWTDTP NYADLLTSYFPCTAGETVRRARIGEQLLSCCRPPRAHKYQVPSLOYLAKVYSDVR SQGENTPWTQWRNRRRLRWAKNSRGDKQRGKRPPTYKANQFPELAKVILGILA"
	CDS	5295. .5633	/gene="vpx"	/db_xref="GI:2828040"	5295. .5633
gene		/product="vpx"	/protein_id="AAB99961.1"	/db_xref="GI:2828040"	/translation="MSDPRERIPGNSGEETIGBAFELWLNRTVEEINREAVNHLPREL IFQVWQRSWEYWHDEQGMSPSYVKYRILCLIQKALFWHCKGRCGLGEGHAGGWRPG PPPPPPGLA"
	CDS	5634. .5939	/gene="vpr"	/db_xref="GI:2828040"	5634. .5939
gene		/product="vpr"	/protein_id="AAB99967.1"	/db_xref="GI:2828046"	/translation="MGGAI SMRRSRPSGDLRQLRLRARGETYGRLLGVEBGYSQSPG GLDKGLSLSCEGQYKQGYMNTWRNPAERSKLAYRKONMODIDREDDDLGVSV RPKVPRTMSYKLAIDMSHF IKEKGGLGEGIYSARRRHLIILYILEKEGIGIPDWQDYT SGPGIRVPKTFGLMWKLVPVNSDEAQDEEHYLMWHPAQTSQWDDPFMGEVLAWKFDPT LAYTYEAYVRYPEEFGSKSLSEBEVRRRLTARGLLNMADKKETR"
	CDS	9307. .10000	/gene="vpr"	/db_xref="GI:2828046"	9307. .10000
gene		/product="vpr"	/protein_id="AAB99962.1"	/db_xref="GI:2828041"	/translation="MEERPENEGQREPWDEWVVELEELKEALKHFDPRLLTALG NHIYNRHGDTLLEGAGELIRILQALFMHFRGGCIHSRIGQPGGNPLSAIPPSRML"
	CDS	5948. .8761	/gene="gag"	/db_xref="GI:2828041"	5948. .8761
gene		/product="gag"	/protein_id="AAB99958.1"	/db_xref="GI:2828037"	/translation="MGRVNSVLGKKKADELEKIRLPNGKKKYMLKHVWAANELDRP GLAELLNKGCCILISVLAPLPTGSENLSKSYNTVCVWCIHABEKVKHTEAQ IVQRLHVEVETTTMTKTSRTPAPSGRGNGYVQIGGYVHLPISPRTLNAWVKL IEEKFAGVPGFALSSEGTPTDINQMLNCVGHQAAMQIIRDIINEEAADWLOH POPAQOQLREPSGSDIAGTTSVDEQIOMYRQONPIPVGNIYRWIOLGLOKQVR MYNPTNLDVKGKPEQSVVDYFYKSLRAEOTDAAKVNMWTTOTLIIQANPDCKLV LKGCVNPTLEMLTACQGVGPGQKARLMAELKAALPVPIPPAAAQGRPKPIK CWNCGKBGSAQCRAPRPGGCKGMDHMAKCPDQAGFLGLGPGWGRKPRFMA QVHQGLMPTAPPDPAVDLLKNYNQLGKQKQREKREKPEVTEDDLHNSLFGG DQ"
	CDS	<1714. .4893	/gene="pol"	/db_xref="GI:2828038"	<1714. .4893
gene		/product="pol"	/protein_id="AAB99959.1"	/db_xref="GI:2828039"	/translation="LELWERTGLCKAMQSPKKTGMLEWKNKGPCYGMQPTGGFFRP WSMGKEAPQFPHGSSAGDANCSPRGSCGSAKELHAGQAERKAERKOREALQGG DRFPAAPQFSLWRPVPVTAHIEGQVEVLLDGDADSIVTGIELGPHYTPKIVGGIGG FINTKYKNVBI EVLGKRIKGTIMGTPTINIFGRNLTALGMSLNPPIAKVEPVKA LPGKDQPKLQWPLSKIEKIVALREICEKMEKQGLEAAPTPYNTPTPAIKKDKN KRWMLIDPRELNRVTQDFTEVLQGI PHPAGLAKKRI TVLDIGDAYFSI PLDEEFQY TAFILPSVNNAPGKRIYIKVLPQMGKSPAIQTIMRWLEPPFRKANPDVLVQYMD DILASDRDTHEDRVLQSKELLNSIGFSPBEKFOKPPQFMGYELMWTKWLQK IELQRETWTVDNIQKLVGLNAAQIYPGIIKTKHLCRLIRGKMTL EEVQWTEMAEA EYBENKI LSQEQGYYQEGKPLEATVIKSDQNSWKIHOEDKILKVGKFAKINT HTNGVRLAHVIOIKGEAIVIGQVPKFLPVEKDVWQWMTDYQVWTIPEWDFIS TPPLVRLVNLKQDPIEGEETYYTDGSCNKQSKGAGYITDRGDKVUKLEOJTNQO AELAFALMALDGSFKNANIVDSQYVMGIIITGPTESERLNVQIIEEMIKKSIYVA WVPAHKGIGNQSDIHLVSQIRQVLFLEKI EPOAEHDKYHSNVKELVPFGPLPRIV ARQIVTCDKCHQGEAIHQANSDLGTWQMDCTHLEGKIIIVAVHVASGFIEAEVLP QETGRQTLAKLAGRWPI THLTDNGANFASQVKVMAWAGIETFGVYPNPQSQ GVRAMNHHLNQIDIRIQANSVETI VLMAVHCMNFKRGGIGDMTPAERLINMITT EQEIQFQOSKSKFNFRVYREGRDOLWKGPGELLWKGEAGVILKVGTDIKVYPRRK AKIINDFGGKEVDSSSHMEDTGEAREVA"
	CDS	4823. .5467	/gene="vif"	/db_xref="GI:2828039"	4823. .5467
gene		/product="vif"	/protein_id="AAB99960.1"	/db_xref="GI:2828039"	/translation="MEERKRWIAYPTWRI PERLWRHSLIKYLYKTKDLQKVCYVPH FKVGAWMTCSRVIFPLQEGSHLEVQGWHLTPBKGMSTYAVRI TWYKNFTWTDTP NYADLLTSYFPCTAGETVRRARIGEQLLSCCRPPRAHKYQVPSLOYLAKVYSDVR SQGENTPWTQWRNRRRLRWAKNSRGDKQRGKRPPTYKANQFPELAKVILGILA"
	CDS	5295. .5633	/gene="vpx"	/db_xref="GI:2828040"	5295. .5633
gene		/product="vpx"	/protein_id="AAB99961.1"	/db_xref="GI:2828040"	/translation="MSDPRERIPGNSGEETIGBAFELWLNRTVEEINREAVNHLPREL IFQVWQRSWEYWHDEQGMSPSYVKYRILCLIQKALFWHCKGRCGLGEGHAGGWRPG PPPPPPGLA"
	CDS	5634. .5939	/gene="vpr"	/db_xref="GI:2828040"	5634. .5939
gene		/product="vpr"	/protein_id="AAB99967.1"	/db_xref="GI:2828046"	/translation="MGGAI SMRRSRPSGDLRQLRLRARGETYGRLLGVEBGYSQSPG GLDKGLSLSCEGQYKQGYMNTWRNPAERSKLAYRKONMODIDREDDDLGVSV RPKVPRTMSYKLAIDMSHF IKEKGGLGEGIYSARRRHLIILYILEKEGIGIPDWQDYT SGPGIRVPKTFGLMWKLVPVNSDEAQDEEHYLMWHPAQTSQWDDPFMGEVLAWKFDPT LAYTYEAYVRYPEEFGSKSLSEBEVRRRLTARGLLNMADKKETR"
	CDS	9307. .10000	/gene="vpr"	/db_xref="GI:2828046"	9307. .10000

misc_feature		/note="3' long terminal repeat"			
9307..9823					
repeat_region		/note="U3 region"			
9824..10000					
		/note="R region"			
ORIGIN					
Query Match 72.5%; Score 1471; DB 14; Length 10000;					
Best Local Similarity 99.0%; Pred. No. 4.5e-296;					
Matches 1480; Conservative 0; Mismatches 15; Indels 0; Gaps 0;					
Qy	52	TGGATCTCGGCTTCGAGATCCATGCTCCTCTGGGATATTGATGATCTGTAGTGTACAGAA	111		
Db	6375	TGGGGGTGGAGATGGGGCACCATGCTCCTTTGGGATGTTGATGATCTGTAGTGTACAGAA	6434		
Qy	112	AAATTTGGGTGACAGTCTATTATTTGGGTTACCTGTGTGGAGAGAGCAACACCACTCTA	171		
Db	6435	AAATTTGGGTGACAGTCTATTATTTGGGTTACCTGTGTGGAGAGAGCAACACCACTCTA	6494		
Qy	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231		
Db	6495	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554		
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT	291		
Db	6555	GCCTGTGTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAT	6614		
Qy	292	TTTAAACATGTGGAAAAATAACATGTGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	351		
Db	6615	TTTAAACATGTGGAAAAATAACATGTGTAGATCAGATGCATGAGGATATAATCAGTTTATGG	6674		
Qy	352	GATGAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATGTCACAT	411		
Db	6675	GATGAAGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATGTCACAT	6734		
Qy	412	AATTTGAATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAG	471		
Db	6735	AATTTGAATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAG	6794		
Qy	472	AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCAAGCATTAAGAAATAAGGTTAAG	531		
Db	6795	AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCAAGCATTAAGAAATAAGGTTAAG	6854		
Qy	532	AAAGAAATATGCATCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAATCTAATAATACT	591		
Db	6855	AAAGAAATATGCATCTTTTAAATAGACTTTGATGTAGTACCAATAGAAAATCTAATAATACT	6914		
Qy	592	AAGTATAGTTAATAAGTTGTGAACACCTCAGTCATTACAGGGCTGTCCAAAGGTTATCC	651		
Db	6915	AAGTATAGTTAATAAGTTGTGAACACCTCAGTCATTACAGGGCTGTCCAAAGGTTATCC	6974		
Qy	652	TTTTCAGCAATTTCCCATACATTAATTTGTGTCGGCTGGTGTGGCATGCTTAAAGTGTAAAC	711		
Db	6975	TTTTCAGCAATTTCCCATACATTAATTTGTGTCGGCTGGTGTGGCATGCTTAAAGTGTAAAC	7034		
Qy	712	AATAAGACATTCATAGGATCAGGACCATGACAAAATGTTCAGCAGTACAATGTACACAT	771		
Db	7035	AATAAGACATTCATAGGATCAGGACCATGACAAAATGTTCAGCAGTACAATGTACACAT	7094		
Qy	772	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	831		
Db	7095	GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	7154		
Qy	832	ATAGTAATTTAGATCTGAAAAATTTTCACAGCAATGCTAAAACCATTAATAGTACAGCTAAAT	891		
Db	7155	ATAGTAATTTAGATCTGAAAAATTTTCACAGCAATGCTAAAACCATTAATAGTACAGCTAAAT	7214		
Qy	892	GAACTGTAGTAATTTAATTTGTACAAGACCCCAACAATACAAAGAGAGGTTTATCTATA	951		
Db	7215	GAACTGTAGTAATTTAATTTGTACAAGACCCCAACAATACAAAGAGAGGTTTATCTATA	7274		
Qy	952	GGACAGGGAGAGCAATTTTATGCAAGAGAGAAAACATAATAGGAGATATAAGCAAGCAACAT	1011		

Db	7275	GGACAGGGAGAGCATTTTATGCAAGAAACAACTAATAGGAGATATAAGACAACCAT	7334
Qy	1012	TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATATAAATAAGA	1071
Db	7335	TGTAACATTAGTAGAGCAAAAATGGAATAACACTTTTACAACAGATAGTTATATAAATAAGA	7394
Qy	1072	GAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGAGCCAGAAAT	1131
Db	7395	GAAAAATTTAGGAATAAAAACAATAGCCTTTAATCAATCCTCAGGAGGGAGCCAGAAAT	7454
Qy	1132	GTAATGACACAGTTTAAATTTGGAGGGAAATTTCTTACTGTAAATACAGCACAACTGTTT	1191
Db	7455	GTAATGACACAGTTTAAATTTGGAGGGAAATTTCTTACTGTAAATACAGCACAACTGTTT	7514
Qy	1192	AATAGTACTTGGAAATGTTTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATACA	1251
Db	7515	AATAGTACTTGGAAATGTTTACTGGAGGGCAAAATGGCACTGAAGGAAATGACATAATACA	7574
Qy	1252	CTCAATGCAAGATAAAAACAATTTAATAATATGCGGCAAGAAAGTAGGAAAAGCAATGTAT	1311
Db	7575	CTCAATGCAAGATAAAAACAATTTAATAATATGCGGCAAGAAAGTAGGAAAAGCAATGTAT	7634
Qy	1312	GCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	1371
Db	7635	GCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	7694
Qy	1372	AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGAT	1431
Db	7695	AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGAT	7754
Qy	1432	ATGAGGACAAATTTGGAGAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1491
Db	7755	ATGAGGACAAATTTGGAGAGTGAATTTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	7814
Qy	1492	GGAGTAGCACCACCCAGCGGCAAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGAGAGAG	1546
Db	7815	GGAGTAGCACCACCCAGCGGCAAGAGAGACAGTGCAGAGAGAGAGAGAGAGAGAGAGAG	7869
RESULT 2			
LOCUS	CQ753919 2046 bp DNA linear PAT 01-MAR-2004		
DEFINITION	Sequence 24 from Patent WO2004001051.		
ACCESSION	CQ753919		
VERSION	CQ753919.1 GI:44845220		
KEYWORDS	Human immunodeficiency virus 1 (HIV-1)		
SOURCE	Human immunodeficiency virus 1		
ORGANISM	Human immunodeficiency virus 1		
REFERENCE	1		
AUTHORS	Tangy, F., Lorin, C., Mollet, L. and Delebecque, F.		
TITLE	Recombinant measles viruses expressing epitopes of antigens of rna		
JOURNAL	viruses - use for the preparation of vaccine compositions		
FEATURES	Patent: WO 2004001051-A 24 31-DEC-2003;		
source	INSTITUT PASTEUR (FR)		
ORIGIN	Location/Qualifiers		
Query Match	71.7%; Score 1453.4; DB 6; Length 2046;		
Best Local Similarity	98.3%; Pred. No. 2.7e-292;		
Matches 1469; Conservative	0; Mismatches 26; Indels 0; Gaps 0;		
Qy	52	TGGATCTCGGCTTCAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAA	111
Db	37	TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTGTACAGAA	96
Qy	112	AAATTTGGGTGACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACTCTA	171

412 AATTTGAATATCACTAAGAACTACTAATCCACTAGTAGCAGCTGGGAAATGATGAG 471
Db |||||
397 AATTTGAATATCACTAAGAACTACTAATCCACTAGTAGCAGCTGGGAAATGATGAG 456
Qy 472 AAAGGAGAAATAAAAAATGCTCTTCTATATACCAACGACATTAAGAAATAGGTAAG 531
Db 457 GAAGGAGAAATAAAAAATGCTCTTCTATATACCAACGACATTAAGAAATAGGTAAG 516
Qy 532 AAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAATAATACT 591
Db 517 AAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAATAATACT 576
Qy 592 AAGTATAGTTAATAGTTTAAACCTCAGTCATTAACAGGCTGTCCAAAGGTATCC 651
Db 577 AAGTATAGTTAATAGTTTAAACCTCAGTCATTAACAGGCTGTCCAAAGGTATCC 636
Qy 652 TTTTACGCCAATCCCATATATTGTGTCGCCGCTGGTTTGCATGCTAAAGGTATAC 711
Db 637 TTTTACGCCAATCCCATATATTGTGTCGCCGCTGGTTTGCATGCTAAAGGTATAC 696
Qy 712 AATAAGACATTCATAGGATCAGGACATGCACAAATGTACGACATGATGATACAT 771
Db 697 AATAAGACATTCATAGGATCAGGACATGCACAAATGTACGACATGATGATACAT 756
Qy 772 GGAATTAGGCCAGTGGTCACTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGAC 831
Db 757 GGAATTAGGCCAGTGGTCACTCAACTCACTGCTTTAAATGGCAGTCTAGCAGAAAGAC 816
Qy 832 ATAGTAATTAGTCTGAAATTTTACAGACATGCTTAAACCATTAATAGTACAGTAAAT 891
Db 817 ATAGTAATTAGTCTGAAATTTTACAGACATGCTTAAACCATTAATAGTACAGTAAAT 876
Qy 892 GAATCTGTAGTAATTAATTTGTAACAGACCCCAACAAATACAAAGAAAGGTTATCTATA 951
Db 877 GAATCTGTAGTAATTAATTTGTAACAGACCCCAACAAATACAAAGAAAGGTTATCTATA 936
Qy 952 GGACAGGGAGAGCAATTTATGCAAGAGAGAAACATAATAGGAGATATAAGCAACACAT 1011
Db 937 GGACAGGGAGAGCAATTTATGCAAGAGAGAAACATAATAGGAGATATAAGCAACACAT 996
Qy 1012 TGTAACATTAGTAGCAAAATGGAATTAACACTTTTACACAGATAGTTATAAATTAAGA 1071
Db 997 TGTAACATTAGTAGCAAAATGGAATTAACACTTTTACACAGATAGTTATAAATTAAGA 1056
Qy 1072 GAAAAATTTAGGAATAAAACAATAGCCTTTTATCAATCTCAGGAGGGACCCAGAAAT 1131
Db 1057 GAAAAATTTAGGAATAAAACAATAGCCTTTTATCAATCTCAGGAGGGACCCAGAAAT 1116
Qy 1132 GTAATGCAAGTTTAAATTTGAGGGGAAATCTTCTACTGTAAATACAGCAACTGTTT 1191
Db 1117 GTAATGCAAGTTTAAATTTGAGGGGAAATCTTCTACTGTAAATACAGCAACTGTTT 1176
Qy 1192 AATAGTACTGGAATTTTACTGGAGGAGCAAAATGACACTGAAGGAATGACATATACAC 1251
Db 1177 AATAGTACTGGAATTTTCTGGAGGGGCAAAATGACACTGAAGGAATGACATATACAC 1236
Qy 1252 CTCCAATGCAAGTAATAAACAATTAATATGTCGCAAGAGTAGGAGAAAGCAATGAT 1311
Db 1237 CTCCAATGCAAGTAATAAACAATTAATATGTCGCAAGAGTAGGAGAAAGCAATGAT 1296
Qy 1312 GCCCTCCCATCACAGGCAAAATTAGATGTTTCAATCAAAATATTACAGGCTGCTACTAACA 1371
Db 1297 GCCCTCCCATCACAGGCAAAATTAGATGTTTCAATCAAAATATTACAGGCTGCTACTAACA 1356
Qy 1372 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAT 1431
Db 1357 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAT 1416
Qy 1432 ATGAGGGCAATTTGAGAGAGTGAATTTATATAAATATAAGTAGTAAGAAATGAACCAATA 1491
Db 1417 ATGAGGGCAATTTGAGAGAGTGAATTTATATAAATATAAGTAGTAAGAAATGAACCAATA 1476

Qy 1492 GGAGTAGCACCACAGGGCAAGAGAGAAAGACAGTGCAGAGAGAAAAAGACCGG 1546
Db 1477 GGAGTAGCACCACAGGGCAAGAGAGAAAGACAGTGCAGAGAGAAAAAGACGAG 1531
RESULT 4
AF217181
LOCUS Simian-Human immunodeficiency virus SHIV-C2/1, linear VRL 01-JAN-2002
DEFINITION Simian-Human immunodeficiency virus SHIV-C2/1, complete genome.
ACCESSION AF217181
VERSION AF217181.1 GI:18026826
KEYWORDS
SOURCE Simian-Human immunodeficiency virus
ORGANISM Simian-Human immunodeficiency virus
VIRUSES; Retrovirdae; Retroviridae; Lentivirus; Primate
lentiivrus group.
REFERENCE 1 (bases 1 to 9860)
AUTHORS Sakai,K., Shinohara,K., Takahashi,E., Ami,Y., Sasaki,Y., Suzuki,Y., Nakasone,T. and Honda,M.
TITLE Comparative genetic analysis of simian/human immunodeficiency viruses (SHIVs) with pathogenic property
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9860)
AUTHORS Sakai,K., Shinohara,K., Takahashi,E. and Honda,M.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1999) AIDS Research Center, National Institute of Infectious Diseases, Gakuen 4-7-1, Musashimurayama, Tokyo 208-0011, Japan
FEATURES
Location/Qualifiers
source 1..9860
/organism="Simian-Human immunodeficiency virus"
/viroion
/mol_type="genomic RNA"
/strain="SHIV-C2/1"
/specific_host="cynomolgus monkey"
/db_xref="taxon:57667"
misc_feature 1..5938
/note="obtained from monkey plasma"
LTR 1..301
/note="derived from SIVmac239"
repeat_region 1..177
/note="R region"
misc_feature 178..301
/note="U5 region"
gene 536..2068
/gene="gag"
CDS 536..2068
/gene="gag"
/codon_start=1
/product="gag protein"
/protein_id="AAL55638.1"
/db_xref="GI:18026827"
/translation="MGVRSVLGSKKADLEKIRLPRNGKKYMLKHVVMAANELDRF
GLASLENKEGCKILSLVLAFLVPTGSENLKSLYNTVCVLCIHAERKVKHTEAKQ
IVORHVVETVETTTMPTKSRPTAPSGRGNGYVQQIGNYVHLPLSPRTLNAAWVKL
IEEKFGAEVVPFGFALSEGCTPYDINQMLNCVGDHQAAMQIIRIDINEEAADWDLOH
PAPQOQGLREPSGSDIAGTSSVDEQIOMMYRQNPPIVGNITVYRWIQLGLQKCVR
MYNPNTILDVKQKPEPFQSVDFYKSLRAEQDAAVKNWMTOTLLTQNAAPDCKLV
LKGLVNPTEEMLTACQGVGCGQKARLMAEALKEALAPVPIPAQAQGRPKPIK
CWNGCKGHSARQCRAPRQCGKCGKMDHVMKAPQROAGFLGLGPGWKKPRPFPMA
QVHGLITAPPEDPAVDLLKNVMQLGKQREKQREKPYKEVTEDLLHLNLSLFGG
DQ"
gene <1711..4893
/gene="pol"
CDS <1711..4893
/gene="pol"
/codon_start=1
/product="pol protein"
/protein_id="AAL55639.1"
/db_xref="GI:18026828"
/translation="VLELWERTGLCKAMQSPKTKMLMKNKNGPCYCOMPRTGGFFR
PWSMGKGAQFPHGSGADATNCSPGSPGSAKELHAVQQAERKAERKQREALQG
GDRGFAAPQFSLWRRPVVTAHIEQGPVEVLDTGADDSIVTGIELGPHYTPKIVGGIG

Db 6555 GCTCTGTGATCCACAGACCCCAACCCCAAGAAGTAGTATTGGGAAATGTGACAGAAAT 6614
Qy 292 TTAAACATGCTGGAATAAACAATGCTAGATCAGATGCGCATGAGGATATTAATCAGTTTATGG 351
Db 6615 TTAAACATGCTGGAATAAACAATGCTAGATCAGATGCGCATGAGGATATTAATCAGTTTATGG 6674
Qy 352 GATGAAGCCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 411
Db 6675 GATGAAGCCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 6734
Qy 412 AATTGGAATATCACAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 471
Db 6735 AATTGGAATATCACAAGAACTACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGAG 6794
Qy 472 AAAGAGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATTAAGAAATAAGGTAAG 531
Db 6795 GAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATTAAGAAATAAGGTAAG 6854
Qy 532 AAAGAAATATGCACTTTTAAATAGACTTGATAGTACCAATAGAAAACTAAATTAATCT 591
Db 6855 AAAGAAATATGCACTTTTAAATAGACTTGATAGTACCAATAGAAAACTAAATTAATCT 6914
Qy 592 AAGTATAGTTAAATAGTTGAACACCTCAGTCATTACAGGCGCTGTCCAAAGGTATCC 651
Db 6915 AAGTATAGTTAAATAGTTGAACACCTCAGTCATTACAGGCGCTGTCCAAAGGTATCC 6974
Qy 652 TTTACGCCAATCCCATACATTATTTGTGTCGGGCTGGGTTTGGCATGCTAAAGTGTAAC 711
Db 6975 TTTACGCCAATCCCATACATTATTTGTGTCGGGCTGGGTTTGGCATGCTAAAGTGTAAC 7034
Qy 712 AATAAGACATCAATGGATCAGGACCATGCAACAAATGTGACACAGTCAATGTACACAT 771
Db 7035 AATAAGACATCAATGGATCAGGACCATGCAACAAATGTGACACAGTCAATGTACACAT 7094
Qy 772 GGAATTAGGCCAGTGGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 831
Db 7095 GGAATTAGGCCAGTGGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAAGAC 7154
Qy 832 ATAGTAATTAGATCTGAAATTTTACAGACAATGCTAAACCATTAATAGTACAGCTAAT 891
Db 7155 ATAGTAATTAGATCTGAAATTTTACAGACAATGCTAAACCATTAATAGTACAGCTAAT 7214
Qy 892 GAATCTGTAGTAATTAATTTGTAACAAGACCCCAACAATACAAGAGAAGGTTATCTATA 951
Db 7215 GAATCTGTAGTAATTAATTTGTAACAAGACCCCAACAATACAAGAGAAGGTTATCTATA 7274
Qy 952 GCACAGGAGAGCATTTTATGCAAGAGAACAATTAATAGGAGATATAAGACAGACAT 1011
Db 7275 GCACAGGAGAGCATTTTATGCAAGAGAACAATTAATAGGAGATATAAGACAGACAT 7334
Qy 1012 TGTAACATTAGTAGAGCAAAATGGAAATAACCTTTTACAACAGATAGTTATAAAATTAAGA 1071
Db 7335 TGTAACATTAGTAGAGCAAAATGGAAATAACCTTTTACAACAGATAGTTATAAAATTAAGA 7394
Qy 1072 GAAAAATTTAGGAATTAACAATAGCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAT 1131
Db 7395 GAAAAATTTAGGAATTAACAATAGCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAT 7454
Qy 1132 GTAATGCACAGTTTAAATTTGGAGGGGAATTTCTTCTACTGTAAATACAGCACACTGTTT 1191
Db 7455 GTAATGCACAGTTTAAATTTGGAGGGGAATTTTCTTCTACTGTAAATACAGCACACTGTTT 7514
Qy 1192 AATAGTACTTGAATTTTACTGGAGGGACAATAGCCTGAAGGAAATGACATAATCACA 1251
Db 7515 AATAGTACTTGAATTTTCTGCTGGAGGGACAATAGCCTGAAGGAAATGACATAATCACA 7574
Qy 1252 CTCCTAATGCAGATAAAACAAATTAATAATGTGCGAGAAATAGGAAAAAGCAATGTAT 1311
Db 7575 CTCCTAATGCAGATAAAACAAATTAATAATGTGCGAGAAATAGGAAAAAGCAATGTAT 7634
Qy 1312 GCCCCTCCCATCAGAGGACAAATTAAGATTGTTTCATCAATATATACAGGGCTGCTACTAACA 1371

Db 7635 GCCCTCCCATCAGAGCAAAATTAGATGTTTCATCAATATATACAGGGCTGCTACTAACA 7694
Qy 1372 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1431
Db 7695 AGAGATGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 7754
Qy 1432 ATGAGGNCATTTGGAGAGTGAATTTATATAATATAAGTAGTAAGATTGAACCAATA 1491
Db 7755 ATGAGGNCATTTGGAGAGTGAATTTATATAATATAAGTAGTAAGATTGAACCAATA 7814
Qy 1492 GGAGTAGCACCCACAGGGCAAGAGAAAGACAGTCGAAAGAGAAAAAGACCCG 1546
Db 7815 GGAGTAGCACCCACAGGGCAAGAGAAAGACAGTCGAAAGAGAAAAAGACAGCAG 7869
RESULT 5
SIU89134
LOCUS SIU89134 9860 bp DNA linear VRL 21-MAY-1997
DEFINITION Simian-Human immunodeficiency virus strain SHIV-89.6P, complete genome.
ACCESSION U89134
VERSION U89134.1 GI:2108163
KEYWORDS
SOURCE
ORGANISM Simian-Human immunodeficiency virus
Simian-Human immunodeficiency virus
Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
REFERENCE
1 (bases 1 to 9860)
AUTHORS Karlsson,G.B., Halloran,M., Li,J., Park,I.W., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J. Characterization of molecularly cloned simian-human immunodeficiency viruses causing rapid CD4+ lymphocyte depletion in rhesus monkeys
J. Virol. 71 (6), 4218-4225 (1997)
MEDLINE 97296224
PUBMED 9151808
REFERENCE
2 (bases 1 to 9860)
AUTHORS Karlsson,G.B., Halloran,M., Li,J., Park,I., Gomila,R., Reimann,K.A., Axthelm,M.K., Iliff,S.A., Letvin,N.L. and Sodroski,J. Direct Submission
TITLE Submitted (10-FEB-1997) Human Retrovirology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA
JOURNAL
FEATURES
location/Qualifiers
source
1. .9860
/organism="Simian-Human immunodeficiency virus"
/proviral
/mol_type="genomic DNA"
/strain="SHIV-89.6P"
/db_xref="taxon:57667"
/clone="SHIV-89.6KB9"
1. .5946
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/note="derived from SIV"
5947. .8778
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/note="derived from HIV-1"
8779. .9860
/organism="Simian-Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:57667"
/note="derived from SIV"
1. .301
/note="5' LTR"
1. .177
/note="R region"
178. .301
/note="U5 region"
536. .2068
/gene="gag"
misc_feature
LTR
misc_feature
misc_feature
gene

Best Local Similarity 98.3%; Pred. No. 2.1e-292; Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
Qy	52	TGGATCTCGGCTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTCTCAGAAA	111
Db	6375	TGGGGTGGAGATGGGCGACCATGCTCTTGGGATTTGATGATCTGTAGTCTCAGAA	6434
Qy	112	AAATGTGGGTGACAGTCTATTATGGGTPACCTGTGTGGAGAGAACCAACCACTCTA	171
Db	6435	AAATGTGGGTGACAGTCTATTATGGGTPACCTGTGTGGAGAGAACCAACCACTCTA	6494
Qy	172	TTTTGTGCATCAGATCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	6495	TTTTGTGCATCAGATCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	6554
Qy	232	GCCTGTGTACCCACAGACCCCAACCCACAAAGAGTAGTATTGGGAAATGTGACAGAAAT	291
Db	6555	GCCTGTGTACCCACAGACCCCAACCCACAAAGAGTAGTATTGGGAAATGTGACAGAAAT	6614
Qy	292	TTTAACTGTGGAAAAATAACATGTTAGATGATGATGATGATGATGATGATGATGATGATG	351
Db	6615	TTTAACTGTGGAAAAATAACATGTTAGATGATGATGATGATGATGATGATGATGATGATG	6674
Qy	352	GATGAAGCCTAAAGCCATGTGTAAATTTAACCCCACTCTGTGTTACTTTTAAATTCGACT	411
Db	6675	GATGAAGCCTAAAGCCATGTGTAAATTTAACCCCACTCTGTGTTACTTTTAAATTCGACT	6734
Qy	412	AAATTTGAATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	471
Db	6735	AAATTTGAATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAG	6794
Qy	472	AAAGAGAAATAAAAATTTGCTTTCTATATCAACAAGCATTAAGAAATAAGTTAAAG	531
Db	6795	AAAGAGAAATAAAAATTTGCTTTCTATATCAACAAGCATTAAGAAATAAGTTAAAG	6854
Qy	532	AAAGAAATGCACTTTTAAATAGATCTGATGTAGTACCAATAGAAATCTAATAATACT	591
Db	6855	AAAGAAATGCACTTTTAAATAGATCTGATGTAGTACCAATAGAAATCTAATAATACT	6914
Qy	592	AAGTATAGTTAATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCTAAAGGTATCC	651
Db	6915	AAGTATAGTTAATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCTAAAGGTATCC	6974
Qy	652	TTTCAGCAATTCCTCATATTTTGTGTCGGCTGGGTTTGCATGCTCAAAGTGTAAAC	711
Db	6975	TTTCAGCAATTCCTCATATTTTGTGTCGGCTGGGTTTGCATGCTCAAAGTGTAAAC	7034
Qy	712	AATAAGACATTCATGGATCAGGACCATGCACAAATGTGCAGACAGTACAATGTACAT	771
Db	7035	AATAAGACATTCATGGATCAGGACCATGCACAAATGTGCAGACAGTACAATGTACAT	7094
Qy	772	GGAAATTAGGCCAGTGGTCACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAC	831
Db	7095	GGAAATTAGGCCAGTGGTCACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAGAC	7154
Qy	832	ATAGTAATTTAGATCTGAAATTTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAAT	891
Db	7155	ATAGTAATTTAGATCTGAAATTTTCACAGCAATGCTTAAACCATTAATAGTACAGCTAAAT	7214
Qy	892	GAATCTGTAGTAATTAATTTGTAACAAGCCCAACCAATACAAAGAAAGGTTATCTATA	951
Db	7215	GAATCTGTAGTAATTAATTTGTAACAAGCCCAACCAATACAAAGAAAGGTTATCTATA	7274
Qy	952	GGACAGGAGAGAGATTTTATGCAAGAGAAACATAATAGGAGATATAAGCAACACAT	1011
Db	7275	GGACAGGAGAGAGATTTTATGCAAGAGAAACATAATAGGAGATATAAGCAACACAT	7334
Qy	1012	TGTAACTATTAGTAGCAAAAATGGAATAACCTTTTCAACAGATAGTTTATAAATTAAGA	1071
Db	7335	TGTAACTATTAGTAGCAAAAATGGAATAACCTTTTCAACAGATAGTTTATAAATTAAGA	7394
Qy	1072	GAAAAATTTAGGAATAAAACAAATAGCCTTTTAAATCAATCTCTAGGAGGGGACCCAGAAAT	1131

Db	7395	GAAAAATTTAGGAATAAAACAAATAGCCTTTTAAATCAATCCTCAGGAGGGGCCAGAAAT	7454
Qy	1132	GTAATGCACAGTTTTTAATTTGGAGGGGAAATTTCTTACTGTAATACAGCAACATGTTT	1191
Db	7455	GTAATGCACAGTTTTTAATTTGGAGGGGAAATTTTCTTACTGTAATACAGCAACATGTTT	7514
Qy	1192	AATAGTACTTGGAAATGTTTACTGGAGGCAAAATGGCACTGGAAGAAATGACATATCACA	1251
Db	7515	AATAGTACTTGGAAATGTTTCTGGAGGGCAAAATGGCACTGGAAGAAATGACATATCACA	7574
Qy	1252	CTCCAAATGCAGATAAAAAAATAAATATAAATATGTGCGAGAAAGTAGGAAAAAGCAATGTAT	1311
Db	7575	CTCCAAATGCAGATAAAAAAATAAATATAAATATGTGCGAGAAAGTAGGAAAAAGCAATGTAT	7634
Qy	1312	GCCCTCCCATCAGAGCAAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACA	1371
Db	7635	GCCCTCCCATCAGAGCAAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACA	7694
Qy	1372	AGAGATGAGGATTAATAGTACTGAGCTGAGACTGAGATCTTCAGACCTGGAGGAGAT	1431
Db	7695	AGAGATGAGGATTAATAGTACTGAGCTGAGACTGAGATCTTCAGACCTGGAGGAGAT	7754
Qy	1432	ATGAGGACAAATTTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTCGAACCAATA	1491
Db	7755	ATGAGGACAAATTTGGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTCGAACCAATA	7814
Qy	1492	GGAGTAGCACCCACAGGCGCAAGAGAAAGACAGTCGAAAGAGAAAAAGACCGG	1546
Db	7815	GGAGTAGCACCCACAGGCGCAAGAGAAAGACAGTCGAAAGAGAAAAAGACAG	7869
RESULT 6			
BD161892			
LOCUS			
Nonhuman primate model of acquired immunodeficiency syndrome.			
10501 bp DNA linear PAT 17-JAN-2003			
BD161892			
Nonhuman primate model of acquired immunodeficiency syndrome			
BD161892.1 GI:27867650			
JP 2002159296-A/1.			
Simian-Human immunodeficiency virus			
Simian-Human immunodeficiency virus			
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate			
lenti virus group.			
1 (bases 1 to 10501)			
Shinohara, K., Sakai, K. and Honda, M.			
Nonhuman primate model of acquired immunodeficiency syndrome			
Patent: JP 2002159296-A 1 04-JUN-2002;			
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE			
ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH			
OS Simian-human immunodeficiency virus			
PN JP 2002159296-A/1			
PD 04-JUN-2002			
PF 27-NOV-2000 JP 2000360274			
PI KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA			
PC C12N15/09,A01K67/027,C12N7/00,C12N7/02,G01N33/15,G01N33/50//			
PC G01N33/569,			
PC (C12N7/00,C12R1:93),(C12N7/02,C12R1:93),C12N15/00 CC genomic			
DNA			
CC strain='SHIV-C2/1'			
CC derived from SIMmac239			
CC 5' long terminal repeat			
CC U3 region			
CC R region			
CC U5 region			
CC gag			
CC pol			
CC vif			
CC vpx			
CC vpr			
CC tat			
CC rev			
CC vpu			
CC env			

[illegible]

gene	6060..6302	
CDS	/gene="vpu"	
	6060..6302	
	/gene="vpu"	
	/citation=[2]	
	/codon_start=1	
	/product="VPU protein"	
	/protein_id="AA81042.1"	
	/db_xref="GI:1055036"	
	/translation="MLSQILAI VALVVAIIIAIIVWSIVFIEYRKILRQRKIDRLID	
	RIREREDSGNESGDDEELALERGLHLPWDVDDL"	
gene	6223..8784	
CDS	/gene="env"	
	6223..8784	
	/gene="env"	
	/citation=[2]	
	/codon_start=1	
	/product="ENV polyprotein precursor"	
	/protein_id="AA81043.2"	
	/db_xref="GI:9409798"	
	/translation="MRVKEIRKNQHLRGGILLGLMLMICSAAKEKTWVTIYGVPM	
	REATTILFCASDAKAYDEHVNWATHACVPTDENPQEVILGNVTIENMKNNDVQ	
	MHEDIILSWDESLKPCVKLTPLCVTLNLTNLTNTNPTSSGMMKEIKRCPH	
	YITTSIRNKVKEALFNRLDVPENTNTNRYLISCVTSVITQACPKEVQPIPIH	
	YCVAPGAPLAKNNKTENGSPCTNVSTVQCTHGIRPVSQTLLGLSLABEDIVRS	
	ENFTDNKTIIVOLNESVINCTRPNNTRRLSIGPGRAFARNNIIGDIRQAHENI	
	SRKNNLTQIIVIKLEKPFNTIAFNQSSGDPRIVMHSPNCGGFFFCNTAQLFN	
	STWNTGTGTBGNDIITLOCRKIQIINMQKVGKMYAPPTIGQIRCSNITGLLL	
	TRDGNSTETETIIFRPGGDMRDNRSLELYKIVKVRLEPIGVAPTAKRRTVQREKR	
	AVGAGVPLFGIAGSTMGAAVSVLTVQARLLSGIVQQNNLLRAIEAQHMLQLT	
	VMGIKQARVALERYLDQQLMGIWGCCKLICTTSPVWNVSWSKNSVDDIWNMT	
	WMWEREDTNDTVIYDLLEKSOTQOEKNEKELLELDKWSLWNWFDITNMLWIRLP	
	IMIYGGILGIRLFAVLSIVNRVQGSPLSFOTLLPASRGPDPEPTEEREGGERDR	
	RSGLVNGFLAFWDLNRNLCIFLYHLRLNLLIVTRIVELLRRGHEALKYWNLLQ	
mat_peptide	YSGELKNSAVSLNLTALIAVAEGTDRVIKIVQACRAIRNIPTRIRQGLERALL"	
	6223..7746	
	/gene="env"	
	/product="glycoprotein 120"	
	/citation=[2]	
mat_peptide	7747..8781	
	/gene="env"	
	/product="glycoprotein 41"	
	/citation=[2]	
gene	8786..9400	
CDS	/gene="nef"	
	8786..9400	
	/gene="nef"	
	/citation=[2]	
	/codon_start=1	
	/product="NEF protein"	
	/protein_id="AA81044.1"	
Query Match	71.4%; Score 1447.6; DB 14; Length 9713;	
Best Local Similarity	99.2%; Pred. No. 3.4e-291;	
Matches 1466; Conservative	0; Mismatches 9; Indels 3; Gaps 1;	
QY	72	CATGCTCTGGGATATTGATGATCTGTAGTGCT---ACAGAAAATTTGGGTACAGT 128
DB	6273	CTTGCTCTGGGATGTTGATGATCTGTAGTGCTGCAAAAGAAAACGTGGGTACCAAT 6332
QY	129	CTATTATGGGGTACCTGTGTGAGAGAGAACACCACTCTATTTTTGTGATCAGATGC 188
DB	6333	CTATTATGGGTACCTGTGTGAGAGAGAACACCACTCTATTTTTGTGATCAGATGC 6392
QY	189	TAAAGCCTTATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 248
DB	6393	TAAAGCCTTATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGA 6452
QY	249	CCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAATTTTAACATGTGAAAAA 308
DB	6453	CCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAATTTTAACATGTGAAAAA 6512
QY	309	TAACATGGTAGATCAGATGAGGATATATATCAGTTTATGGGATGAAAGCCTTAAAGCC 368

DB	6513	TAACATGGTAGATCAGATGAGGATATATATCAGTTTATGGGATGAAAGCCTTAAAGCC 6572
QY	369	ATGTGTAATAATAACCCCACTCTGTGTACTTTTAAATTTGCACATAATTTGAATATACACTAA 428
DB	6573	ATGTGTAATAATAACCCCACTCTGTGTACTTTTAAATTTGCACATAATTTGAATATACACTAA 6632
QY	429	GAATACTACTAATCCCACTAGTAGCAGCTGGGGATGATGGAGAAAGAGAGAAATAAAAAA 488
DB	6633	GAATACTACTAATCCCACTAGTAGCAGCTGGGGATGATGGAGAAAGAGAGAAATAAAAAA 6692
QY	489	TTGCTCTTTTATATACCAACACATAGAGATAAGGTAAAGGTAAAGAAATATGCATTTT 548
DB	6693	TTGCTCTTTTATATACCAACACATAGAGATAAGGTAAAGGTAAAGAAATATGCATTTT 6752
QY	549	TAATAGACTTGATGTAGTACCAATAGAAAATCTAATAATTAATTAAGTATAGTTTAATAG 608
DB	6753	TAATAGACTTGATGTAGTACCAATAGAAAATCTAATAATTAATTAAGTATAGTTTAATAG 6812
QY	609	TTGTAAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTATCCTTTACGCCAATTTCCCAT 668
DB	6813	TTGTAAACACCTCAGTCAATTACACAGGCTGTCCAAAGGTATCCTTTACGCCAATTTCCCAT 6872
QY	669	ACATTATTGTCTCCCGCTGGGTTTGGCATGCTAAAAGTGTAAACAATAAGACATTTCAATGG 728
DB	6873	ACATTATTGTCTCCCGCTGGGTTTGGCATGCTAAAAGTGTAAACAATAAGACATTTCAATGG 6932
QY	729	ATCAGGACCATGCACAAATGTGCACACATGTAACATGTAACATGGAATTTAGCCAGTGGT 788
DB	6933	ATCAGGACCATGCACAAATGTGCACACATGTAACATGTAACATGGAATTTAGCCAGTGGT 6992
QY	789	GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTTAGATCTGA 848
DB	6993	GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTTAGATCTGA 7052
QY	849	AAATTTACACAGCAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTAGTAATTAA 908
DB	7053	AAATTTACACAGCAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTAGTAATTAA 7112
QY	909	TTGTACAGACCCACACACATACAGAGAGAGGTATTCTATAGGACACAGGAGAGACATT 968
DB	7113	TTGTACAGACCCACACACATACAGAGAGAGGTATTCTATAGGACACAGGAGAGACATT 7172
QY	969	TTATGCAAGAGAAACATAATAGGAGATATAGACACACATTTGTAACATTAGTAGAGC 1028
DB	7173	TTATGCAAGAGAAACATAATAGGAGATATAGACACACATTTGTAACATTAGTAGAGC 7232
QY	1029	AAAAATGGAAATAACCTTTTACACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATA 1088
DB	7233	AAAAATGGAAATAACCTTTTACACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATA 7292
QY	1089	AACAAATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCACAGAAATTTGTAATGCACAGTTTAA 1148
DB	7293	AACAAATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCACAGAAATTTGTAATGCACAGTTTAA 7352
QY	1149	TTGTGGAGGGGAATTTCTTCTACTGTAAATACAGCACTGTTTAAATAGTACTTTGGAATGT 1208
DB	7353	TTGTGGAGGGGAATTTTCTACTGTAAATACAGCACTGTTTAAATAGTACTTTGGAATGT 7412
QY	1209	TACTGGAGGGGACAAATGGCCTGAAAGAAATGACATAATCACTCCCAATGCAGAAATAA 1268
DB	7413	TACTGGAGGGGACAAATGGCCTGAAAGAAATGACATAATCACTCCCAATGCAGAAATAA 7472
QY	1269	ACAAATTAATAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAGG 1328
DB	7473	ACAAATTAATAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAGG 7532
QY	1329	ACAAATTAAGATGTTTCATCAAAATATTACAGGGCTGCTACTTAAACAGAGATGGAGGTAATAG 1388
DB	7533	ACAAATTAAGATGTTTCATCAAAATATTACAGGGCTGCTACTTAAACAGAGATGGAGGTAATAG 7592
QY	1389	TACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGGAACAATTTGGAG 1448

JOURNAL Submitted (04-MAR-2003) NCID/DASTLR/HARB/VETS, Centers for Disease Control & Prevention, 1600 Clifton Rd., Mail Stop G-19, Atlanta, GA 30333, USA

FEATURES

source

Location/Qualifiers

1. .2553

/organism="Human immunodeficiency virus 1"

/proviral

/mol_type="genomic DNA"

/isolate="81NJ"

/db_xref="taxon:11676"

/country="USA: New Jersey"

/note="sampled in 1981"

subtype: B"

<1. .2553

/gene="env"

1. .2553

/gene="env"

/note="gp160"

/codon_start=1

/product="envelope glycoprotein"

/protein_id="AAP37149.1"

/db_xref="GI:30794653"

/translation="MRVKEIRKNYQHLWRWGTMLLGIIMICSAAEKLVVTVYGVVW
KEATTLPCASDAKAYDTEVHNWATHACVPTDPNPQVLENTENENMKNNVQ
MHEDIISUDOSLPCVKLTCLVTLNCTDURNATNITSSGGTWERGEIKNCFNIT
TSIRKQKEVALFYKLDVDPIDNDNTTTSYRLISCNSTSVIQCPRVSPFPIHYC
TPAGFAILKDKXKFNFGTGPCTNVSTVQCTHGRIPVSTQLLNGSLAEEBWIIRSDN
FTDNAKTIIVOLKEVSEINCTRNPNNTKSHIIGPRAFYTGIBIIGDIOAHNLSR
AKWNTLKOIVRKLEORFQNKTIIVFNOSGGDPEIVHSPNCGEFPVCDSTOLFNSR
WNVTGSNNTGNITLPLCRKQIOLINMQEVRGAMVAPPRIQQIRGSSNITGLLLTR
DGNNESEITEIPRGGGDMRDNWSELYKIVKIEPIGVAPTAKRVRVOREKRAVG
IGVPLFLGFAAGSTGMAASMTLVQARLLLSGVQQNNLLRAIEAQHLLQLTVWG
IKQLQARVLAVERYLKDQLLGIWGCSEKLICTTTPWNASWSNKSLDKIWNNTWME
WERBNNTSVIYTLIESQNOEKELELLELKWASLWNNFDITKWLVIKIPIMI
VGLVGLFIVAVLSIIVNRVQVSPISFOTELPABGPDRPEGIEBEGGERDRSG
RLVGLFLFVWDLSRLCLFSYHRLRDLILLIVTRIVELLRRGHEVLKYWNLLQYWS
QELKNSAVSLNLNATAIAVAEGTDRVIEVQLQRTCRAILHIPIRIQGUERALL"

ORIGIN

Query Match 62.3%; Score 1262.8; DB 14; Length 2553;

Best Local Similarity 92.1%; Pred No. 1.3e-252;

Matches 1369; Conservative 0; Mismatches 102; Indels 15; Gaps 3;

Qy	64	TCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGGGTC	123
Db	46	TGGGACCACTGCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTGGGTC	105
Qy	124	ACAGTCTATTATGGGTCCTGTGGAGAGCAACCACTCTATTTTTGGCATCA	183
Db	106	ACAGTCTATTATGGGTCCTGTGGAGAGCAACCACTCTATTTTTGGCATCA	165
Qy	184	GATGCTAAAGCTATGATACAGAGGTACATAATGTTGGGCGCACACATGCTGTATCCC	243
Db	166	GATGCTAAAGCATATGATACAGAGGTACATAATGTTGGGCGCACACATGCTGTATCCC	225
Qy	244	ACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGG	303
Db	226	ACAGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAAATTTAAACATGTGG	285
Qy	304	AAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAGCCTA	363
Db	286	AAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAGCCTA	345
Qy	364	AAGCCATGTGTAATAATTAACCCCTCTGTGTACTTTAAATTTGACCTAAATTTGAATATC	423
Db	346	AAGCCATGTGTAATAATTAACCCCTCTGTGTACTTTAAATTTGACCTAAATTTGAATATC	399
Qy	424	ACTAAGAATCTACTTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGGAGAAATA	483
Db	400	---AGGAATGCTACTTAATCACCCTAGTAGTAGCGGGGNAACGATGGAGAGGAGAAATA	456
Qy	484	AAAAATTCCTCTTTCTATATACCAACAGCATTAAGAAATAAGGTTAAAGAAAGATATGCA	543

RESULT 11
AY426111

LOCUS AY426111 2568 bp DNA linear VRL 28-JUN-2004
DEFINITION HIV-1 clone BaL-lp isolate BaL from USA envelope glycoprotein (env)
gene, complete cds.
ACCESSION AY426111
VERSION AY426111.1 GI:37962967
KEYWORDS
SOURCE
ORGANISM Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retroviridae; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 (bases 1 to 2568)
Pastore, C., Ramos, A. and Mosier, D.E.
TITLE Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
Coreceptor Switching
J. Virol. 78 (14), 7565-7574 (2004)
JOURNAL
PUBMED 15220431
REFERENCE 2 (bases 1 to 2568)
Pastore, C., Ramos, A. and Mosier, D.E.
AUTHORS Direct Submission
TITLE Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
JOURNAL Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
Location/Qualifiers
1..2568
/organism="Human immunodeficiency virus 1"
/proviral
/mol_type="genomic DNA"
/isolate="BaL"
/isolation_source="RSX4 mutant of BaL isolated after
multiple passages in CXCR4 expressing cells"
/db_xref="taxon:11676"
/clone="BaL-lp"
/country="USA"
1..2568
/gene="env"
1..2568
/gene="env"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AA05835.1"
/db_xref="GI:37962968"
translation="MRVKEKYQHLWRGWRGWTLLGLMLTCSATEKLWVTVYGVVPV
WKEATTLFCASDAKAYDEVHNWATHACVPTDPNPOEVELENVFNFMKNMKN
OMHEDI LSWQDLPKPCVKLPCLVCLPTDLNNTNGNDNTTSSRNMWGGMGME
CSFKITNNRKQVKEYALFYKLDIVPDDNNRNRYLISNTSVITQACPKISFEPI
PIHVCAPAGPAILCKDKKFKNGKPCNSVSTVQCTHGRPVVSTQLLNGSLABEEV
IRSEFNADNKTIIIVOLNESVEINCTRENNTNRKSIHIGPGRALITTKGI LDIRQAH
LNFSTNVTEESNTVENNTITLPCRIKQIIMWQVGRAMYAPP IRQIRCSNITG
LLLRDGGPDENKTEVPFPGGDMRDNRSLEYKYVKVIEPLGVAPTKAKRVVQRE
CNLSRKNWDTLNKIVIKLREQFGNKTIVFKHSSGGDPEIVTHFNCGEFFYCNSTQ
KRVGIGAVLGFILGAGSTWGAASMTLTVOARLLSGIVQOKNLLRAIEAQOHLLO
LTVWGIKQLQARLVAERYLRDQQLLGTWGSGLKICTTAVPWRNWSNKSINKLWDN
MTWMEWDREINNTYSIIYSLIEESQNKQKNELELDKWSLWNNWFEITEWELWYIK
IFIMIGLIGLIRIVFSLSIMNRVQGYSPLSFQTHLPASRGDPDRPGGIEBEGGERD
RDRSRLVNGSLATWDLRSCLFVSYHRLRDLIIIVTRI VELLGRRWGAEALKYWNIL
LQWNSQELKNSAVSLNATATAVABGTDVRVIEVQGCACRAIRHPRIRQGLERILL"
ORIGIN
Query Match 61.3%; Score 1242.2; DB 14; Length 2568;
Best Local Similarity 90.2%; Pred. No. 2.4e-248;
Matches 1354; Conservative 0; Mismatches 138; Indels 9; Gaps 2;
Qy 52 TGGATCTGGCTTCAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGCACAGAA 111
Db 37 TGGGGGTGGAGATGGGGCACCATGCTCTTGGGATGTTGATGATCTGTAGTGCACAGAA 96
Qy 112 AAATTTGGGTACACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACACCACTCTTA 171
Db 97 AAATTTGGGTACACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 156
Qy 172 TTTTGTGCATCAGATCTTAAGCCTATGATACAGAGGTACATAATATGTTTGGGCCACACAT 231
Db 157 TTTTGTGCATCAGATCTTAAGCCTATGATACAGAGGTACATAATATGTTTGGGCCACACAT 216

Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGCAGAAAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTGGGAAATGTGCAGAAAAAT 276
Qy 292 TTTAACATGTGGAAAAATAACATCGGTAGATCAGATGCATGAGGATATATATCAGTTTATGG 351
Db 277 TTTAACATGTGGAAAAATAACATCGGTAGAACAGATGCATGAGGATATATATCAGTTTATGG 336
Qy 352 GATCAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 411
Db 337 GATCAAGCCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 396
Qy 412 AATTGTAATATCACTA-----AGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 397 GATTTGAGGATATCTACTAATGGGAATGACACTAATACCCTAGTAGTAGCAGGGAATG 456
Qy 466 ATGGAGAAAGAGAAAAATAAAAAATTCCTTTCTATATCACCACAGCATAGAAATAAG 525
Db 457 ATGGGGGAGAGAAAAATGAAAAATTCCTTTCTTTCAAAATCACCACAAAATAGAGGTAAAG 516
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAAT 585
Db 517 GTGCAGAAAGAAATATGCACCTTTTAAATAGTATAGTACCAATAGTAAATAATAGT 576
Qy 586 AATACTAAGTATAGCTTAATAAGTTGTAAACACCTCAGTCATTACACAGCCCTGTCCAAAG 645
Db 577 AATTAATAGATATAGTTGATTAAGTTGTAAACCTCAGTCATTACACAGCCCTGTCCAAAG 636
Qy 646 GTATCCTTTAGCCAAATTCCTCATCATTTATGTGTCCCGCTGGTGGTTCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATTCCTCATCATTTATGTGTCCCGCTGGTGGTTCGATGCTAAAG 696
Qy 706 TGTAAACAATAGACATCAATGGAATCAGGACCATGCAAAATGTCCAGCACAGTACAATGT 765
Db 697 TGTAAAGATAAGAAAGTTCAATGGAAAGGACATGTTCAAAATGTCCAGCACAGTACAATGT 756
Qy 766 ACACATGGAATTAGGCCAGTGTGTCAACTCAACTGTCTGTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGGATTAGGCCAGTAGTAGTCAACTCAACTGTCTGTGTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTAGATCTGAAAAATTTTCACAGCAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGATCTGAAAAATTTTCGCGGCAATGCTTAAACCATATAGTACAG 876
Qy 886 CTAATGAATCTGTAGTAATTAATTGTACAGACCCCAACCAATACAAAGAAAGAGGTATA 945
Db 877 CTGAATGAATCTGTAGAAATTAATTGTACAGACCCCAACCAATACAAAGAAAGAGTATA 936
Qy 946 TCTATAGGACCCAGGAGAGAGCATTTTATGCAAGAGAAAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCCAGGAGAGCATTTATACACAGGAAAAATAATAGGAGATATAAGACAA 996
Qy 1006 GCACATTGTAACTATGTAGAGCAAAATGGGAATAACACTTTTACACAGATAGTTATAAA 1065
Db 997 GCACATTGTAACTATGTAGAGCAAAATGGGAATGACACTTTTAAATAGATAGTTATAAA 1056
Qy 1066 TTAAGAAAAATTTAGCAATAAACAATAGCTTTTAATCACTCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAACAATTTGGGAAATAAAACAATAGTCTTTTAAGCATTTCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGCAAGTTTTAAATTTGTGGAGGGGAATTTCTTCTACTGTAATACAGACAA 1185
Db 1117 GAAATTTGCAAGCAGTTTTAAATTTGTGGAGGGGAATTTTCTACTGTAATTTCAACACAA 1176
Qy 1186 CTGTTTAAATAGTACTTTGGAATGTTACTGGAGGGAATAATGGGCACCTGAAGGAAATGACATA 1245
Db 1177 CTGTTTAAATAGTACTTTGGAATGTTACTGAAGAGTCAAAATTAACACTGTAGAAAAATTAACACA 1236
Qy 1246 ATCACACTCCCAATGCAGATAAACAATAATATAATATGTGGCAGAAAGTAGGAAAAAGCA 1305
Db 1237 ATCACACTCCCAATGCAGATAAACAATAATATAATATGTGGCAGAAAGTAGGAAAAAGCA 1296
Qy 1306 ATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAATATTATACAGGGCTGCTA 1365

```

Db      1297 ATGTATGCCCTCCCATCAGAGGACAAATTTAGATGTTTATCAAAATTTACAGGCGTGTCTA 1356
Qy      1366 CTAACAAGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGA 1425
Db      1357 TTAACAAGAGATGGTGG---TCCAGAGGACCAACAGACCGAGGCTTCAGACCTGGAGGA 1413
Qy      1426 GGAGATAGAGGACAAATGGAGAGTGAATATATATAATATAATTAAGTAGTAAAGTGA 1485
Db      1414 GGAGATATGAGGACAAATGGAGAGTGAATATATATAATATAATTAAGTAGTAAAGTGA 1473
Qy      1486 CCAATAGGATGAGACCCACAGGCGCAAGAGAGAGAACAGTGCACCAAGAGAGAGAGACCG 1545
Db      1474 CCAATAGGATGAGACCCACAGGCGCAAGAGAGAGAGAGTGGTGCAGAGAGAGAGAGCA 1533
Qy      1546 G 1546
Db      1534 G 1534

RESULT 12
LOCUS   AY426112
DEFINITION HIV-1 clone BaL-1A isolate BaL from USA envelope glycoprotein (env)
ACCESSION AY426112
VERSION   1
KEYWORDS  HIV-1, complete cds.
SOURCE   Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
          Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate
          lentivirus group.
REFERENCE 1 (bases 1 to 2568)
AUTHORS  Pastore,C., Ramos,A. and Mosier,D.E.
TITLE    Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
          Coreceptor Switching
JOURNAL  J. Virol. 78 (14), 7565-7574 (2004)
PUBMED  15220431
REFERENCE 2 (bases 1 to 2568)
AUTHORS  Pastore,C., Ramos,A. and Mosier,D.E.
TITLE    Direct Submission
JOURNAL  Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
          Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
     source
         1. .2568
            /organism="Human immunodeficiency virus 1"
            /proviral
            /mol_type="genomic DNA"
            /isolate="BaL"
            /isolation_source="RSX4 mutant of BaL isolated after
            multiple passages in CXCR4 expressing cells"
            /db_xref="taxon:11676"
            /clone="BaL-1A"
            /country="USA"
         2. .2568
            /gene="env"
         3. .2568
            /gene="env"
            /codon_start=1
            /product="envelope glycoprotein"
            /protein_id="AAR05836.1"
            /db_xref="GI:37962970"
            /translation="MRVKEKYQHLWRGWRGTMGLMLMICSATEKLWVTYYGVVP
            WKEATTLFCADAKAYDTEVHNWATHACVPTDNPQVELENTFNFMKNMVE
            OMHED11SLWDSLKPCVKLPLVCLNCTDLRNTGNDNTNTSSREWMGGMKN
            CSFKITNIRKQVEALFYKLDIVPIDNNRNRYRLISNTSVITQACPKISPEPI
            PIHYCAPAGAILKDKKNGKPCSKVSTVQCTHGRVPVSTOLLGSLABEEVV
            IRSFNADNAKTIIVQLNESVEINCTRENNTKSIHIGPRALYTTGKIIGIRQAH
            NLGRKWNLDLNIKVLREQFGNKTIVFKHSGSDPEIVTHSFNCGEFPYCNSTQ
            LFNSTWNTESNNVENTTLPCKIKOILNMQKVRAMYAPPIRGOIRCSNITG
            LLLTRDGPENKTEVPRPGGDMRDNRSLEYKYKVKIEPLGVAPTKAKRVVORE
            KRVGIGAVGLGLAGSTMGAAASMTLVQARLLLSGIVQQNNLRLRAIEAQHLLR
            LTVNGIKQLQARVLAVERYLRDQQLLGIWCGSGKLICTTAVPMNSWSLNKIWDN

```

```

MTWWEDEBNNTSYIIYSLEESONQOEKNEOELLELDKWSLWNPFEITELMWYIK
IFIMILGLIGLRIVFVSLIMNRVQGYSPLSFQTHLPASGRDPRPGGIBEEGGERD
RDSRGLNGLSLALIWDLRLSLFYSYHRLDLLLI VTRIVELLRGWEALKYWNLL
LOYWSOLKNSAVSLNATAIAVAEGTDRVIEVVGACRAIRHPRIRROGLERILL"

Query Match      61.2%; Score 1240.6; DB 14; Length 2568;
Best Local Similarity 90.1%; Pred. No. 5.2e-248; Indels 9; Gaps 2;
Matches 1353; Conservative 0; Mismatches 139;

ORIGIN
Qy      52 TGGATCTCGGCTTCGAGATCCATGCTCTTCGGGATATTGATGATCTGTAGTGTCTACAGAA 111
Db      37 TGGGGGTGGAGATGGGCGACCATGCTCTTCGGGATGTTGATGATCTGTAGTGTCTACAGAA 96
Qy     112 AAATTTGGGTGCACAGTCTATTATTTGGGTACTCTGTGTGGAGAGAGCAACCACTCTCTA 171
Db      97 AAATTTGGGTGCACAGTCTATTATTTGGGTACTCTGTGTGGAAAGAGCAACCACTCTCTA 156
Qy     172 TTTTGTGCATCAGATGCTTAAAGCCTATGATACAGAGGTACATATATTTTGGGCCACACAT 231
Db     157 TTTTGTGCATCAGATGCTTAAAGCATATGATACAGAGGTACATATATTTTGGGCCACACAT 216
Qy     232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAT 291
Db     217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTAAATTTGAAAATGTGACAGAAAAT 276
Qy     292 TTTAACATGTGGAAAAATAACATGCTAGATCAGATGCATGAGGATATATCAGTTTATGG 351
Db     277 TTTAACATGTGGAAAAATAACATGCTAGAACAGATGCATGAGGATATATCAGTTTATGG 336
Qy     352 GATCAAGCCTTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACT 411
Db     337 GATCAAGCCTTAAAGCCATGTGTAATAATTAACCTCTCTGTGTACTTTAAATTTGCACT 396
Qy     412 AATTTGAATATCACTA-----AGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db     397 GATTTGAGGATACTACTAATGGGAAATGACACTAATACCCTAGTAGTAGCAGGGAATG 456
Qy     466 ATGAGAGAGAGAGAAATAAAAAATTTGCTTTCTATATATCACCAAGCATTAAGAAATAG 525
Db     457 ATGGGGGAGAGAGAAATGAAAAATTTGCTCTTTCAAAATCACCAAAACATAAGAGGTAG 516
Qy     526 GTAAAGAGAGATATGACATTTTAAATAGACTTGATGTAGTAGTACCAATAGAAAATACTAAT 585
Db     517 GTGCAGAGAGAAATATGCATTTTATAAACTTGATATAGTACCAATAGATAAATAATAGT 576
Qy     586 AATACTAAGTATAGTTAATAAGTTGTAAACACCTCAGTCATTACACAGCGCTGTCCAAAG 645
Db     577 AATAATAGATATAGTTGATAGTTGTAACACCTCAGTCATTACACAGCGCTGTCCAAAG 636
Qy     646 GTATCCTTTTCAGCCAAATTCACATACATTTATTTGTGCCGGCTGGGTTTTCGATGCTAAAG 705
Db     637 ATATCCTTTGAGCCAATTCACATACATTTATTTGTGCCCGGCTGGTTCGATGCTTAAAG 696
Qy     706 TGTAAACAATAAGACATTCATGATGATCAGGACCATGACAAATATGTCAGACAGTACAAATGT 765
Db     697 TGTAAAGATAGAAAGTTCAATGGAAAAGGACCATGTTTCAAAAGTCAGACAGTACAAATGT 756
Qy     766 ACACATGGAATTTAGCCAGTGTCTCAACTCAACTGCTTTAAATTTGAGGAGTCTAGCAGAA 825
Db     757 ACACATGGAATTTAGCCAGTGTATCAACTCAACTGCTTTAAATTTGAGGAGTCTAGCAGAA 816
Qy     826 GAAGACATAGTAAATTAGATCTGAAAAATTTTCA CAGACAAATGCTTAAACCATTAATAGTACAG 885
Db     817 GAAGAGGTAGTAAATTAGATCTGAAAAATTTTTCGCGGACCAATGCTTAAACCATTAATAGTACAG 876
Qy     886 CTAATAGATCTGTAGTAAATTAATTTGTAACAGACCCCAACCAATATACAGAGAGAGTTA 945
Db     877 CTGAATGAATCTGTAGAAATTTAATTTGTAACAGACCCCAACCAATATACAGAGAGAGTTA 936
Qy     946 TCTATAGACACAGGAGAGCAATTTTATGCAAGAGAGAAACATAATAGGAGATATTAAGACAA 1005
Db     937 CATATAGGACACAGGAGAGCAATTTATATACAGAGAGAAATTAATAGGAGATATTAAGACAA 996

```


Qy	1006	GCACATTGTACATTAGTAGGCAAAATGGATTAACACATCTTTACACAGATAGTTATAAA	1065
Db	997	GCACATTGTAACTTAGTAGAGCAAAATGGAAATGACACTTTAAATAAGATAGTTATAAA	1056
Qy	1066	TTAAGAGAAAATTTAGGAATAAAACAATAGCCTTTAATCAATCCTCAGGAGGGAGCCCA	1125
Db	1057	TTAAGAGAACAAATTTGGGAATAAAACAATAGCTTTTAAGCAATCCTCAGGAGGGAGCCCA	1116
Qy	1126	GAATTTGATGACACAGTTTTAATGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAA	1185
Db	1117	GAATTTGTGACGACACAGTTTTAATTTGTGGAGGGGAATTTTCTACTGTAAATCAACACAA	1176
Qy	1186	CTGTTTAATAGTACTTGAATGTTTACTGGAGGACAAATGGCACTGAAGGAAATGCACATA	1245
Db	1177	CTGTTTAATAGTACTTGAATGTTTACTGAAGAGTCAAAATAACACTGTAGAAAATAACACA	1236
Qy	1246	ATCACACTCCCAATGCAGATAAAACAATTAATAATATGTGGCAGAAAGTAGGAAAAGCA	1305
Db	1237	ATCACACTCCCATGCAGATAAAACAATTAATAACATGTGGCAGAAAGTAGGAAAGCA	1296
Qy	1306	ATGATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTAACAGGCTGCTA	1365
Db	1297	ATGATGCCCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTAACAGGCTGCTA	1356
Qy	1366	CTAACAGAGTAGGAGTAAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGA	1425
Db	1357	TTAAACAAGAGATGGTGG---TCCAGAGACAAACAGACCGAGGTCTTCAGACCTGGAGGA	1413
Qy	1426	GGAGATATGAGGGACAAATGGAGAGTGAATTTATATAATATAAAGTAGTAAGAAATGAA	1485
Db	1414	GGAGATATGAGGGACAAATGGAGAGTGAATTTATATAATATAAAGTAGTAAGAAATGAA	1473
Qy	1486	CCAATAGAGTAGCACCCACAGGCAAAAGAGAGAACAGTGCAGAAAGAGAAAAAGACCG	1545
Db	1474	CCATTAGAGTAGCACCCACAGGCAAAAGAGAGAGTGGTGCAGAGAGAAAAAGAGCA	1533
Qy	1546	G 1546	
Db	1534	G 1534	

RESULT 13
AY426118
LOCUS
DEFINITION HIV-1 clone BaL-4p isolate BaL from USA envelope glycoprotein (env) gene, complete cds.
ACCESSION AY426118
VERSION AY426118.1 GI:37962981
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1 (HIV-1)
REFERENCE
AUTHORS
TITLE Viruses; Retrovirus; Retroviridae; Lentivirus; Primate lentivirus group.
1 (bases 1 to 2568)
Pastore,C., Ramos,A. and Mosier,D.E.
Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching
J. Virol. 78 (14), 7565-7574 (2004)
JOURNAL
PUBMED 15220431
REFERENCE
AUTHORS
TITLE Pastore,C., Ramos,A. and Mosier,D.E.
JOURNAL Direct Submission
Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
Location/Qualifiers
1. .2568
/organism="Human immunodeficiency virus 1"
/proviral
/mol_type="genomic DNA"
/isolate="BaL"
/isolation.sources="RSX4 mutant of BaL isolated after multiple passages in CXCR4 expressing cells"

gene	
CDS	

```
/db xref="taxon:11676"
/clone="BaL-4p"
/country="USA"
1. .2568
/genes="env"
1. .2568
/genes="env"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AAR05842.1"
/db xref="GI:37962982"
translation="MRVKEKYQHLRWGRWGTMLLGMLIMCSATEKLWTVTVYGVV
WKATTTFLCASDAKAYDEVHNVWATHACVPTDPNPQVELEVENVFNFWKNNMKE
QMEDIISLDQSLKPCVLTPLCVTLNCTDLRNATNGDNTTSSREMMGGGEMKN
CSKHITNIGSKVQKALFYKLDIVPDNNSNRVRLISNTSVITQACPKIFEPI
PIHCAAPAGFAILKCKDKKENGKPGPCNSVSTQCTHGRVPSVQLLNGSLAEVV
IRSENFADNAKTIIVQLNESVEINCTPNNTNKRSHIHGPRALITTKLIGDIRQAH
CNISRAKNDTILNKIVIKLEQFNGKTIIVFKHSGSGDPEIVTHSFNGGEPFYCNSTQ
LFLNVTWTESENKTEVENPFGGDMRDNRSELYKYKVVKIPLGVATPKAKRRVQRE
LLLTRDQGPEDNKTVEPRGGDMRDNRSELYKYKVVKIPLGVATPKAKRRVQRE
KBAVGICQALFPLGAGSTMGASMTLTQVQRLLSGIVQQNNLRLAIEAQOHLLO
LTVWGIKQALQARVLAVERYLRDQQLGIWCSGSKLICTTAVPWNASHNSKLNKWDN
MTMWEDEINNTYIIISLIEESQOQEKNEQELLEDKWSLWNNFEITEWELWYIK
IFIMIIGLGLRIIVSVLSIMNRVQGYPLSFQTHLPASRGPDGPGIBEEGERD
RDRSGRLVNGSLALIWDLRLSLFVSHRLDLLIVTRIVELGLRRGEALKYWNIL
LQWYSQELKNSAVSLNATAIAVAEGTDRVIEVVQGACRAIRHPRIRIQGLERILL"
```

Query Match 61.1%; Score 1239; DB 14; Length 2568;
Best Local Similarity 90.1%; Pred. No. 1.1e-247;
Matches 1352; Conservative 0; Mismatches 140; Indels 9; Gaps 2;

Qy	52	TGGATCTCGGCTCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGCTACAGAA	111
Db	37	TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATTTGATGATCTGTAGTGCTACAGAA	96
Qy	112	AAATTGTGGGTCAACAGTCTATTATGGGGTACTCTGTGGAGAGAGAACACCACCTCTA	171
Db	97	AAATTGTGGGTCAACAGTCTATTATGGGGTACTCTGTGGAGAGAGAACACCACCTCTA	156
Qy	172	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	157	TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	216
Qy	232	GCCTGTGTACCCACAGACCCCAACCAAGTAGTAGTATTGGGAAATGTGCACAGAAAT	291
Db	217	GCCTGTGTACCCACAGACCCCAACCAAGTAGTAGTATTGGGAAATGTGCACAGAAAT	276
Qy	292	TTTAAACATGTGGAATAATAACATGTTAGATCAGATGATGAGGATATATCAGTTTATGG	351
Db	277	TTTAAACATGTGGAATAATAACATGTTAGATCAGATGATGAGGATATATCAGTTTATGG	336
Qy	352	GATGAAGCCTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTAAATGGCACT	411
Db	337	GATCAAGCCTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTAAATGGCACT	396
Qy	412	AATTGTA-----ATATCACTAAGAAATACTACTTAATCCACTAGTAGCAGCTGGGGAATG	465
Db	397	GATTGTAGGAATGCTACTAATGGGAATGACACTTAATACCTAGTAGTAGCAGGGAATG	456
Qy	466	ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATAGAATAAG	525
Db	457	ATGGGGGAGGAGAAATGAAAAATTTGCTCTTTCAAAATCACCACAACATAAGAGGTAAG	516
Qy	526	GTAAGAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT	585
Db	517	GTGCAGAAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT	576
Qy	586	AATACTAGTAGTGTAAATAGTTGTAAACACCTCAGTCATTTACACAGCCCTGTCCAAAG	645
Db	577	AATACTAGTAGTGTAAATAGTTGTAAACACCTCAGTCATTTACACAGCCCTGTCCAAAG	636
Qy	646	GTATCTTTTCAGCCAAATTTCCCATACATATTATTGTGTCCCGGTGGGTTTTGCCGATGATAAG	705

ORIGIN

Db 337 GATCAAGCGCTAAAGCCATGTGTAAATTAATCCACTCTGTGTACTTTAAATTTGCACT 396
Qy 412 AATTGTA-----ATATCACTAAGAAATACTACTAATCCACTAGTAGCAGCTGGGGAATG 465
Db 337 GATTTTGAGGAATGCTACTAATGGGAATGACACTAATACCACTAGTAGTAGCAGGGAATG 456
Qy 466 ATGGAGAAGGAGAAATAAAAAATTCCTTTCTATATCACCACAAGCATAGAATAAAG 525
Db 457 ATGGGGGAGGAGAAATGAAATTTGCTCTTTCAAAATCACCACAAACATAAGAGGTAAG 516
Qy 526 GTAAGAAGAATATGCACTTTTAAATAGACTGTAGTAGTACCAATAGAAAATACTAAT 585
Db 517 GTGCAGAAGAATATGCACTTTTATGAATCTGATATAGTACCAATAGATAAATAGT 576
Qy 586 AATACTAAGTATAGTTAATAGTTGTAACTCAGTCAGTCATTACACAGCCCTGTCCAAG 645
Db 577 AATAATAGATATAGTTGTAAGTTGTAACTCAGTCAGTCATTACACAGCCCTGTCCAAG 636
Qy 646 GTATCCTTTTCAGCCCAATTTCCCATACATTAATTTGTGTCGCGCTGGGTTTTCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCCAATTTCCCATACATTAATTTGTGTCGCGCTGGGTTTTCGATTTCAAAG 696
Qy 706 TGTAAACAATAGACATTCATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 765
Db 697 TGTAAAGATAAAGAGTTCAATGGAAAGGACCATGTTCAAAATGTCAGCACAGTACAATGT 756
Qy 766 ACACATGGAATTTAGCCAGTGTGTCACTCACTCACTGTTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTTAGCCAGTGTGTCACTCACTCACTGTTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCCGAATTTTCGCGGACATGCTTAAACCATATAGTACAG 876
Qy 886 TTAATGTAATCTGTAGTAAATTTGTGTAAGACCCCAACAATACAGGAAGAGGTTA 945
Db 877 CTGAATGAATCTGTAGAAATTAATTTGTACAGACCCCAACAATACAGGAAGAGGTTA 936
Qy 946 TCTATAGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
Db 937 CATATAGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 996
Qy 1006 GCACATTTGTAACATTTAGTAGCAAAATGGAATAACACTTTTACACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGTAACATTTAGTAGCAAAATGGAATGACACTTTTAAATAGATAGTTATAAAA 1056
Qy 1066 TTAAGAGAAAATTTAGGAATAAACAATAGCCTTTAATCAATCTCAGGAGGGAGCCCA 1125
Db 1057 TTAAGAGAACAAATTTGGGAATAAACAATAGTCTTTAAAGCATTCCTCAGGAGGGAGCCCA 1116
Qy 1126 GAAATTTGTAATGACAGTCTTTAATTTGTGAGGGGAAATTTCTTCTACTGTAAATACACAAA 1185
Db 1117 GAAATTTGTAATGACAGTCTTTAATTTGTGAGGGGAAATTTTCTCTGTAAATTTCAACAAA 1176
Qy 1186 CTGTTTAAATAGTACTTGAATCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1245
Db 1177 CTGTTTAAATAGTACTTGAATCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1236
Qy 1246 ATCACATCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305
Db 1237 ATCACATCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1296
Qy 1306 ATGTATGCGCCCTCCCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1365
Db 1297 ATGTATGCGCCCTCCCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1356
Qy 1366 CTAACAAGAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1425
Db 1357 TTAACAAGAGATGGTGG---TCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1413
Qy 1426 GGAGATATGAG 1485
Db 1414 GGAGATATGAG 1473

Qy 1486 CCAATAGGAGTAGCACCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1545
Db 1474 CCAATAGGAGTAGCACCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1533
Qy 1546 G 1546
Db 1534 G 1534

RESULT 15
AY426113
LOCUS
DEFINITION HIV-1 clone Bal-1B isolate Bal from USA envelope glycoprotein (env)
ACCESSION AY426113
VERSION AY426113.1 GI:37962971
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
VIRUSES: Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.

REFERENCE 1 (Bases 1 to 2568)
Pastore, C., Ramos, A. and Mosier, D.E.
Intrinsic Obstacles to Human Immunodeficiency Virus Type 1
Coreceptor Switching
J. Virol. 78 (14), 7565-7574 (2004)
PUBMED 15220431
REFERENCE 2 (Bases 1 to 2568)
Pastore, C., Ramos, A. and Mosier, D.E.
Direct Submission
Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
JOURNAL Location/Qualifiers
FEATURES
source
1..2568
/organism="Human immunodeficiency virus 1"
/proviral
/mol_type="genomic DNA"
/isolate="Bal"
/isolation_source="R5X4 mutant of Bal isolated after
multiple passages in CXCR4 expressing cells"
/db_xref="taxon:11676"
/clone="Bal-1B"
/country="USA"
1..2568
/gene="env"
1..2568
/gene="env"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AAR05837.1"
/db_xref="GI:37962972"
/translation="MRVKEKYQHLWRGWRNGTLLGLMIMICSTATEKLWTVVYGVVPV
WKEATTLFCASDAKAYDEVHNVWATHACVTPDPNPOEVELENTENFNMKNKNNVE
QMHEDIISLWDQSLKPCVKLPLCLVTLNCTDLRNTNGDNTNTSSRMWGGGEMKN
CSFKITTLNKGQVQKAYLKYLDIVPIDNNNNRRLISNTSVITQACPKISEPI
PIHYCAPAGPAILKCKDKFKGKPCSNVSTVQCTGIRPVVSTOLLGLABREVV
IRSENADNAKTIIVOLNESVEINCTRENNTKRSIHIGPKRKIVTTGKIIGDIRQAH
CNLSRAKNDTLINKIVIKLRFQGNKTIIVFKHSSGGDEIVTHSPNCGGEFPYCSTQ
LLFNSTWNTVEESNNTVENNTITLPCRITQIKQIIMMWKQVGRAMTAPPIRQIKCSNITG
LLNTRDGGPDNKTVEFPGGMDRDNWRSLEYKYVKVIEPLGVAPTAKRRVVORE
KRAVIGIGAVLIGFLCAAGTGAASMTLTVOARLSLGIIVQOQNNLLRAIQAQHLQ
LTVNGIKOQARVLAVERLDQOLIGIWGCGSKLICITTAVPWNASWNSKSLKNDN
MTWMBDEINNTYSIIYSLIEESONOEKNEOELLELDKWSLWNNWFEITELWYIK
IFIMIGLIGLIRIVFVSLIMNRVQSYSLSFQTHLPASRGDPRPGIIEEGGERD
RDRSGRLVNGSLALIDWDLRSCLFVYHRLDLLLIVTRIVELLGRRGWEAKLYWNVL
LQYWSQELKNSAVSLNATAVAEGTDRVIEVVGQACRAIRHPRIRQGLERILL"

ORIGIN

Query Match 61.0%; Score 1237.4; DB 14; Length 2568;
Best Local Similarity 90.0%; Pred. No. 2.4e-247; Indels 9; Gaps 2;
Matches 1351; Conservative 0; Mismatches 141;

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2028	100.0	2028	4	AAf82931	AAf82931 HIV-1 gp1
2	1972.8	97.3	2070	4	AAf82930	AAf82930 HIV-1 gp1
3	1838	90.6	2209	4	AAf82929	AAf82929 HIV-1 gp1
4	1786.4	88.1	2252	4	AAf82928	AAf82928 HIV-1 gp1
5	1453.4	71.7	2046	12	ACa63265	ACa63265 HIV-1 im
6	1453.4	71.7	2610	12	ACa63266	ACa63266 HIV-1 im
7	1447.6	71.4	2051	10	AAf56171	AAf56171 HIV trun
8	1447.6	71.4	2562	10	AAf56170	AAf56170 Human im
9	1339.4	66.0	2010	12	ACa63267	ACa63267 HIV-1 im
10	1339.4	66.0	2574	12	ACa63268	ACa63268 HIV-1 im
11	1225.4	60.4	3806	2	AAx04767	AAx04767 Env gene
12	1225.4	60.4	3807	2	AAf58551	AAf58551 Human im
13	1221.8	60.2	9540	12	ADo52562	ADo52562 Human im
14	1321.8	60.2	9540	12	ADp20074	ADp20074 Human im
15	1219	60.1	3807	2	AAg14753	AAg14753 HIV-1 BA-
16	1207.4	59.5	2553	1	AAp80949	AAp80949 HIV prote
17	1198.8	59.1	2612	12	ADJ92821	ADJ92821 Human im
18	1198.8	59.1	8896	12	ADp20082	ADp20082 Human im
19	1197.59	59.0	1512	5	AAf87100	AAf87100 HIV-1 gp1
20	1179.8	58.2	1422	12	ADp74731	ADp74731 HIV-1 iso
21	1174.2	57.9	3808	2	AAy58244	AAy58244 Insert re

PA (HAYD/) HAYDEN-LEDBETTER M S.

XX Ledbetter JA, Hayden-Ledbetter MS;

XX WPI; 2001-281790/29.

DR P-PSDB; AAB62336.

XX DNA vaccine for improving antigen-specific humoral and cellular immune

PT responses, comprising one or more antigens linked to a domain that binds

PT at least one receptor.

XX Example 1; Fig 3B; 55pp; English.

XX The invention provides a vaccine comprising one or more antigens linked

CC to a domain that binds at least one receptor to improve the antigen-

CC specific humoral and cellular immune response. The DNA vaccines induce

CC strong antigen-specific humoral and cellular immune responses. The

CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The

CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154

CC short form extracellular domain fusion protein linked by a ProhepPro

CC linker. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 2028; DB 4; Length 2028;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2028; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTGGCGGCGATGCTGTATACCTCTCAGCTGTGTAGGACTACTTCTGTTTGGATCTCG 60

DB 1 AAGCTTGGCGGCGATGCTGTATACCTCTCAGCTGTGTAGGACTACTTCTGTTTGGATCTCG 60

QY 61 GCTTCGAGATCCATGCTCTTGGGATATGATGATCTGTAGTGTCTACAGAAAAATTGTGG 120

DB 61 GCTTCGAGATCCATGCTCTTGGGATATGATGATCTGTAGTGTCTACAGAAAAATTGTGG 120

QY 121 GTCACAGTCTATTATGGGGTACCTGTGGGAGAGCAACACCACCTCTATTTTGTGCA 180

DB 121 GTCACAGTCTATTATGGGGTACCTGTGGGAGAGCAACACCACCTCTATTTTGTGCA 180

QY 181 TCAGATGCTAAGCCATGATACAGAGGTACATATGTTTGGGCGACACATGCCCTGTGTA 240

DB 181 TCAGATGCTAAGCCATGATACAGAGGTACATATGTTTGGGCGACACATGCCCTGTGTA 240

QY 241 CCCACAGACCCCAACCCACAGAGTAGTATTGGGAATGTGACAGAAAAATTAAACATG 300

DB 241 CCCACAGACCCCAACCCCAAGAGTAGTATTGGGAATGTGACAGAAAAATTAAACATG 300

QY 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAAAGC 360

DB 301 TGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAAAGC 360

QY 361 CTAAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTCACATAATTGAAT 420

DB 361 CTAAAGCCATGTGTAATAATTAAACCCACTCTGTGTACTTTTAAATTCACATAATTGAAT 420

QY 421 ATCCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAA 480

DB 421 ATCCTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAA 480

QY 481 ATAAAAAATTCCTCTTTCTATATCACCACAGCATAAGGAATAAGGTAAAGAAAGAAATAT 540

DB 481 ATAAAAAATTCCTCTTTCTATATCACCACAGCATAAGGAATAAGGTAAAGAAAGAAATAT 540

QY 541 GCACCTTTTAAATAGATCTGATGTAGTACCAATAGAAAAATCTAATAATCTAAGTATAGG 600

DB 541 GCACCTTTTAAATAGATCTGATGTAGTACCAATAGAAAAATCTAATAATCTAAGTATAGG 600

QY 601 TTAATAAGTTGTAACACCTCAGTCTATTACAGGGCTGTCCAAAGGATTCCTTTACGCCA 660

DB 601 TTAATAAGTTGTAACACCTCAGTCTATTACAGGGCTGTCCAAAGGATTCCTTTACGCCA 660

QY 661 ATTCCTCATACATATTGTGTCGCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA 720

DB 661 ATTCCTCATACATATTGTGTCGCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA 720

QY 721 TTCAATGGATCAGGACCATGCAAAATGTGACGACAGTACAAATGTACACATGGAAATTAGG 780

DB 721 TTCAATGGATCAGGACCATGCAAAATGTGACGACAGTACAAATGTACACATGGAAATTAGG 780

QY 781 CCAGTGTGTCAACTCACTGCTTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATT 840

DB 781 CCAGTGTGTCAACTCACTGCTTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATT 840

QY 841 AGATCTGAAAAATTTTACAGACAAATGCTAAAAACCAATAATAGTACAGTAAATGAATCTGTA 900

DB 841 AGATCTGAAAAATTTTACAGACAAATGCTAAAAACCAATAATAGTACAGTAAATGAATCTGTA 900

QY 901 GTAATTAATTGTAACAAGCCCAACAAACAAATACAGAGAGAGGTTTATCTATAGGACGAGG 960

DB 901 GTAATTAATTGTAACAAGCCCAACAAACAAATACAGAGAGAGGTTTATCTATAGGACGAGG 960

QY 961 AGAGCATTTTATGCAAGAGAAACATATAGGAGATATAAGACAAGCACATTTGTAAACATT 1020

DB 961 AGAGCATTTTATGCAAGAGAAACATATAGGAGATATAAGACAAGCACATTTGTAAACATT 1020

QY 1021 AGTAGACAAAATGGAATAACACTTTTCAACACAGATAGTTATAAAAATTAAAGAGAAAAATTT 1080

DB 1021 AGTAGACAAAATGGAATAACACTTTTCAACACAGATAGTTATAAAAATTAAAGAGAAAAATTT 1080

QY 1081 AGGAATAAAAACAATAGCCTTTAATCAATCTCAGAGGGGACCCAGAAAATTTGTAATGCAC 1140

DB 1081 AGGAATAAAAACAATAGCCTTTAATCAATCTCAGAGGGGACCCAGAAAATTTGTAATGCAC 1140

QY 1141 AGTTTAAATTCGTGGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACT 1200

DB 1141 AGTTTAAATTCGTGGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACT 1200

QY 1201 TGGGAATGTTACTGGAGGACAAATGGCACTCAAGGAAATGCATAATCACACTCCAATGC 1260

DB 1201 TGGGAATGTTACTGGAGGACAAATGGCACTCAAGGAAATGCATAATCACACTCCAATGC 1260

QY 1261 AGAATAAAAACAATTAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCC 1320

DB 1261 AGAATAAAAACAATTAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCC 1320

QY 1321 ATACAGACAAAATTAGATGTTTCAATATTTACAGGGCTGCTACTAAACAGAGATGGA 1380

DB 1321 ATACAGACAAAATTAGATGTTTCAATATTTACAGGGCTGCTACTAAACAGAGATGGA 1380

QY 1381 GGTAAATAGTACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGAC 1440

DB 1381 GGTAAATAGTACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATGAGGAC 1440

QY 1441 AATTGGAGAAAGTAAATTAATAATATAAGTAGTAAGAAATGAACCAATAGGAGTAGCA 1500

DB 1441 AATTGGAGAAAGTAAATTAATAATATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCA 1500

QY 1501 CCCACCGGGCAAGAGAGAAACAGTGCAGAGAAAAAGACCGGATCCAGAAAAACAGC 1560

DB 1501 CCCACCGGGCAAGAGAGAAACAGTGCAGAGAAAAAGACCGGATCCAGAAAAACAGC 1560

QY 1561 TTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGTATAGTGAGGCC 1620

DB 1561 TTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGTATAGTGAGGCC 1620

QY 1621 AGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1680

DB 1621 AGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACACCATGAGCAAC 1680

QY 1681 AACTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTAT 1740

DB 1681 AACTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTTAAAGACAAGGACTCTATTAT 1740

QY 1741 ATCTATGCCCAAGTCAACCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTATA 1800

Db 1741 ATCTATGCCCAAGTCACCTTCTGTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTATTA 1800
Qy 1801 GCCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTCAAAAT 1860
Db 1801 GCCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACTCAGAGCTCAAAAT 1860
Qy 1861 ACCGACAGTTCGGCCAAACCTTGGCGGGGCAAAATCAATTCATCTTGGGAGGAGTATTGAA 1920
Db 1861 ACCGACAGTTCGGCCAAACCTTGGCGGGGCAAAATCAATTCATCTTGGGAGGAGTATTGAA 1920
Qy 1921 TTGCAACAGAGTCTCGTGTCTTCTCAATGTGACTGATCCAAAGCCAAGTGAAGCCATGCG 1980
Db 1921 TTGCAACAGAGTCTCGTGTCTTCTCAATGTGACTGATCCAAAGCCAAGTGAAGCCATGCG 1980
Qy 1981 ACTGGCTTCACGCTCTTTGGCTTACTCAAACTCGAGTGATATCTAGA 2028
Db 1981 ACTGGCTTCACGCTCTTTGGCTTACTCAAACTCGAGTGATATCTAGA 2028

RESULT 2
ID AAF82930
XX AAF82930 standard; cDNA; 2070 BP.
XX AAF82930;
AC AAF82930;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..2070
FT /tag= a
FT sig_peptide 13..72
FT /tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1593
FT /tag= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 1594..2070
FT /tag= e
FT /note= "human CD154 short form extracellular domain coding sequence"

XX WO200126608-A2.
PN 19-APR-2001.
XX 13-OCT-2000; 2000WO-US028414.
XX 14-OCT-1999; 99US-0159690P.
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
PI Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62335.
XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.

XX Example 1; Fig 3B; 55pp; English.
XX The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC short form extracellular domain fusion protein linked by (Gly4Ser)3
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;
Query Match 97.3%; Score 1972.8; DB 4; Length 2070;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2026; Conservative 0; Mismatches 2; Indels 42; Gaps 1;
Qy 1 AAGCTTGGCGGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCCATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGG 120
Db 61 GCTTCGAGATCTATGCTCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGTGG 120
Qy 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCCACCTCTATTTTGTGCA 180
Db 121 GTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCCACCTCTATTTTGTGCA 180
Qy 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTTGGGCCACACATGCTGTGTA 240
Db 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTTGGGCCACACATGCTGTGTA 240
Qy 241 CCCACAGACCCCAACCCACCAAGAGTACTATTGGGAATGTGACAGAAAAATTAAACATG 300
Db 241 CCCACAGACCCCAACCCCAAGAGTACTATTGGGAATGTGACAGAAAAATTAAACATG 300
Qy 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Db 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC 360
Qy 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATGTCATTAATTGAT 420
Db 361 CTAAAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATGTCATTAATTGAT 420
Qy 421 ATCACTAAGATATCTACTTAATCCCACTAGTACGCTGCGGAATCATGGAGAAAGAGAA 480
Db 421 ATCACTAAGATATCTACTTAATCCCACTAGTACGCTGCGGAATCATGGAGAAAGAGAA 480
Qy 481 ATAAAAAATTGCTCTTCTTATATCAACCAAGCATAAGAAATTAAGTAAAGAAAGATAT 540
Db 481 ATAAAAAATTGCTCTTCTTATATCAACCAAGCATAAGAAATTAAGTAAAGAAAGATAT 540
Qy 541 GCACCTTTTAAATAGACTTTGATGATCAATATAGAAAAATCTAATAATCTAAGTATAGG 600
Db 541 GCACCTTTTAAATAGACTTTGATGATCAATATAGAAAAATCTAATAATCTAAGTATAGG 600
Qy 601 TTAATAGTTCTACACCTCAGTCAATACAGGCTCTCCAAAGGATCCTTTTCAGCCA 660
Db 601 TTAATAGTTCTACACCTCAGTCAATACAGGCTCTCCAAAGGATCCTTTTCAGCCA 660
Qy 661 ATTCACATACATTATTGTGTCCTGGCTGGGTTTGGGATGCTAAAGTAAACAATAGACA 720
Db 661 ATTCACATACATTATTGTGTCCTGGCTGGGTTTGGGATGCTAAAGTAAACAATAGACA 720
Qy 721 TTCAATGGATCAGGACCATGCAAAATCTCAGCACAGTACATGATGACATGGAATTAGG 780
Db 721 TTCAATGGATCAGGACCATGCAAAATCTCAGCACAGTACATGATGACATGGAATTAGG 780
Qy 781 CCAGTGGTCTCACTCACTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT 840
Db 781 CCAGTGGTCTCACTCACTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT 840

```
QY 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATAGTAGACAGCTAAATGAATCTCTGA 900
Db 841 AGATCTGAAAAATTTTCACAGACAATGCTAAAAACCATATAGTAGACAGCTAAATGAATCTCTGA 900
QY 901 GTAATTAATTTGTACAAGACCCCAACAACCAATACAAGAAGAAGTTATCTATAGGACCCAGGG 960
Db 901 GTAATTAATTTGTACAAGACCCCAACAACCAATACAAGAAGAAGTTATCTATAGGACCCAGGG 960
QY 961 AGAGCATTTTATGCAAGAGAAAAACAATAATAGGAGATATAAGACAAGCACTTGTAAACATT 1020
Db 961 AGAGCATTTTATGCAAGAGAAAAACAATAATAGGAGATATAAGACAAGCACTTGTAAACATT 1020
QY 1021 AGTAGAGCAAAATGCAATTAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAAATTT 1080
Db 1021 AGTAGAGCAAAATGCAATTAACACTTTTACAACAGATAGTTATAAAATTAAGAGAAAAAATTT 1080
QY 1081 AGGAATAAAAAAATAGACCTTTTAATCAATCCTCAGAGGGGACCCAGAAAATTTGTAATGCAC 1140
Db 1081 AGGAATAAAAAAATAGACCTTTTAATCAATCCTCAGAGGGGACCCAGAAAATTTGTAATGCAC 1140
QY 1141 AGTTTTAATTTGTGGAGGGGAATTTCTTCTACTGTAATACAGACAACCTGTTTAATAGTACT 1200
Db 1141 AGTTTTAATTTGTGGAGGGGAATTTCTTCTACTGTAATACAGACAACCTGTTTAATAGTACT 1200
QY 1201 TGGATGTTACTGGAGGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGC 1260
Db 1201 TGGATGTTACTGGAGGGACAAATGGCACTGAAGGAATGACATAATCACACTCCAATGC 1260
QY 1261 AGAATAAAAAAATTAATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320
Db 1261 AGAATAAAAAAATTAATAATATGTGGCAGAAAAGTAGGAAAAGCAATGTATGCCCTCCC 1320
QY 1321 ATCAGAGACAATAATAGATGTTTCATAAATATTACAGGGCTGCTACTAACAGAGATGGA 1380
Db 1321 ATCAGAGACAATAATAGATGTTTCATAAATATTACAGGGCTGCTACTAACAGAGATGGA 1380
QY 1381 GGTATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC 1440
Db 1381 GGTATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGATATAGGGAC 1440
QY 1441 AATTGGAGAAGTGAATTTATAAATATAAAGTAGTAAGAATTTGAACCAATAGGAGTAGCA 1500
Db 1441 AATTGGAGAAGTGAATTTATAAATATAAAGTAGTAAGAATTTGAACCAATAGGAGTAGCA 1500
QY 1501 CCCACAGGGCAAGAGAAGAACAGTGCACAGAGAAAAA----- 1540
Db 1501 CCCACAGGGCAAGAGAAGAACAGTGCACAGAGAAAAA----- 1540
QY 1541 -----GACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGT 1578
Db 1541 -----GACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGT 1578
QY 1579 GATCAGAATCTCTCAAATTCGGGCACATGTCTAAAGTGAGGGCAGCAGTAACCAACATCT 1638
Db 1579 GATCAGAATCTCTCAAATTCGGGCACATGTCTAAAGTGAGGGCAGCAGTAACCAACATCT 1638
QY 1639 GTGTTACAGTGGCTGAAAAAGGATACCTACCATGAGCAACAATTGGTAACCCCTGAA 1698
Db 1639 GTGTTACAGTGGCTGAAAAAGGATACCTACCATGAGCAACAATTGGTAACCCCTGAA 1698
QY 1699 AATGGGAACAGCTGACCGTTAAAGACAAAGGACTTATTATCTATGCCCCAGTCAACC 1758
Db 1699 AATGGGAACAGCTGACCGTTAAAGACAAAGGACTTATTATCTATGCCCCAGTCAACC 1758
QY 1741 AATGGGAACAGCTGACCGTTAAAGACAAAGGACTTATTATCTATGCCCCAGTCAACC 1800
Db 1741 AATGGGAACAGCTGACCGTTAAAGACAAAGGACTTATTATCTATGCCCCAGTCAACC 1800
QY 1759 TTCTGTTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAG 1818
Db 1759 TTCTGTTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAG 1818
QY 1801 TTCTGTTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAG 1860
Db 1801 TTCTGTTTCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAG 1860
QY 1819 TCCCCCGGTAGATTTCAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAA 1878
Db 1819 TCCCCCGGTAGATTTCAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAA 1878
QY 1861 TCCCCCGGTAGATTTCAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAA 1920
Db 1861 TCCCCCGGTAGATTTCAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAA 1920
```

```
QY 1879 CTTTGGGGCAACAATCCATTCACTTGGAGGAGTATTGAATTGCAACACAGGTCTTCG 1938
Db 1879 CTTTGGGGCAACAATCCATTCACTTGGAGGAGTATTGAATTGCAACACAGGTCTTCG 1938
QY 1939 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAAGCCATGGCCTTACAGTCCCTTT 1998
Db 1939 GTGTTTGTCAATGTGACTGATCCAAAGCCAAAGTGAAGCCATGGCCTTACAGTCCCTTT 1998
QY 1999 GGCTTACTCAAACTCGAGTGATTAATCTAGA 2028
Db 1999 GGCTTACTCAAACTCGAGTGATTAATCTAGA 2028
QY 2041 GGCTTACTCAAACTCGAGTGATTAATCTAGA 2070
Db 2041 GGCTTACTCAAACTCGAGTGATTAATCTAGA 2070

RESULT 3
AAF82929 standard; cDNA; 2209 BP.
XX AAF82929;
AC AC
XX AC
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX DT
DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
XX DE
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX KW
OS Human immunodeficiency virus 1.
XX OS
PH Homo sapiens.
XX PH
FT Key Location/Qualifiers
FT CDS 13..2209
FT sig_peptide /tag= a
FT /tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1551
FT /tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 1552..2209
FT /tag= e
FT /note= "human CD154 long form extracellular domain coding
sequence"
XX FT
XX FT
XX FT
XX WO200126608-A2.
XX PN
XX 19-APR-2001.
XX PD
XX 13-OCT-2000; 2000WO-US028414.
XX PF
XX 14-OCT-1999; 99US-0159690P.
XX PR
XX (LEDB/) LEDBETTER J A.
XX PA (HAYD/) HAYDEN-LEDBETTER M S.
XX PI Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
XX DR P-PSDB; AAB62334.
XX PT DNA vaccine for improving antigen-specific humoral and cellular immune
responses, comprising one or more antigens linked to a domain that binds
at least one receptor.
XX PT
XX Example 1; Fig 3A; 55pp; English.
XX PS
XX The invention provides a vaccine comprising one or more antigens linked
to a domain that binds at least one receptor to improve the antigen-
specific humoral and cellular immune response. The DNA vaccines induce
CC CC
```


CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be use against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC long form extracellular domain fusion protein linked by a ProAspPro
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;

Query Match 90.6%; Score 1838; DB 4; Length 2209;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 2028; Conservative 0; Mismatches 0; Indels 180; Gaps 1;

Qy	1	AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG	60
Db	1	AAGCTTGGCCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTGTTTGGATCTCG	60
Qy	61	GCTTCGAGATCAATGCTCTCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGGG	120
Db	61	GCTTCGAGATCAATGCTCTCTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTGGG	120
Qy	121	GTACAGTCTATTATTTGGGTCCTGTGTGGAGAGCAACCACTCTATTTTTGCA	180
Db	121	GTACAGTCTATTATTTGGGTCCTGTGTGGAGAGCAACCACTCTATTTTTGCA	180
Qy	181	TCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTA	240
Db	181	TCAGATGCTAAAGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGTA	240
Qy	241	CCACAGACCCCAACCCCAAGAGTGTATTGGGAAATGTGACAGAAAAATTTTAAACATG	300
Db	241	CCACAGACCCCAACCCCAAGAGTGTATTGGGAAATGTGACAGAAAAATTTTAAACATG	300
Qy	301	TGGAAAAATAACATGGTGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC	360
Db	301	TGGAAAAATAACATGGTGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGC	360
Qy	361	CTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTTAAATGTCATTTTGAAT	420
Db	361	CTAAAGCCATGTGTAATAATTAACCCACTCTGTGTACTTTTAAATGTCATTTTGAAT	420
Qy	421	ATCCTAAGAAATPACTACTTAATCCCACTAGTACAGCTGGGAAATGATGAGAAAGAGAA	480
Db	421	ATCCTAAGAAATPACTACTTAATCCCACTAGTACAGCTGGGAAATGATGAGAAAGAGAA	480
Qy	481	ATAAAAAATTTGCTTCTTCTATATACCACATAGAAATAAGTTAAAGAAAGATAT	540
Db	481	ATAAAAAATTTGCTTCTTCTATATACCACATAGAAATAAGTTAAAGAAAGATAT	540
Qy	541	GCACCTTTTATAGACTGTAGTACCAATAGAAAAATACATAATACTAAAGTATAGG	600
Db	541	GCACCTTTTATAGACTGTAGTACCAATAGAAAAATACATAATACTAAAGTATAGG	600
Qy	601	TTAATAAGTGTAAACACCTCAGTCAATACAGAGGCTGTCCAAAGGATCCTTTTCAGCCA	660
Db	601	TTAATAAGTGTAAACACCTCAGTCAATACAGAGGCTGTCCAAAGGATCCTTTTCAGCCA	660
Qy	661	ATTCCCATACATTAATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA	720
Db	661	ATTCCCATACATTAATTGTGTCCCGCTGGGTTTGGGATGCTAAAGTGTAAACAATAAGACA	720
Qy	721	TTCATATGATCAGGACCAATGTGCAAAATGTACAGCAAGTACAAATGTACATGGAATTAGG	780
Db	721	TTCATATGATCAGGACCAATGTGCAAAATGTACAGCAAGTACAAATGTACATGGAATTAGG	780
Qy	781	CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT	840
Db	781	CCAGTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGACATAGTAATT	840
Qy	841	AGATCTGAAAAATTTTACAGACAAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTA	900
Db	841	AGATCTGAAAAATTTTACAGACAAATGCTAAAAACATAATAGTACAGCTAAATGAATCTGTA	900
Qy	901	GTAATTAATTGTACAAAGCCCAACCAATACAAAGAAAGGTTATCTATAGGACCGGG	960

Db	901	GTAATTAATTGTACAAAGCCCAACCAATACAAAGAAAGGTTATCTATAGGACCGGG	960
Qy	961	AGAGCATTTTATGCAAGAAAGAAACATATAGGAGATATAAGACAAGCACATTTGTAACTTT	1020
Db	961	AGAGCATTTTATGCAAGAAAGAAACATATAGGAGATATAAGACAAGCACATTTGTAACTTT	1020
Qy	1021	AGTGAGCAAAATGGAATAACACTTTTCAACAGATAGTTATATAAATTAAAGAGAAAAATTT	1080
Db	1021	AGTGAGCAAAATGGAATAACACTTTTCAACAGATAGTTATATAAATTAAAGAGAAAAATTT	1080
Qy	1081	AGGATATAAACAATAGCCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCAC	1140
Db	1081	AGGATATAAACAATAGCCCTTTAATCAATCCTCAGAGGGGACCCAGAAATTTGTAATGCAC	1140
Qy	1141	AGTTTAAATTTGAGAGGGGAAATTTCTTCTACTGTATACAGCACAACTGTTTAAATAGTACT	1200
Db	1141	AGTTTAAATTTGAGAGGGGAAATTTCTTCTACTGTATACAGCACAACTGTTTAAATAGTACT	1200
Qy	1201	TGGAATGTTACTGAGAGGACAAATGGCACTGGAAGAAATGACATAATCACACTCCAATGC	1260
Db	1201	TGGAATGTTACTGAGAGGACAAATGGCACTGGAAGAAATGACATAATCACACTCCAATGC	1260
Qy	1261	AGATATAAACAATTTATAAATATGTGSCAGAAAGTAGGAAAGCAATCTATGCCCTCCC	1320
Db	1261	AGATATAAACAATTTATAAATATGTGSCAGAAAGTAGGAAAGCAATCTATGCCCTCCC	1320
Qy	1321	ATCAGAGACAAATTTAGATGTTTCAATATTTACAGGGCTGCTACTAACAGAGATGGA	1380
Db	1321	ATCAGAGACAAATTTAGATGTTTCAATATTTACAGGGCTGCTACTAACAGAGATGGA	1380
Qy	1381	GGTAAATAGTACTGAGACTGAGATCTTTCAGACCTTGGAGGAGGAGATATGAGGAC	1440
Db	1381	GGTAAATAGTACTGAGACTGAGATCTTTCAGACCTTGGAGGAGGAGATATGAGGAC	1440
Qy	1441	AAATGGGAACTGAAATTTATATAAATATTAAGTGTAGAAATTTGAACCAATAGGAGTAGCA	1500
Db	1441	AAATGGGAACTGAAATTTATATAAATATTAAGTGTAGAAATTTGAACCAATAGGAGTAGCA	1500
Qy	1501	CCCAAGGACAAAGAGAGAAAGCAAGTCAAAAGAGAAAAAGACCGGATCC	1550
Db	1501	CCCAAGGACAAAGAGAGAAAGCAAGTCAAAAGAGAAAAAGACCGGATCCCAAGAGGTTG	1550
Qy	1551	-----	1550
Db	1551	-----	1550
Qy	1561	GACAAGATAGAAAGTGAAGGAATCTTTCATGAAGATTTTGTATTTCATGAAGAAACGATACAG	1620
Db	1561	GACAAGATAGAAAGTGAAGGAATCTTTCATGAAGATTTTGTATTTCATGAAGAAACGATACAG	1620
Qy	1551	-----	1550
Db	1551	-----	1550
Qy	1621	AGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGAGATTAAAGCCAG	1680
Db	1621	AGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGAGATTAAAGCCAG	1680
Qy	1551	-----	1550
Db	1551	-----	1550
Qy	1681	TTTGAAGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAAAGAAACAGC	1740
Db	1681	TTTGAAGCTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAAAGAAACAGC	1740
Qy	1561	TTTGAATGCAAAAGAGTGTAGTACAGAACTCTCAAAATTTGGGACACATGTCTAAGTGAGGCC	1620
Db	1741	TTTGAATGCAAAAGAGTGTAGTACAGAACTCTCAAAATTTGGGACACATGTCTAAGTGAGGCC	1800
Qy	1621	AGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATCTACCATGAGCAAC	1680
Db	1801	AGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATCTACCATGAGCAAC	1860
Qy	1681	AACCTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTTAAAGACAAAGGACTCTATTAT	1740
Db	1861	AACCTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTTAAAGACAAAGGACTCTATTAT	1920
Qy	1741	ATCTATGCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCAGGTCAAGCTCCATTTATA	1800
Db	1921	ATCTATGCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCAGGTCAAGCTCCATTTATA	1980
Qy	1801	GCACGCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAAATCTTACTCAGAGCTCAAT	1860
Db	1801	GCACGCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAAATCTTACTCAGAGCTCAAT	1860

Db 1981 GCCAGCTCTGCTAAAGTCCCGGTAGATTGCGAGAGAATCTTACTCAGAGCTGCAAAAT 2040
Qy 1861 ACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAA 1920
Db 2041 ACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAGGAGTATTTGAA 2100
Qy 1921 TTGCAACAGAGTGCTTCGGTGTGTTGCTCAATGTGACTGATCCAAGCCAAGTCAGGCCATGGC 1980
Db 2101 TTGCAACAGAGTGCTTCGGTGTGTTGCTCAATGTGACTGATCCAAGCCAAGTCAGGCCATGGC 2160
Qy 1981 ACTGCTTTCAGTCTCTTTGGCTTACTCAAACTCGAGTGAATAATCTAGA 2028
Db 2161 ACTGCTTTCAGTCTCTTTGGCTTACTCAAACTCGAGTGAATAATCTAGA 2208

RESULT 4
AAF82928
ID AAF82928 standard; cDNA; 2252 BP.
XX AC AAF82928;
XX DT 11-SEP-2003 (revised)
XX DT 29-JUN-2001 (first entry)
XX DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
XX KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX OS Homo immunodeficiency virus 1.
OS Homo sapiens.
XX FH Key
FH CDS Location/Qualifiers
FT sig_peptide /tag= a
FT sig_peptide /tag= b
FT misc_feature /note= "synthetic secretory signal peptide"
FT misc_feature /tag= c
FT misc_feature /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature /tag= d
FT misc_feature /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature /tag= e
FT misc_feature /note= "human CD154 long form extracellular domain coding sequence"

PN WO200126608-A2.
XX PD 19-APR-2001.
XX PF 13-OCT-2000; 2000WO-US028414.
XX PR 14-OCT-1999; 99US-0159690P.
XX PA (LEDB/) LEDBETTER J A.
XX PA (HAYD/) HAYDEN-LEDBETTER M S.
XX PI Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
XX DR P-PSDB; AAB62333.
XX PT DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX Example 1; Fig 3A; 55pp; English.
XX PS The invention provides a vaccine comprising one or more antigens linked
XX CC

CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC long form extracellular domain fusion protein linked by (Gly4Ser)³
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;
Query Match 88.1%; Score 1786.4; DB 4; Length 2252;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 6; Indels 222; Gaps 1;
Qy 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGG 120
Db 61 GCTTCGAGATCTATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTTGGG 120
Qy 121 GTCAAGTCTATTATGGGGTACCTGTGTGAGAGAGCAACACCACTCTATTTTGTGCA 180
Db 121 GTCAAGTCTATTATGGGGTACCTGTGTGAGAGAGCAACACCACTCTATTTTGTGCA 180
Qy 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTGGCCACACATGCTGTCTGTA 240
Db 181 TCAGATGCTAAAGCCTATGATACAGAGTACATATGTTGGCCACACATGCTGTCTGTA 240
Qy 241 CCCACAGACCCCAACCCACAGAGTAGTATTGGGAATGTGACAGAAAAATTTAAACATG 300
Db 241 CCCACAGACCCCAACCCACAGAGTAGTATTGGGAATGTGACAGAAAAATTTAAACATG 300
Qy 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAAAGC 360
Db 301 TGGAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGATGAAAGC 360
Qy 361 CTAAGCCATGCTGTAATAATTAACCCCTCTGTTTAAATTTGACCTAAATTTGAAT 420
Db 361 CTAAGCCATGCTGTAATAATTAACCCCTCTGTTTAAATTTGACCTAAATTTGAAT 420
Qy 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGAGAA 480
Db 421 ATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGAATGATGGAGAAAGAGAA 480
Qy 481 ATAAAAAATGCTCTTTCTATATCAACAAGCATATAAGAAATAGGTAAAGAAAGAAATAT 540
Db 481 ATAAAAAATGCTCTTTCTATATCAACAAGCATATAAGAAATAGGTAAAGAAAGAAATAT 540
Qy 541 GCACCTTTTAATAGACTTGTAGTACCAATAGAAAATCTAATAATCTAAAGTATAGG 600
Db 541 GCACCTTTTAATAGACTTGTAGTACCAATAGAAAATCTAATAATCTAAAGTATAGG 600
Qy 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGATCTCTTTTCAGCCA 660
Db 601 TTAATAAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGATCTCTTTTCAGCCA 660
Qy 661 ATTCCCATACATTAATGTGTCCTGGGTTGGGATGCTAAAGTGTAAACAATTAAGACA 720
Db 661 ATTCCCATACATTAATGTGTCCTGGGTTGGGATGCTAAAGTGTAAACAATTAAGACA 720
Qy 721 TTCATGGATCAGGACCATGACAAATGTCAGCAGTACATGATGATGATGATGATGATGAT 780
Db 721 TTCATGGATCAGGACCATGACAAATGTCAGCAGTACATGATGATGATGATGATGATGAT 780
Qy 781 CCAGTGGTGTCAACTCTGCTTAAATGGCAGTCTAGCAGAGAAAGACATAGTAATT 840
Db 781 CCAGTGGTGTCAACTCTGCTTAAATGGCAGTCTAGCAGAGAAAGACATAGTAATT 840
Qy 841 AGATCTGAAAAATTTTCACAGACAATGCTGCTAAATGGCAGTCTAGCAGTAAATGAAATCTGTA 900
Db 841 AGATCTGAAAAATTTTCACAGACAATGCTGCTAAATGGCAGTCTAGCAGTAAATGAAATCTGTA 900

Db 37 TGGGGTGGAGATGGGGACCATGCTCTTGGGATGTTGATGATCTGTAGTGTACAGAA 96
Qy 112 AAAATTGTGGGTACACAGTCTATTATGGGGTGAAGTGTGGGAGAGAGAACACCACTCTTA 171
Db 97 AAAATTGTGGGTACACAGTCTATTATGGGGTGAAGTGTGGGAGAGAGAACACCACTCTTA 156
Qy 172 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 231
Db 157 TTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT 216
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db 217 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 276
Qy 292 TTTAACATGTGGAAAAATAAATGATGGTAGATCAGATGATGATGATGATGATGATGATG 351
Db 277 TTTAACATGTGGAAAAATAAATGATGGTAGATCAGATGATGATGATGATGATGATGATG 336
Qy 352 GATGAAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 411
Db 337 GATGAAAGCCTAAAGCCATGTGTAATTAACCCCACTCTGTGTACTTTTAAATTTGCACT 396
Qy 412 AATTGTGAATATCACTAAGAAATCTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAG 471
Db 397 AATTGTGAATATCACTAAGAAATCTACTAATCTCACTAGTAGCAGCTGGGGAAATGATGGAG 456
Qy 472 AAAGAGAAATAAAAAATTTGCTCTTTCTATATCAACCAAGCAGATGATGATGATGATGATG 531
Db 457 GAAGAGAAATAAAAAATTTGCTCTTTCTATATCAACCAAGCAGATGATGATGATGATGATG 516
Qy 532 AARGAATGACATCTTTTAAATAGACTGATGATGATGATGATGATGATGATGATGATGATG 591
Db 517 AARGAATGACATCTTTTAAATAGACTGATGATGATGATGATGATGATGATGATGATGATG 576
Qy 592 AAGTATAGTTTAAATAGTTTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCC 651
Db 577 AAGTATAGTTTAAATAGTTTAAACACCTCAGTCAATACACAGGCTGTCCAAAGGTATCC 636
Qy 652 TTTACGCAATTTCCCAATATTTGTTGTCGGCTGGGTTTGGGATGCTAAAGTGTAAAC 711
Db 637 TTTACGCAATTTCCCAATATTTGTTGTCGGCTGGGTTTGGGATGCTAAAGTGTAAAC 696
Qy 712 AATAGACATTTCAATGGATCAGGACCATGCAACAAATGTCAGACAGTACATGATGACAT 771
Db 697 AATAGACATTTCAATGGATCAGGACCATGCAACAAATGTCAGACAGTACATGATGACAT 756
Qy 772 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTGTAAATGGCAGTCTAGCAGAGAAGAC 831
Db 757 GGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTGTAAATGGCAGTCTAGCAGAGAAGAC 816
Qy 832 ATAGTAATTAGATCTGAAAAATTTCAAGACAAATGCTAAACCATATAGTACAGCTAAAT 891
Db 817 ATAGTAATTAGATCTGAAAAATTTCAAGACAAATGCTAAACCATATAGTACAGCTAAAT 876
Qy 892 GAATCTGTAGTAATTAATTTGACAGACCCCAACCAATACAGAGAGCTTATCTATA 951
Db 877 GAATCTGTAGTAATTAATTTGACAGACCCCAACCAATACAGAGAGCTTATCTATA 936
Qy 952 GGACCAAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAGCAACAGCAGAT 1011
Db 937 GGACCAAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAGCAACAGCAGAT 996
Qy 1012 TGTAACATTTAGTAGCAAAAATGGAATAACACTTTTACACAGATAGTTTAAATTAAGA 1071
Db 997 TGTAACATTTAGTAGCAAAAATGGAATAACACTTTTACACAGATAGTTTAAATTAAGA 1056
Qy 1072 GAAAAATTTAGGAATAAACAATACCTTTTAAATCAATCTCAGGAGGGGACCCAGAAAT 1131
Db 1057 GAAAAATTTAGGAATAAACAATACCTTTTAAATCAATCTCAGGAGGGGACCCAGAAAT 1116
Qy 1132 GTAATGCAAGTTTTAAATTTGGAGGGGAATTTCTTACTGTGTAATACAGCAACATGTTT 1191

Db 1117 GTAATGCAAGTTTTAAATTTGGAGGGGAATTTTCTACTGTAAATACAGCAACACTGTTT 1176
Qy 1192 AATAGTACTTTGGATGTTTACTTGGAGGACAAATGGCACTGAAGAAATGACATATACACA 1251
Db 1177 AATAGTACTTTGGATGTTTCTTGGAGGACAAATGGCACTGAAGAAATGACATATACACA 1236
Qy 1252 CTCCAATGCGAGATATAAAATTAATATATGTCGAGAGAAAGTAGGAAAAGCAATGTAT 1311
Db 1237 CTCCAATGCGAGATATAAAATTAATATATGTCGAGAGAAAGTAGGAAAAGCAATGTAT 1296
Qy 1312 GCGCTCTCCATCAGACAGCAAAATAGATGTTTCATCAAAATATACAGGCTCTCTACTACA 1371
Db 1297 GCGCTCTCCATCAGACAGCAAAATAGATGTTTCATCAAAATATACAGGCTCTCTACTACA 1356
Qy 1372 AGAGATCGAGGTATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1431
Db 1357 AGAGATCGAGGTATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGGAGAT 1416
Qy 1432 ATGAGGACCAATTTGGAGAGTGAATTTATATAAATATAAAGTAGTAAGAATTTGAACCAATA 1491
Db 1417 ATGAGGACCAATTTGGAGAGTGAATTTATATAAATATAAAGTAGTAAGAATTTGAACCAATA 1476
Qy 1492 GGAGTAGCACCCACAGGCGAAAGAGAGAACACAGTGCAGAGAGAGAGAGAGAGAGAGAG 1546
Db 1477 GGAGTAGCACCCACAGGCGAAAGAGAGAACACAGTGCAGAGAGAGAGAGAGAGAGAGAG 1531

RESULT 6
ACA63266
ID ACA63266 standard; DNA; 2610 BP.
XX ACA63266;
XX ACA63266;
DT 22-APR-2004 (first entry)
XX HIV-1 immunogenic sequence #2.
DE Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;
KW immunogenic; virucide; ds.
XX Human immunodeficiency virus type 1.
OS WO2004001051-A2.
PN 31-DEC-2003.
PD 20-JUN-2003; 2003WO-EP007146.
PF 20-JUN-2002; 2002EP-00291550.
PR (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
XX Tangy F, Lorin C, Mollet L, Delebecque F;
XX WPI; 2004-082508/08.
DR New recombinant mononegavirales measles virus expressing a heterologous
XX amino acid, useful for preparing immunogenic or vaccine composition for
PT the prophylaxis or treatment of measles.
PT Disclosure; Fig 16C; Opp; English.
XX The present invention relates to a recombinant mononegavirales measles
CC virus expressing a heterologous amino acid, which is capable of eliciting
CC a humoral and/or cellular immune response against the heterologous amino
CC acid sequence including in individuals having pre-existing measles virus
CC immunity. The recombinant virus is useful for preparing immunogenic or
CC vaccine composition for the prophylaxis or treatment of measles. The
CC present sequence is a HIV immunogenic sequence shown in the
CC exemplification of the invention
XX Sequence 2610 BP; 885 A; 442 C; 643 G; 640 T; 0 U; 0 Other;
SQ

Query Match			
Best Local Similarity 98.3%; Pred. No. 3.8e-286;			
Matches 1469; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
QY	52	TGGATCTCGGCTTCAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAA	111
Db	37	TGGGGGTGGAGATGGGGCACCATGCTCTTGGGATGTTGATGATCTGTAGTGTACAGAA	96
QY	112	AAATTTGGGGTACACAGTCTATTATATGGGGTACCTGTGTGGAGAGAGCAACACCACTCTA	171
Db	97	AAATTTGGGGTACACAGTCTATTATATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA	156
QY	172	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	231
Db	157	TTTTTGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACAT	216
QY	232	GCCTGTGTACCCACAGAGCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAT	291
Db	217	GCCTGTGTACCCACAGAGCCCAACCCACAAGAAGTAGTATTGGGAAATGTGACAGAAAAT	276
QY	292	TTTAACTGTGGAAAAATAAATGCTAGATCAGATGCATGAGGATATATCAAGTTTATGG	351
Db	277	TTTAACTGTGGAAAAATAAATGCTAGATCAGATGCATGAGGATATATCAAGTTTATGG	336
QY	352	GATGAAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTGTTACTTTAAATGCACT	411
Db	337	GATGAAAGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTGTTACTTTAAATGCACT	396
QY	412	AATTTGAATATCAGTAAAGTACTACTAATCCCATGCTAGCAGCTGGGATGATGGAG	471
Db	397	AATTTGAATATCAGTAAAGTACTACTAATCCCATGCTAGCAGCTGGGATGATGGAG	456
QY	472	AAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATAAAGAAATAGGTAAG	531
Db	457	GNAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAAGCATAAAGAAATAGGTAAG	516
QY	532	AAAGAAATATGCATTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAAATAACT	591
Db	517	AAAGAAATATGCATTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAAATAACT	576
QY	592	AAATATAGTTAAATAGTTGTAACACCTCAGTCAATACACAGGCTGTCCAAAGTATCC	651
Db	577	AAATATAGTTAAATAGTTGTAACACCTCAGTCAATACACAGGCTGTCCAAAGTATCC	636
QY	652	TTTCAGCAATCCCATACATATTGTTGTCCGGCTGGGTTTGCATGCTAAAGTGAAC	711
Db	637	TTTCAGCAATCCCATACATATTGTTGTCCGGCTGGGTTTGCATGCTAAAGTGAAC	696
QY	712	AATAAGACATCAATGGATCAGGACCATGCAAAATGTGAGCACAGTACAAATGTACACAT	771
Db	697	AATAAGACATCAATGGATCAGGACCATGCAAAATGTGAGCACAGTACAAATGTACACAT	756
QY	772	GGAATTAGCCAGTGGTGTCACTCACTCACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	831
Db	757	GGAATTAGCCAGTGGTGTCACTCACTCACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGAC	816
QY	832	ATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAACCATATAGTACAGCTAAAT	891
Db	817	ATAGTAATTAGATCTGAAAAATTTACAGACAAATGCTTAAACCATATAGTACAGCTAAAT	876
QY	892	GAATCTGTAGTAATTAATTGTAACAAGCCCAACCAACAATAACAAGAAAGGTTATCTATA	951
Db	877	GAATCTGTAGTAATTAATTGTAACAAGCCCAACCAACAATAACAAGAAAGGTTATCTATA	936
QY	952	GGACAGGGAGAGCAATTTTATGCAAGAGAAACATATAGGAGATATTAAGCAAGCACAT	1011
Db	937	GGACAGGGAGAGCAATTTTATGCAAGAGAAACATATAGGAGATATTAAGCAAGCACAT	996
QY	1012	TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAGA	1071
Db	997	TGTAACATTAGTAGAGCAAAATGGAATAACACTTTTACAAACAGATAGTTATAAAATTAGA	1056

QY	1072	GAATAATTTAGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGAGCCAGAAATT	1131
Db	1057	GAATAATTTAGGAATAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGAGCCAGAAATT	1116
QY	1132	GTAATGCACAGCTTTTAAATTGTTGGAGGGGAAATTTCTTACTGTGTAATACAGCAACTGTTT	1191
Db	1117	GTAATGCACAGCTTTTAAATTGTTGGAGGGGAAATTTCTTACTGTGTAATACAGCAACTGTTT	1176
QY	1192	AATAGTACTTGGAAATGTTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA	1251
Db	1177	AATAGTACTTGGAAATGTTTACTGGAGGGACAAATGGCACTGAAGGAAATGACATAATCACA	1236
QY	1252	CTCCAATGCAGAAATAAAACAATTTATAAATATGTGGCAGAAATAGGAAAAGCAATGTAT	1311
Db	1237	CTCCAATGCAGAAATAAAACAATTTATAAATATGTGGCAGAAATAGGAAAAGCAATGTAT	1296
QY	1312	GCCCTCCCATCAGAGCAAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	1371
Db	1297	GCCCTCCCATCAGAGCAAAATTTAGATGTTTCATCAATATTTACAGGCTGCTACTAACA	1356
QY	1372	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAT	1431
Db	1357	AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAT	1416
QY	1432	ATGAGGACAAATGGAGAAAGTAAATTTATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1491
Db	1417	ATGAGGACAAATGGAGAAAGTAAATTTATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1476
QY	1492	GGAGTAGCACCACCCAGGGCAAGAGAAAGACAGTGCAGAGAGAAAAGACCCG	1546
Db	1477	GGAGTAGCACCACCCAGGGCAAGAGAAAGACAGTGCAGAGAGAAAAGAGCAG	1531

RESULT 7

AAL56171
ID AAL56171 standard; DNA; 2051 BP.

XX AC AAL56171;

XX DT 11-MAR-2004 (first entry)

XX DE HIV truncated envelope glycoprotein 160 coding sequence.

XX KW HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;
XX KW gene; ds; anti-HIV; truncated.

XX OS Human immunodeficiency virus.

FH Key Location/Qualifiers
FT CDS 1..2001
FT /*tag= a
FT /product= "truncated gp 160"

XX WO2003077838-A2.

XX 25-SEP-2003.

XX 05-MAR-2002; 2002WO-US007144.

XX 05-MAR-2002; 2002WO-US007144.

XX (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.

XX Dimitrov DS, Chow Y, Phogat SK, Broder CC;

XX WPI; 2003-779074/73.

XX P-PSDB; ABU64219.

XX New HIV antigenic composition comprising an HIV envelope glycoprotein 160
XX PT having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
XX PT subunit useful for protecting a human from HIV infection.

XX PS Disclosure; Page 62-63; 65pp; English.

XX The present invention relates to an HIV antigenic composition, comprising
CC an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
CC subunit, where the carboxy-terminal end of gp120 is covalently linked
CC through a peptide linker of at least 5 amino acids, to the amino-terminal
CC end of gp41. The HIV antigenic composition is useful for protecting a
CC human from HIV infection, potentially in the form of a vaccine. The
CC present sequence is the HIV truncated gp160 coding sequence
XX
SQ Sequence 2051 BP; 749 A; 333 C; 467 G; 502 T; 0 U; 0 Other;
Query Match 71.4%; Score 1447.6; DB 10; Length 2051;
Best Local Similarity 99.2%; Pred. No. 5.6e-285;
Matches 1466; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
72 CATGCTCTGGGATATTGATGATCTGTAGTGCT---ACAGAAAATTTGGTGTCACAGT 128
Db CTTGCTCTGGGATGTTGATGATCTGTAGTGCTGCAAAAAGAAAACGTGGGTCACAAT 110
129 CTATTATGGGTACTGTGTGGAGAGAGCAACCACTCTATTTTTGTGCATCAGATGC 188
Db CTATTATGGGTACTGTGTGGAGAGAGCAACCACTCTATTTTTGTGCATCAGATGC 170
189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGA 248
Db TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGA 230
249 CCCCACCCCAAGAAGTAGTATGGGAAATGTGACAGAAAATTTTAAACATGTGGAAAAA 308
Db CCCCACCCCAAGAAGTAGTATGGGAAATGTGACAGAAAATTTTAAACATGTGGAAAAA 290
309 TAAACATGTCAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
Db TAAACATGTCAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 350
369 ATGTGTAATAATTAACCCCACTCTGTGTTACTTTTAAATTCGCACTAATTTGAATATCACTAA 428
Db ATGTGTAATAATTAACCCCACTCTGTGTTACTTTTAAATTCGCACTAATTTGAATATCACTAA 410
429 GAATACCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAGAAATAAAAA 488
Db GAATACCTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAGAAATAAAAA 470
489 TTGCTCTTTCTATATACCAACAGCATAGAAATAGCTTAAGTAAGTAAGTAAGTAAGTCTTT 548
Db TTGCTCTTTCTATATACCAACAGCATAGAAATAGCTTAAGTAAGTAAGTAAGTCTTTT 530
549 TAATAGACTTGTATGTAGTACCAATAGAAAATACTAATAATCTAAGTATAGTAAATAG 608
Db TAATAGACTTGTATGTAGTACCAATAGAAAATACTAATAATCTAAGTATAGTAAATAG 590
609 TTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTACGCCAATTCCTAT 668
Db TTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTACGCCAATTCCTAT 650
669 ACATTATTGTGTCGGCTGGGTTTGGGATGCTGTAAGTGAACAATAAGACATCAATGG 728
Db ACATTATTGTGTCGGCTGGGTTTGGGATGCTGTAAGTGAACAATAAGACATCAATGG 710
729 ATCAGGACCATGCACAAATGTGAGCAGCAGTACAATGTACATGGAATTTAGGCCAGTGGT 788
Db ATCAGGACCATGCACAAATGTGAGCAGCAGTACAATGTACATGGAATTTAGGCCAGTGGT 770
789 GTCAACTCACTGCTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTTAGATCTGA 848
Db GTCAACTCACTGCTGTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTTAGATCTGA 830
849 AAATTTTCAGACAAATGCTTAAACCATATAGTACAGCTTAAATGATCTGTAGTAATTA 908
Db AAATTTTCAGACAAATGCTTAAACCATATAGTACAGCTTAAATGATCTGTAGTAATTA 890
909 TTGTACAAGACCCCAACAATACAGAAGAGAGGTTATCTATAGGACCGAGGAGCAATT 968
|||||

Db 891 TTGTACAAGACCCCAACAATACAGAAGAAGGTTATCTATAGGACCCAGGAGAGCAATT 950
Qy TTATGCAAGAGAAACATATAGGAGATATAAGACAAGCACATTGTAACTATTAGTAGAGC 1028
Db TTATGCAAGAGAAACATATAGGAGATATAAGACAAGCACATTGTAACTATTAGTAGAGC 1010
Qy AAAATGGAATAACACTTTTACACACAGATAGTTTATAAAATTTAAGAGAAAAATTTAGGAATAA 1088
Db AAAATGGAATAACACTTTTACACACAGATAGTTTATAAAATTTAAGAGAAAAATTTAGGAATAA 1070
Qy AACAAATGACCTTTTAAATCAATCCTCAGGAGGGAACCCAGAAATTTGTAATGCAACAGTTTAA 1148
Db AACAAATGACCTTTTAAATCAATCCTCAGGAGGGAACCCAGAAATTTGTAATGCAACAGTTTAA 1130
Qy TTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTTGGAATGT 1208
Db TTGTGGAGGGGAATTTTCTTCTACTGTAATACAGCACAACTGTTTAAATAGTACTTTGGAATGT 1190
Qy TACTGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCCAATGCAGAAATAA 1268
Db TACTGGAGGGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCCAATGCAGAAATAA 1250
Qy ACAAATTAATAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGG 1328
Db ACAAATTAATAATATGTGGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGG 1310
Qy ACAAATTAGATGTTTCATCAATATTTACAGGCTGCTACTAACAAGAGATGAGGTAATAG 1388
Db ACAAATTAGATGTTTCATCAATATTTACAGGCTGCTACTAACAAGAGATGAGGTAATAG 1370
Qy TACTGAGACTCAGACTCAGATCTTTTACAGCTGGAGGAGGAGATATGAGGGAACAATTGGAG 1448
Db TACTGAGACTCAGACTCAGATCTTTTACAGCTGGAGGAGGAGATATGAGGGAACAATTGGAG 1430
Qy AAGTGAATTAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCAG 1508
Db AAGTGAATTAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCACCAG 1490
Qy GGCAAGAGAGAAACAGTGCACAAAGAGAAAAAGACCCG 1546
Db GGCAAGAGAGAAACAGTGCACAAAGAGAAAAAGAGCAG 1528
RESULT 8
AAL56170
ID AAL56170 standard; DNA; 2562 BP.
XX
AC AAL56170;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human immunodeficiency virus envelope glycoprotein 160 coding sequence.
XX
KW HIV; envelope glycoprotein; gp 160; antigen; gp 120; gp 41; vaccine;
KW gene; ds; anti-HIV.
XX
OS Human immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT CDS 1..2559
FT /*tag= a
FT /product= "gp 160"
XX
PN WO2003077838-A2.
XX
PD 25-SEP-2003.
XX
PF 05-MAR-2002; 2002WO-US007144.
XX
PR 05-MAR-2002; 2002WO-US007144.
XX (NAHE-) NAT INST HEALTH OFFICE TECHNOLOGY TRANSF.
XX

PI Dimitrov DS, Chow Y, Phogat SK, Broder CC;
XX WPI; 2003-779074/73.
DR P-PSDB; ABU64218.
XX
PT New HIV antigenic composition comprising an HIV envelope glycoprotein 160
PT having a glycoprotein 120 subunit covalently linked to a glycoprotein 41
PT subunit useful for protecting a human from HIV infection.
XX
PS Disclosure; Page 61-62; 65pp; English.
XX
CC The present invention relates to an HIV antigenic composition, comprising
CC an HIV envelope glycoprotein (gp) 160 having a gp120 subunit and a gp41
CC subunit, where the carboxy-terminal end of gp120 is covalently linked
CC through a peptide linker of at least 5 amino acids, to the amino-terminal
CC end of gp41. The HIV antigenic composition is useful for protecting a
CC human from HIV infection, potentially in the form of a vaccine. The
XX present sequence is the HIV gp160 coding sequence
SQ Sequence 2562 BP; 897 A; 433 C; 604 G; 628 T; 0 U; 0 Other;
Query Match 71.4%; Score 1447.6; DB 10; Length 2562;
Best Local Similarity 99.2%; Pred. No. 5.7e-285;
Matches 1466; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
QY 72 CATGCTCCTGGGATATTGATGATCTGTAGTGCT---ACAGAAAAAATTTGGGTCAAGT 128
DB 51 CTTGCTCCTGGGATGTTGATGATCTGTAGTGCTGCAAAAGAAAAACGTGGGTCACAAT 110
QY 129 CTATTATGGGTACCTGTGTGGAGAGACACACCACTCTATTTTTGTGCATCAGATGC 188
DB 111 CTATTATGGGTACCTGTGTGGAGAGACACACCACTCTATTTTTGTGCATCAGATGC 170
QY 189 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACACAGA 248
DB 171 TAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACACAGA 230
QY 249 CCCCACCCACAAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTGTGGAAAAA 308
DB 231 CCCCACCCACAAAGAAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTGTGGAAAAA 290
QY 309 TAAATGCTAGTACAGATGCATGAGGATATATCAATGTTTATGGGATGAAGCCTTAAAGCC 368
DB 291 TAAATGCTAGTACAGATGCATGAGGATATATCAATGTTTATGGGATGAAGCCTTAAAGCC 350
QY 369 ATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAATATCACTAA 428
DB 351 ATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTCGACTAATTTGAATATCACTAA 410
QY 429 GAATACTACTAATCCCACTAGTACGCTGGGGAATGATGGAGAAAGAGAGAAATAAAAAA 488
DB 411 GAATACTACTAATCCCACTAGTACGCTGGGGAATGATGGAGAAAGAGAGAAATAAAAAA 470
QY 489 TTGCTCTTCTATATACCAACAGCATAAAGTAAGTTAAAGAAAGATATGCACTTTT 548
DB 471 TTGCTCTTCTATATACCAACAGCATAAAGTAAGTTAAAGAAAGATATGCACTTTT 530
QY 549 TAAATGACTTGTATGTAGTACCAATAAGAAATACTAATACTAAGTATAGTTAATAAG 608
DB 531 TAAATGACTTGTATGTAGTACCAATAAGAAATACTAATACTAAGTATAGTTAATAAG 590
QY 609 TTGTAAACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTTCAGCCAAATCCCAT 668
DB 591 TTGTAAACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTTCAGCCAAATCCCAT 650
QY 669 ACATTATTGTGTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 728
DB 651 ACATTATTGTGTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 710
QY 729 ATCAGGACCATGACAAATGTGACAGACAGTACAAATGATGACATGGAATTTAGGCCAGTGGT 788
DB 711 ATCAGGACCATGACAAATGTGACAGACAGTACAAATGATGACATGGAATTTAGGCCAGTGGT 770

QY 789 GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTTAGATCTGA 848
DB 771 GTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAGAAGACATAGTAATTTAGATCTGA 830
QY 849 AAATTTTACAGACATGCTTAAACCCATTAATAGTACAGCTAAATGAATCTGTAGTAATTA 908
DB 831 AAATTTTACAGACATGCTTAAACCCATTAATAGTACAGCTTAAATGAATCTGTAGTAATTA 890
QY 909 TTGTACAAAGACCCCAACCAATACAAAGAAAGGTTTATCTATAGGACACAGGGAGAGCAATT 968
DB 891 TTGTACAAAGACCCCAACCAATACAAAGAAAGGTTTATCTATAGGACACAGGGAGAGCAATT 950
QY 969 TTATGCAAGAGAAACATTAATAGGAGATATAAGACACACATTTTCACTATAGTAGAGC 1028
DB 951 TTATGCAAGAGAAACATTAATAGGAGATATAAGACACACATTTTCACTATAGTAGAGC 1010
QY 1029 AAAATGGAATAACACTTTTCAACACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATAA 1088
DB 1011 AAAATGGAATAACACTTTTCAACACAGATAGTTTATAAAATTAAGAGAAAAATTTAGGAATAA 1070
QY 1089 AACATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAAATTTGTAATGCACAGTTTTAA 1148
DB 1071 AACATAGCCTTTTAAATCAATCCTCAGGAGGGAGCCAGAAAAATTTGTAATGCACAGTTTTAA 1130
QY 1149 TTGTGGAGGGGAATTTCTTCTACTGTAATACAGCACAACCTGTTTAAATAGTACTTGGAAATGT 1208
DB 1131 TTGTGGAGGGGAATTTTCTTCTACTGTAATACAGCACAACCTGTTTAAATAGTACTTGGAAATGT 1190
QY 1209 TACTGGAGGGACAATGCGCACTGGAAGGAAATGACATATCACTCCCAATGCAGAAATAA 1268
DB 1191 TACTGGAGGGACAATGCGCACTGGAAGGAAATGACATATCACTCCCAATGCAGAAATAA 1250
QY 1269 ACAAAATTAATAATATGTGCGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGG 1328
DB 1251 ACAAAATTAATAATATGTGCGCAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCACAGG 1310
QY 1329 ACAAAATTAGATGTTTCAATCAAAATATACAGGCTGCTACTTAAACAGAGATGGAGTAATAG 1388
DB 1311 ACAAAATTAGATGTTTCAATCAAAATATATACAGGCTGCTACTTAAACAGAGATGGAGTAATAG 1370
QY 1389 TACTGAGACTCAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGACAAATTTGGAG 1448
DB 1371 TACTGAGACTCAGACTGAGATCTTCAGACCTGGAGGAGAGATATGAGGACAAATTTGGAG 1430
QY 1449 AAGTGAATTAATAATAATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCAACCCACAG 1508
DB 1431 AAGTGAATTAATAATAATAAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCAACCCACAG 1490
QY 1509 GGCAAAGAGAAAGACAGTGCACAAAGAGAAAAAAGACCCG 1546
DB 1491 GGCAAAGAGAAAGACAGTGCACAAAGAGAAAAAAGAGCAG 1528
RESULT 9
ACA63267
ID ACA63267 standard; DNA; 2010 BP.
XX ACA63267;
AC ACA63267;
XX
DT 22-APR-2004 (first entry)
XX
DE HIV-1 immunogenic sequence #3.
XX
KW Measles virus; measles; epitope; HIV; antigen; RNA virus; vaccine;
XX immunogenic; virucide; ds.
XX
OS Human immunodeficiency virus type 1.
XX
FN WO2004001051-A2.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-EP007146.

XX DE Env gene of the BA-L strain of Human immunodeficiency virus type 1.
XX KW HIV-1; HIV-1 strain BA-L; env protein; vaccine; immunotherapy;
XX KW HIV infection; immunogen; HIV-1 diagnosis; ds.
XX OS Human immunodeficiency virus 1.
XX FH Location/Qualifiers
XX FT 648..3214
XX FT /*tag= a
XX FT /product= "env protein"
XX FT /transl_except= (pos: 678..678, aa: Gln)
XX PN US869313-A.
XX PD 09-FEB-1999.
XX XX 14-MAY-1996; 96US-00647714.
XX PR 17-OCT-1990; 90US-00599491.
XX PR 25-FEB-1993; 93US-00022835.
XX PR 15-FEB-1995; 95US-00368809.
XX XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX XX Gallo RC, Franchini G, Reitz MS, Lori FC, Popovic M, Gartner S;
XX PI Markham PD;
XX XX WPI; 1999-152779/13.
XX DR P-PSDB; AAW88113.
XX PT DNA encoding env protein of the human immune deficiency virus isolate BA-
XX PT L - useful for producing protein for use in vaccines, as assay reagent
XX PT and to generate antibodies.
XX PS Claim 2; Fig 8A-H; 87pp; English.
XX XX The present sequence encodes the envelope protein of the BA-L (ATCC
XX CC 40890) strain of Human immunodeficiency virus type 1 (HIV-1) strain MN-
XX CC STL. BA-L is more typical of United States isolates of HIV-1 than
XX CC previously known strains. Recombinant, complete env protein of the BA-L
XX CC strain is used as a vaccine component and for immunotherapy of existing
XX CC HIV infections, to detect HIV-specific antibodies, e.g. in donated blood,
XX CC and as an immunogen to raise specific antibodies, for HIV-1 diagnosis.
XX CC (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 3806 BP; 1306 A; 662 C; 937 G; 901 T; 0 U; 0 Other;
Query Match 60.4%; Score 1225.4; DB 2; Length 3806;
Best Local Similarity 90.2%; Pred. No. 9.9e-240;
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;
72 CATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGGGTACAGTCTA 131
700 CATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAAATTTGGGTACAGTCTA 759
132 TTATGGGGTACTGTGTGGAGAGAGCAACCACTCTATTTTGTGATCAGATGCTAA 191
760 TTATGGGGTACTGTGTGGAGAGAGCAACCACTCTATTTTGTGATCAGATGCTAA 819
192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGACCC 251
820 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTACCCACAGACCC 879
252 CAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTACATGTGGAAAAATAA 311
880 CAACCCACAAGAGTAGAATTGAAAAATGTGACAGAAAAATTTTACATGTGGAAAAATAA 939
312 CATGTAGATCAGATGAGATATTAATCAGTTTATGGGATGAAAGCCCTAAAGCCATG 371
940 CATGGTAGAACAAATGCAATGAGGATATAATCAGTTTATGGGATCAAGCCCTAAAGCCATG 999

Qy 372 TGTAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGA-----ATATCAC 425
Db |||||
Qy 1000 TGTAAATTAACCCCACTCTGTGTACTTTAAATTCACATAATTTGAAGGAATGCTACTAA 1059
Db |||||
Qy 426 TAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAAATAAA 485
Db |||||
Qy 1060 TGGGAATGACACTAATACCACTAGTAGTAGCAGGGAATGCTGGGGGAGAGAAATGAA 1119
Db |||||
Qy 486 AAATTTGCTCTTTCTATATACCAAGCATAGAAATAAAGGTAAAGAAAGAAATATGCACT 545
Db |||||
Qy 1120 AAATTTGCTCTTTCTAATATACCAAAACATAGAGGTAAAGGTGCAGAAAGAAATATGCACT 1179
Db |||||
Qy 546 TTTTAATAGACTTGATGTAGTACCAATAGAAAACTAATAATTAATTAATAGTATAGTTAAT 605
Db |||||
Qy 1180 TTTTATAAATCTTGATATAGCACCATAAGATAATAATAGTAAATAATAGTATAGTTGAT 1239
Db |||||
Qy 606 AAGTTGTAACACCTCAGTCATTACAGGCGCTGTCCAAAGGTATCCTTTTACGCCAATTTCC 665
Db |||||
Qy 1240 AAGTTGTAACACCTCAGTCATTACAGGCGCTGTCCAAAGGTATCCTTTTACGCCAATTTCC 1299
Db |||||
Qy 666 CATACATATTGTGTCCCGCTGGTTCGATGCTAAAGGTAAACATTAAGACATTAAGACATTC 725
Db |||||
Qy 1300 CATACATATTGTGTCCCGCTGGTTCGATGCTAAAGGTAAACATTAAGACATTAAGACATTC 1359
Db |||||
Qy 726 TGGATCAGGACCATGCAAAATGTACAGCACTAGTACAAATGTACACATGGAATTAGGCCAGT 785
Db |||||
Qy 1360 TGGAAAGGACCATGTACAAATGTACAGCACTAGTACAAATGTACACATGGAATTAGGCCAGT 1419
Db |||||
Qy 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAAATTAGATC 845
Db |||||
Qy 1420 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGAGAGGTAGTAAATTAGATC 1479
Db |||||
Qy 846 TGAATAATTTACACACATGCTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTAAT 905
Db |||||
Qy 1480 CGCCAAATTTTCGCGACCAATGCTAAAGTCAATTAATAGTACAGCTGAATGAATCTGTAGAAAT 1539
Db |||||
Qy 906 TAATTTGTACAGACCCCAACAAATACAAAGAAAGGTATCTATAGGACCAAGGAGAGC 965
Db |||||
Qy 1540 TAATTTGTACAGACCCCAACAAATACAAAGAAAGGTATATATAGGACCAAGGAGAGC 1599
Db |||||
Qy 966 ATTTTATGCAAGAGAAACATAATAGGAGATATTAAGCAACACACATTTGTACATAGTAG 1025
Db |||||
Qy 1600 ATTTTATCAACAGAGAAATTAATAGGAGATATTAAGCAACACATTTGTAACTTGTAGTAG 1659
Db |||||
Qy 1026 AGCAAAATGGAAATACACTTTTACACAGATAGTTATATAAATTAAGAGAAAAATTTAGCAA 1085
Db |||||
Qy 1660 AGCAAAATGGAAATGACACTTTAAATTAATAGTATAGTTATATAAATTAAGAGAAACAAATTTGGAA 1719
Db |||||
Qy 1086 TAAACAAATAGCCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTTGTAATGCACAGTTT 1145
Db |||||
Qy 1720 TAAACAAATAGCTTTTAAGCACTCCTCAGGAGGGGACCCAGAAATTTGTGACGACAGTTT 1779
Db |||||
Qy 1146 TAATTTGGAGGGGAATTTCTTCTACTGTAATACAGCACTGTTTAAATAGTACTTGAA 1205
Db |||||
Qy 1780 TAATTTGGAGGGGAATTTTCTACTGTAATTAACACACTGTTTAAATAGTACTTGAA 1839
Db |||||
Qy 1206 TGTTTACTGGAGGGAACAATGCACTGAGGAAATGACATAATCACTCCCAATGCAGAAAT 1265
Db |||||
Qy 1840 TGTACTGAAGAGTCAAAATAACCTGTAGAAAAATTAACAAATCACTCCCAATGCAGAAAT 1899
Db |||||
Qy 1266 AAAACAAATTAATAATATGTCGCAAGAAAGTAGGAAAAAGCAATGTATGCCCTCCCATCAC 1325
Db |||||
Qy 1900 AAAACAAATTAATAACATGTGCGAGGAATAGGAAGAGCAATGTATGCCCTCCCATCAG 1959
Db |||||
Qy 1326 AGGCAAAATTAGATGTTTCATCAAAATATTAAGGGCTGCTACTTAACAGAGATGGAGTTAA 1385
Db |||||
Qy 1960 AGGCAAAATTAGATGTTTCATCAAAATATTAAGGGCTGCTATTAACAGAGATGGTGG--- 2016
Db |||||
Qy 1386 TAGTACTGAGACTGAGACTGAGATCTTCAGACCTTGGAGGAGAGATATAGGAGCAATTTG 1445
Db |||||
Qy 2017 TCCTTGAGGACAAACAGACCGAGGTCTTCAGACCTTGGAGGAGAGATATAGGAGTAAATTTG 2076
Db |||||
Qy 1446 GAGAGTGAATTTATATAAATATAAAGTAGTAGTAAGAAATTGAAACCAATAGGAGTAGCCAC 1505
Db |||||

1781	TAAATTGGAGGGGAAATTTTTC	TACTGTAATCAACAACTGTTTAATAGTACTGGAA	1840
1206	TGTTACTGGAGGACAAATGGCACT	GAAGGAAATGACATAATCACACTCCAAATGCAGAAT	1265
1841	TGTTACTGAAGAGTCAAAATACACT	GTAGAAAATACACAATCACACTCCATGCAGAAT	1900
1266	AAAACAAAATTTAAATATATGTG	CGCAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC	1325
1901	AAAACAAAATTTAAACATGTGGC	AGGAAGTATGTATGCCCTCCCATCAG	1960
1326	AGNCAAAATTAGATGTTTCATCA	ATAATTACAGGGCTGCTACTAACACAGAGATGGAGTAA	1385
1961	AGGACAAATTAGATGTTTCATCA	ATAATTACAGGGCTGCTATTACACAGAGATGGTGG---	2017
1386	TAGTACTGAGACTGAGACTCAGAT	CTTTCAGACCTGGAGGAGGAGATATAGGGACAAATTG	1445
2018	TCCTGGAGCAACAAAGACCGAGGT	CTTTCAGACCTGGAGGAGGAGATATAGGGATTAATTG	2077
1446	GAGAAGTGAATTTATATAAATAT	ATAAGTAGTAAAGAAATTTGAACCAATAGGAGTAGCACCCAC	1505
2078	GAGNAGTGAATTTATATAAATAT	ATAAAGTAGTAAAAATTTGAACCATTAGGAGTAGCACCCAC	2137
1506	CAGGGCAAGAGAGAAACAGCTCA	AGTCAAGAGAAAAAAGACCGG	1546
2138	CAAGGCAAAAGAGAGAGTGTGTCA	GAGAGAAAAAAGAGCAG	2178

RESULT 13

AD052562	432	TACTTAACTCCACTAGCTAGCAGCTGGGGAATCATGGAGAAAGGAGAAATATAAAAAATTC	QY
ID	AD052562	standard; DNA; 9540 BP.	
XX	AC		
AC	AD052562;		
XX	XX		
DT	12-AUG-2004	(first entry)	
XX	XX		
XX	XX		
DE	Human immunodeficiency virus 1 parent JRCSF DNA.		
XX	XX		
KW	Human immunodeficiency virus 1; HIV-1; HIV-1 infection; gene therapy;		
KW	vaccine; ds.		
XX	XX		
OS	Human immunodeficiency virus 1.		
XX	XX		
PN	US2004101823-A1.		
XX	XX		
PD	27-MAY-2004.		
XX	XX		
PF	19-DEC-2002; 2002US-00325468.		
XX	XX		
PR	21-DEC-2001; 2001US-0343524P.		
XX	XX		
PA	(MAXY-) MAXYGEN INC.		
XX	XX		
PI	Soong NW, Pekrun K, Shibata R;		
XX	XX		
DR	WPI; 2004-399670/37.		
DR	GENBANK; M38429.		
XX	XX		
PT	New HIV-1 chimeric or recombinant nucleic acids, useful in preparing a		
PT	composition for treating or preventing infection caused by HIV-1.		
XX	XX		
PS	Disclosure; SEQ ID NO 46; 310pp; English.		
XX	XX		
CC	The present invention relates to human immunodeficiency virus 1 (HIV-1)		
CC	viral variants and nucleic acids and polypeptides thereof having improved		
CC	replication properties for development of suitable animal models for the		
CC	study of HIV-1 pathogenesis. The invention is useful for treating and		
CC	preventing HIV-1 infection. The invention is also useful in gene therapy		
CC	and in the preparation of vaccines. The present sequence is human		
CC	immunodeficiency virus 1 (HIV-1) parent DNA. This sequence is used in the		
CC	invention.		
XX	XX		
SQ	Sequence 9540 BP; 3425 A; 1691 C; 2308 G; 2116 T; 0 U; 0 Other;		

Db 6349 TTATGGGGTACTGTGTGGAAGAAACAAACACACTCTATTTTGTGCATCAGATGCTAA 6408
Qy 192 AGCCTATGATACAGAGTACATAATATGTTTGGGCCACACATCCCTGTGTACCCACAGACCC 251
Db 6409 AGCATATGATACAGAGGTACATAATATGTTTGGGCCACACATCCCTGTGTACCCACAGACCC 6468
Qy 252 CAACCCACAGAGTATGTTGGGAATGTGCACAGAAATTTTAAACATGTGGGAATAA 311
Db 6469 CAACCCACAGAGTATGTTGGGAATGTGCACAGAAATTTTAAACATGTGGGAATAA 6528
Qy 312 CATGTAGATCAGATGAGGATATAATCAGTTTATGGGATGAAGCCCTAAAGCCCATG 371
Db 6529 CATGTAGACAGATGAGGAGGATGTAATCAATTTATGGGATCAAGCTTAAAGCCCATG 6588
Qy 372 TGTAAATTAACCCACACTCTGTGTATCTTTAAATTTGCACTAATTTGAAATCACTAAGAA 431
Db 6589 TGTAAATTAACCCACACTCTGTGTATCTTTAAATTTGCAAGATGT-----GAA 6636
Qy 432 TACTACTAATCCCACTAGTACAGCTGGGGAATGATGGGAAGAGGAATAAATAATTTG 491
Db 6637 TGCTACTAATACCACTAGTATGAGGGAATGATGGAGAGAGAGAAATAAATAACTG 6696
Qy 492 CTCTTTCTATATCACCACAGCATAAAGATAAGGTAAAGAAAGAAATATGCACCTTTTAA 551
Db 6697 CTCCTTCATATACCAAAAGCATAGAGATAGGTGCAGAAAGAAATATGCTCTTTTAA 6756
Qy 552 TAGACTTGATGATGATACCAATAGAAAATCTAATAATCTAAGTATAGTTTAAATGTTG 611
Db 6757 TAACTGGATGTAGTACCATAGATAATAAGAAATAATACCAAAATATAGTTTAAATGTTG 6816
Qy 612 TAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCAAATCCCATACA 671
Db 6817 TAACACCTCAGTCATTACACAAAGCTGTCCAAAGGTATCCTTTAGCCAAATCCCATACA 6876
Qy 672 TTATTGTGTCGGGCTGGGTTTGCATGCTTAAAGTGTAAACAATAAGACATTTCAATGGATC 731
Db 6877 TTATTGTGCCCGGCTGGTGTTCGATTTCTAAAGTGTAAATAAGACATTTCAATGGAA 6936
Qy 732 AGGACCATGCACAAATGTACACACAGTACAAATGTACACATGGAATTAGCCAGTGGTGC 791
Db 6937 AGGACATGTAAATAATGTACACACAGTACAAATGTACACATGGAATTAGCCAGTATATC 6996
Qy 792 AACTCACTGTCTTAAATGGCAGTCTAGCAGAGACACATAGTAAATAGATCTGAAA 851
Db 6997 AACTCACTGTCTTAAATGGCAGTCTAGCAGAGAGAAAGGTGTGAATAGATCTGACAA 7056
Qy 852 TTTCACAGACAATGCTAAACCATAAATAGTACAGCTAAATGAATCTGTAGTAAATTAATTG 911
Db 7057 TTTTACGGACAAATGCTAAACCATAAATAGTACAGCTGAATGAACTGTAAATAATTAATTG 7116
Qy 912 TACAAGACCCACAAACATAACAAGAAAGGTATCTATAGGACAGGAGAGCAATTTTA 971
Db 7117 TACAAGGCCACAGCAACATAACAAGAAAGGTATACATATAGGACAGGAGAGCAATTTTA 7176
Qy 972 TGCAAGAGAACAATAATAGGAGATATAAGACACACATTTGTAACTAGTAGAGCAA 1031
Db 7177 TACAACAGGAGAAATAATAGGAGATATAAGACACACATTTGTAACTAGTAGAGCACA 7236
Qy 1032 ATGGAATAACACTTTTACAACAGATAGTTTATAAATTAAGAGAAAAATTTAGGAATAAAAC 1091
Db 7237 ATGGNATAACACTTTTAAACAGATAGTTTGAATAATTAAGAGNACAATTTAATAAATAC 7296
Qy 1092 AATAGCCTTTAATCAATCCTCAGGAGGGACCCAGAAATGTPAATGCACAGTTTAAATG 1151
Db 7297 AATAGCTTTTACTACTCTCCTCAGGAGGGATCCAGAAATTTGAATGCACAGTTTAAATG 7356
Qy 1152 TGGAGGGGAATTTCTACTGTAAATACAGCACAAGTGTAAATAGTACTTGGAAATTTAC 1211
Db 7357 TGGAGGGGAATTTTCTACTGTAAATTAACACAAGTGTAAATAGTACTTGGAAATTTAC 7416
Qy 1212 TGGAGGGGAATAATGGCACTGAAAGGAATGACATAATCACTCCCAATGCAGAAATAAACA 1271

Db 7417 TGAAGAGTCAAGTGGCACTGAAGGAATGACACCATCATCTCCCATGCAGATAAACA 7476
Qy 1272 AATTATAAATATGTGGCAGAAAGTAGAAAAGCAATGTATGCCCTCCCATCAGAGACA 1331
Db 7477 AATTATAAACATGTGGCAGGAAGTGGGAAAAGCAATGTATGCTCCTCCATTAAGGACA 7536
Qy 1332 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAGAGATGGAGTAAATAGTAC 1391
Db 7537 AATTAGATGTTTCATCAAAATATTACAGGGCTGCTACTAAACAGAGATGGTGGTAA--AAA 7593
Qy 1392 TGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGACAATTTGGAGAAG 1451
Db 7594 TGAGAGTGAGATCAGATCTTTCAGACCTGGAGGAGGAGACATGAGGGACAATTTGGAGAAG 7653
Qy 1452 TGAATTTATATAATATAAGTAGTAAGAAATTTGAACCAATAGGATAGCACCACCAAGGC 1511
Db 7654 TGAATTTATATAATATAAGTAGTAAGAAATTTGAACCAATAGGATAGCACCACCAAGGC 7713
Qy 1512 AAAGAGAAGACACTGCAAAAGAGAAAAAAGACCGG 1546
Db 7714 AAAGAGAAGAGTGTGCAAGAGAAAAAAGAGCAG 7748
RESULT 15
AAQ14753
ID AAQ14753 standard; DNA; 3807 BP.
AC AAQ14753;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-DEC-2001 (revised)
DT 05-FEB-1992 (first entry)
XX
DE HIV-1 BA-L clone.
XX
KW human immunodeficiency virus; United States; MN isolate; AIDS;
KW envelope protein; ss.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
CDS 394..476
FT /*tag= b
FT /product= "rev"
CDS 648..3215
FT /*tag= a
FT /product= "env"
XX
PN USN7599491-N.
XX
PD 15-OCT-1991.
XX
PF 17-OCT-1990; 90US-00183830.
XX
PR 17-OCT-1990; 90US-00599491.
XX
PA (USSH) NAT INST OF HEALTH.
XX
PI Reitz M;
XX
DR WPI; 1991-346752/47.
DR P-FSDB; AAR14905.
XX
PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in
PS therapeutics, vaccines and diagnostic tests.
XX
PS Example 3; Fig 8; 61pp; English.
XX
CC A HindIII fragment of unintegrated viral DNA representing the HIV-1 (BA-
CC L) genome was cloned by standard techniques into lambda phage Charon 28
CC DNA from total DNA of peripheral blood macrophages infected with and
CC producing HIV-1 (BA-L). A positive clone was selected by hybridisation

CC using a HIV-1 envelope probe. This clone, designated BA-L1, contained the
CC entire env gene. The insert was subcloned and sequenced. The BA-L1 plasmid
CC clone has been deposited as ATCC 40890. The sequence also contains the
CC coding region for the rev protein which is needed for efficient
CC expression of the envelope protein in eukaryotic cells. (Note: Revised
CC entry submitted to correct the patent number format of US Government-
CC owned NTIS applications to prevent clashes with ongoing US granted patent
CC numbers. For further information please visit the Derwent web site at
CC www.derwent.com/dwpi/updates/atlis.us.html.) (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ

Sequence 3807 BP; 1307 A; 689 C; 907 G; 904 T; 0 U; 0 Other;

Query Match 60.1%; Score 1219; DB 2; Length 3807;

Best Local Similarity 89.9%; Pred. No. 2e-238;

Matches 1332; Conservative 0; Mismatches 140; Indels 9; Gaps 2;

Qy 72 CATGCTCTCGGATATTGATGATCTGTAGTGTACAGAAAAATTTGTGGTCAAGTCTA 131

Db CATGCTCTCTGGGATATTGATGATCTGTAGTGTAGAAAAATTTGTGGTCAAGTCTA 760

Qy 132 TTATGGGTACTGTGTGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA 191

Db TTATGGGTACTGTGTGAGAGAGCAACCACTCTATTTTGTGCATCAGATGCTAA 820

Qy 192 AGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGACCAAGAGCC 251

Db AGCCTATGATACAGAGTACATAATGTTTGGGCCACACATGCTGTGACCAAGAGCC 880

Qy 252 CAACCCACAGAGTATTGGGAAATGTCACAGAAAAATTTTAACTGTGGAAAAATAA 311

Db CAACCCACAGAGTATTGGGAAATGTCACAGAAAAATTTTAACTGTGGAAAAATAA 940

Qy 312 CATGCTAGATCAGATGAGGATATATCACTTTATGGGATGAAAGCCCTAAAGCCCATG 371

Db CATGCTAGATCAGATGAGGATATATCACTTTATGGGATGAAAGCCCTAAAGCCCATG 1000

Qy 372 TGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTGTA-----ATATCAC 425

Db TGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTGTA-----ATATCAC 1060

Qy 426 TAAGAACTACTACTATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGAGAAATAA 485

Db TAAGAACTACTACTATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGAGAAATAA 1120

Qy 486 AAATTTGCTCTTTCTATATCACCAAGCATTAAGAAATTAAGTAAAGAAAGAAATGCACT 545

Db AAATTTGCTCTTTCTATATCACCAAGCATTAAGAAATTAAGTAAAGAAAGAAATGCACT 1180

Qy 546 TTTTAATAGACTTGATGTAGTACCATAAGAAAAATACTAATAATACTAAGTATAGGTTAAT 605

Db TTTTAATAGACTTGATGTAGTACCATAAGAAAAATACTAATAATACTAAGTATAGGTTAAT 1240

Qy 606 AAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCCAATCC 665

Db AAGTTGTAACACCTCAGTCATTACACAGGCTGTCCAAAGGTATCCTTTAGCCCAATCC 1300

Qy 666 CATACATTATTGTGTCGGCTGGTGTTCGATGCTAAAGTGTAAACATAAGACATTCAA 725

Db CATACATTATTGTGTCGGCTGGTGTTCGATGCTAAAGTGTAAACATAAGACATTCAA 1360

Qy 726 TGGATCAGGACCATGACAAAATGTCAGCACAGTACAATGTACATGGAATTAGGCCAGT 785

Db TGGATCAGGACCATGACAAAATGTCAGCACAGTACAATGTACATGGAATTAGGCCAGT 1420

Qy 786 GGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTAGATC 845

Db GGTGTCAACTCAACTGCTTTAAATGGCAGTCTAGCAGAGAGACATAGTAATTAGATC 1480

Qy 846 TGAAAAATTTACAGACATGCTTAAACCATATAGTACAGCTTAATGAATCTGTAGTAAT 905

Db TGAAAAATTTACAGACATGCTTAAACCATATAGTACAGCTTAATGAATCTGTAGTAAT 1540

Qy 1481 GCCTAATTTTCGGGCAATGCTAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540

Db GCCTAATTTTCGGGCAATGCTAAAGTCATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540

Qy 906 TAATTTGTACAGACCCCAACAATACAGAGAGAGGTTATCTATAGACCAGGGAGAGC 965

Db TAATTTGTACAGACCCCAACAATACAGAGAGAGGTTATCTATAGACCAGGGAGAGC 1600

Qy 966 ATTTTATGCAAGAGAAACATAATAGGAGATATAGCAAGACACATTGTAACATTAGTAG 1025

Db ATTTTATGCAAGAGAAACATAATAGGAGATATAGCAAGACACATTGTAACATTAGTAG 1660

Qy 1026 AGCAAAATGGAATTAACACTTTTCAACAGATAGTTTATAAAAATTAAGAGAAAAATTTAGGAA 1085

Db AGCAAAATGGAATTAACACTTTTCAACAGATAGTTTATAAAAATTAAGAGAAAAATTTAGGAA 1720

Qy 1086 TAAAAACAATAGCCTTTTAACTCCTCAGGAGGGGACCCAGAAAATTTAATGTCACAGTTT 1145

Db TAAAAACAATAGCCTTTTAACTCCTCAGGAGGGGACCCAGAAAATTTGTCACAGTTT 1780

Qy 1146 TAAATTTGGAGGGGAAATTTCTTACTACTGTAAATACAGCAACTGTTTAAATAGTACTTGGAA 1205

Db TAAATTTGGAGGGGAAATTTCTTACTACTGTAAATACAGCAACTGTTTAAATAGTACTTGGAA 1840

Qy 1206 TGTTACTGGAGGGCAAAATGGCACTGAAAGGAAATGACATAATCACTCCCAATGCAGAAAT 1265

Db TGTTACTGGAGGGCAAAATGGCACTGAAAGGAAATGACATAATCACTCCCAATGCAGAAAT 1900

Qy 1266 AAAACAAATTAATAATATGTCGAGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1325

Db AAAACAAATTAATAATATGTCGAGAGAAAGTAGGAAAAGCAATGTATGCCCTCCCATCAC 1960

Qy 1326 AGGACAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTTAAACAGAGATGGAGGTAA 1385

Db AGGACAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTTAAACAGAGATGGAGGTAA 2017

Qy 1386 TAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 1445

Db TAGTACTGAGACTGAGACTGAGATCTTTCAGACCTGGAGGAGGAGATATGAGGGACAATTG 2077

Qy 1446 GAGAAAGTGAATTTATATAATAATAAGTAGTAAAGATTTGAACCAATAGGAGTAGCACCAC 1505

Db GAGAAAGTGAATTTATATAATAATAAGTAGTAAAGATTTGAACCAATAGGAGTAGCACCAC 2137

Qy 1506 CAGGGCAAGAGAGAAACAGTGCACAAAGAGAAAAAGACCCG 1546

Db CAGGGCAAGAGAGAAAGAGTGGTGCAGAGAGAAAAAGAGCAG 2178

Search completed: November 12, 2004, 01:29:44

Job time : 675.232 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 118.359 Seconds
(without alignments)
12178.890 Million cell updates/sec

Title: US-09-687-864A-15
Perfect score: 2028
Sequence: 1 aagcttgccgcagctgtgta.....aactcgagtataatctaga 2028

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225.4	60.4	3807	1	US-08-022-835-5 Sequence 5, Appli
2	1225.4	60.4	3807	1	US-08-388-809-5 Sequence 5, Appli
3	1225.4	60.4	3807	2	US-08-647-714-5 Sequence 5, Appli
C 4	1174.2	57.9	3807	2	US-08-417-210A-78 Sequence 78, Appli
C 5	1174.2	57.9	3807	4	US-09-136-159A-78 Sequence 78, Appli
6	1172.6	57.8	2552	2	US-08-448-603A-27 Sequence 27, Appli
7	1172.6	57.8	2552	3	US-09-134-075-27 Sequence 27, Appli
8	1172.6	57.8	2552	3	US-09-492-739-27 Sequence 27, Appli
9	1172.2	57.8	2571	1	US-08-254-358-3 Sequence 3, Appli
10	1172.2	57.8	2571	1	US-08-475-391-3 Sequence 3, Appli
11	1172.2	57.8	2571	2	US-08-709-609-3 Sequence 3, Appli
12	1172.2	57.8	2571	4	US-09-552-950-3 Sequence 3, Appli
13	1172.2	57.8	2571	4	US-09-936-572-3 Sequence 3, Appli
14	1172.2	57.8	2571	5	PCT-US95-07178-3 Sequence 3, Appli
C 15	1172.2	57.8	6474	3	US-08-651-472-66 Sequence 66, Appli
C 16	1172.2	57.8	6474	3	US-08-358-928-66 Sequence 66, Appli
17	1172.2	57.8	6926	3	US-08-651-472-69 Sequence 69, Appli
18	1172.2	57.8	6926	3	US-08-358-928-69 Sequence 69, Appli
19	1172.2	57.8	9739	1	US-08-022-835-1 Sequence 1, Appli
20	1172.2	57.8	9739	1	US-08-388-809-1 Sequence 1, Appli
21	1172.2	57.8	9739	2	US-08-647-714-1 Sequence 1, Appli
22	1172.2	57.8	9746	1	US-08-022-835-3 Sequence 3, Appli
23	1172.2	57.8	9746	1	US-08-388-809-3 Sequence 3, Appli
24	1172.2	57.8	9746	2	US-08-647-714-3 Sequence 3, Appli
25	1171.4	57.8	1539	3	US-07-956-483-21 Sequence 21, Appli
26	1171.4	57.8	1539	3	US-08-472-240A-13 Sequence 13, Appli
27	1169.4	57.7	2573	2	US-08-448-603A-29 Sequence 29, Appli

28	1169.4	57.7	2573	3	US-09-134-075-29 Sequence 29, Appli
29	1169.4	57.7	2573	3	US-09-492-739-29 Sequence 29, Appli
30	1168.8	57.6	4527	2	US-08-944-449-8 Sequence 8, Appli
31	1168.8	57.6	4527	2	US-09-353-362-8 Sequence 8, Appli
32	1168.6	57.6	1532	2	US-08-037-816A-15 Sequence 15, Appli
33	1168.6	57.6	1532	2	US-08-530-146-15 Sequence 15, Appli
34	1165.4	57.5	1532	2	US-08-037-816A-27 Sequence 27, Appli
35	1165.4	57.5	1532	2	US-08-530-146-27 Sequence 27, Appli
36	1161.8	57.3	1932	4	US-09-475-515-31 Sequence 31, Appli
37	1161.8	57.3	2457	4	US-09-475-515-32 Sequence 32, Appli
38	1161.2	57.3	2570	2	US-08-448-603A-31 Sequence 31, Appli
39	1161.2	57.3	2570	2	US-09-134-075-31 Sequence 31, Appli
40	1161.2	57.3	2570	3	US-09-492-739-31 Sequence 31, Appli
41	1161	57.2	1419	4	US-09-475-515-30 Sequence 30, Appli
42	1160.8	57.2	9737	2	US-08-944-449-7 Sequence 7, Appli
43	1160.8	57.2	9737	3	US-09-353-362-7 Sequence 7, Appli
44	1160	57.2	1527	3	US-07-956-483-26 Sequence 26, Appli
45	1160	57.2	1527	3	US-08-472-240A-19 Sequence 19, Appli

ALIGNMENTS

RESULT 1
US-08-022-835-5
; Sequence 5, Application US/08022835
; Patent No. 5420030
; GENERAL INFORMATION:
; APPLICANT: Reitz Jr., Marvin S.
; APPLICANT: Franchini, Genoveffa
; APPLICANT: Markham, Phillip D.
; APPLICANT: Gallo, Robert C.
; APPLICANT: Lori, Franco C.
; APPLICANT: Popovic, Mikulas
; APPLICANT: Garner, Suzanne
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DAREY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,835
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

1 LOCATION: 648..3215
US-08-022-835-5

Query Match 60.4%; Score 1225.4; DB 1; Length 3807;
Best Local Similarity 90.2%; Pred. No. 8.3e-305;
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

72 CATGCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAATTTGGTGGTCAAGTCTA 131
701 CATGCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAATTTGGTGGTCAAGTCTA 760
132 TTATGGGTACTGTGTGGAGAGAGCAACCACTCTATTTGTGTGCATCAGATGCTAA 191
761 TTATGGGTACTGTGTGGAGAGAGCAACCACTCTATTTGTGTGCATCAGATGCTAA 820
192 AGCCTATCATACAGAGGTACATATGTTTGGGCCACACATCCCTGTGTACCCACAGACC 251
821 AGCATATCATACAGAGGTACATATGTTTGGGCCACACATCCCTGTGTACCCACAGACC 880
252 CAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAAAAATAA 311
881 CAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAAAAATAA 940
312 CATGCTAGATCAGATGCTAGGATATTAATCAGTTTATGGGATGAAGCCCTAAAGCCATG 371
941 CATGCTAGAACAAATGCTAGGATATTAATCAGTTTATGGGATGAAGCCCTAAAGCCATG 1000
372 TGTAATAATTAACCCCACTCTGTGTACCTTTAAATTTGCACTAATTTGA-----ATATCAC 425
1001 TGTAATAATTAACCCCACTCTGTGTACCTTTAAATTTGCACTAATTTGA-----ATATCAC 1060
426 TAAGAAATTAACCCCACTCTGTGTACCTTTAAATTTGCACTAATTTGA-----ATATCAC 485
1061 TGGGAATGACACTAATACACTAGTAGTACAGGGGAATGTTGGGGGAGAGAAATGAA 1120
486 AAATGTCTCTTTATATCACCACAGCATTAAGAAATTAAGGTAAAGAAAGAAATATGCACT 545
1121 AAATGTCTCTTTATATCACCACAGCATTAAGAAATTAAGGTAAAGAAAGAAATATGCACT 1180
546 TTTTATAGACTGTAGTAGTACCAATAGAAAATTAATACTAATAGTATAGTTAAT 605
1181 TTTTATAGACTGTAGTAGTACCAATAGAAAATTAATACTAATAGTATAGTTAAT 1240
606 AAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTATCTTTTCAGCCAAATCC 665
1241 AAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTATCTTTTCAGCCAAATCC 1300
666 CATACATTATTGTGTCGCCGCTGGTTCGATGCTAAAGGTAAAGGTAAAGAAATTAAGCAATCAA 725
1301 CATACATTATTGTGTCGCCGCTGGTTCGATGCTAAAGGTAAAGGTAAAGAAATTAAGCAATCAA 1360
726 TGGATCAGGACCATGCACAAATGTGACAGCAGTACAAATGTACATGGAATTAGGCCAGT 785
1361 TGGAAAGGACCATGCACAAATGTGACAGCAGTACAAATGTACATGGAATTAGGCCAGT 1420
786 GGTGTCACCTCACTGCTTTAAATGGCAGTCTACAGAGAGACATAGTAAATTAGATC 845
1421 AGTATCAACTCACTGCTTTAAATGGCAGTCTACAGAGAGACATAGTAAATTAGATC 1480
846 TGAAAATTTTCAGACAAATGCTTAAACCATTAATAGTACAGCTTAAATGAATCTGTAGTAAAT 905
1481 CGCCAAATTCGGGACATGCTTAAAGTCATATAGTACAGCTGATGAATCTGTAGAAAT 1540
906 TAAATGTCAGAGCCCAACAAATATACAGAGAGAGGTTATCTATAGCACCGGAGAGC 965
1541 TAAATGTCAGAGCCCAACAAATATACAGAGAGAGGTTATCTATAGCACCGGAGAGC 1600
966 ATTTTATCAGAGAGAGAGAGAGATATAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1025
1601 ATTTTATCAGAGAGAGAGAGAGATATAGAGAGAGATATAGAGAGAGAGAGAGAGAGAGAGAG 1660
1026 AGCAAAATGGAAATACACTTTTACACAGATAGTTTAAAAATTAAGAGAAAAATTTAGGAA 1085

Db 1661 AGCAAAATGGAAATGACACTTTTAAATAAGATAGTTATAAAAATAAGAGAAACAAATTTGGAA 1720
Qy TAAACAAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCAAGTTT 1145
Db TAAACAAATAGCCTTTTAAATCAATCCTCAGGAGGGGACCCAGAAAATTTGTAATGCAAGTTT 1780
Qy TAAATGTTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1205
Db TAAATGTTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1840
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1265
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1900
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1325
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1960
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1385
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 2017
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1445
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 2077
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1505
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 2137
Qy TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 1546
Db TGTACTGGAGGGGAAATTTCTTCTACTGTAATTAACACAACTGTTTAAATAGTACTTGGAA 2178

RESULT 2
US-08-388-809-5
; Sequence 5, Application US/08388809
; Patent No. 5576000
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,809
; FILING DATE: 15-FEB-1995
; PRIORITY DATA:
; APPLICATION NUMBER: US 08/022,835
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: LESLIE A. SERUNIAN
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4092US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800

```

; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3215
US-08-388-809-5

Query Match      60.4%; Score 1225.4; DB 1; Length 3807;
Best Local Similarity 90.2%; Pred. No. 8.3e-305;
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

Qy 72 CATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAATTTGCGGTACAGTCTTA 131
Db |||||
Qy 701 CATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAATTTGCGGTACAGTCTTA 760
Db |||||
Qy 132 TTATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCAGATGCTTAA 191
Db |||||
Qy 761 TTATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCAGATGCTTAA 820
Db |||||
Qy 192 AGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 251
Db |||||
Qy 821 AGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACC 880
Db |||||
Qy 252 CAACCCACAGAGTACGATTTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAATTA 311
Db |||||
Qy 881 CAACCCACAGAGTACGATTTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAATTA 940
Db |||||
Qy 312 CATGCTAGATCAGATGATGAGGATATATCAGTTTATGGGATGAAAGCTTAAAGCCATG 371
Db |||||
Qy 941 CATGCTAGACAAATGATGAGGATATATCAGTTTATGGGATGAAAGCTTAAAGCCATG 1000
Db |||||
Qy 372 TGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTGA-----ATATCAC 425
Db |||||
Qy 1001 TGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAGGAATGCTACTAA 1060
Db |||||
Qy 426 TAAGNATCTACTATCCCTAGCTAGGATGATGAGGGAATGTGGAAGAGAGGAATTA 485
Db |||||
Qy 1061 TGGGAATGACATTAATACCTAGTAGTACAGGGGGAATGTGGGGGAGGAGAAATGAA 1120
Db |||||
Qy 486 AAATGCTCTTCTATATACCAAGCATAGAAATTAAGGTAAAGAAAGAAATATGCACT 545
Db |||||
Qy 1121 AAATGCTCTTCTATATACCAAGCATAGAAATTAAGGTAAAGGTGAGAAAGAAATATGCACT 1180
Db |||||
Qy 546 TTTTAAATAGACTGTATGATACCAATAGAAAATTAATAATACTAATAAGTATAGGTTAAT 605
Db |||||
Qy 1181 TTTTAAATAGACTGTATGATACCAATAGAAAATTAATAATACTAATAAGTATAGGTTAAT 1240
Db |||||
Qy 606 AAGTGTAAACCTCAGTCATACAGAGGCTGTCCAAAGGTATCTTTACGCCAATTC 665
Db |||||
Qy 1241 AAGTGTAAACCTCAGTCATACAGAGGCTGTCCAAAGGTATCTTTACGCCAATTC 1300
Db |||||
Qy 666 CATACATTTATGTGTCGGCTGGGTTTGGCATGTCTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAA 725
Db |||||
Qy 1301 CATACATTTATGTGTCGGCTGGGTTTGGCATGTCTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAA 1360
Db |||||
Qy 726 TGGATCAGGACCATGACAAAATGTGACGACAGTACAAATGTACATGGAATTTAGGCCAGT 785
Db |||||
Qy 1361 TGGAAAGGACCATGACAAAATGTGACGACAGTACAAATGTACATGGAATTTAGGCCAGT 1420
Db |||||
Qy 786 GGTGTCAACTCACTGCTGTTAAATGGGAGTCTAGCAGAGAGACATAGTAATTAGATC 845
Db |||||
Qy 1421 AGTATCAACTCACTGCTGTTAAATGGGAGTCTAGCAGAGAGAGGAGTAAATTTAGATC 1480
Db |||||
Qy 846 TGAAAATTTTCAGACAAATGCTAAACCATATAGTACAGCTAAATGATCTGTAGTAAT 905
Db |||||
Qy 1481 GCCTAAATTTTCGGGCAATGCTAAAGTCAATAATAGTACAGCTGAATGAATCTGTAGAAAT 1540
Db |||||

RESULT 3
US-08-647-714-5
; Sequence 5, Application US/08647714
; Patent No. S869313
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C. LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,714
; FILING DATE:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4092US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 648..3215
US-08-647-714-5

Query Match 60.4%; Score 1225.4; DB 2; Length 3807;
Best Local Similarity 90.2%; Pred. No. 8.3e-305;
Matches 1336; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

QY 72 CATGCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTACAGTCTA 131
DB 701 CATGCTCTCTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTACAGTCTA 760
QY 132 TTATGGGGTACTGTGTGGAGAGAGCAACCACTCTATTTGTGTCATCAGATGCTAA 191
DB 761 TTATGGGGTACTGTGTGGAGAGAGCAACCACTCTATTTGTGTCATCAGATGCTAA 820
QY 192 AGCCTATGATACAGAGGTACATTAATTTGGGCCACACATCCCTGTGTACCCACAGACC 251
DB 821 AGCATATGATACAGAGGTACATTAATTTGGGCCACACATCCCTGTGTACCCACAGACC 880
QY 252 CAACCCACAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAACTGTGGAAAAATAA 311
DB 881 CAACCCACAAGAGTAGTATTGAAAATGTGACAGAAAAATTTTAACTGTGGAAAAATAA 940
QY 312 CATGTTAGATCAGATGCGATGAGGATATAATCAGTTTATGGGATGAAAGCCCTAAAGCCATG 371
DB 941 CATGTTAGAACAAATGCCATGAGGATATAATCAGTTTATGGGATCAAAAGCCCTAAAGCCATG 1000
QY 372 TGTAATAATTACCCCACTCTGTGTACTTTAAATTCGACTAATTTGA-----ATATCAC 425
DB 1001 TGTAATAATTACCCCACTCTGTGTACTTTAAATTCGACTAATTTGAGGAAATGCTACTAA 1060
QY 426 TAAGAAATACTACTAATCCCACTGTAGTACAGTGTGGGAAATGTAGGAGAAAGAGAAATAAA 485
DB 1061 TGGGAATGCACATAATACCACTAGTAGAGGGGGAATGGTGGGGGGGAGGAAATGAA 1120
QY 486 AAATTCCTCTTTCTATATCACCAAGCATAGAAATAAGGTAAAGAAAGAAATATGCACT 545
DB 1121 AAATTCCTCTTTCTATATCACCAAGCATAGAAATAAGGTAAAGAAAGAAATATGCACT 1180
QY 546 TTTTAAATAGACTTGATAGTACCAATAGAAATACTAATATCTAGTATAGTTAAT 605
DB 1181 TTTTAAATAGACTTGATAGTACCAATAGAAATACTAATATCTAGTATAGTTAAT 1240
QY 606 AAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCTTTACGCCAATCC 665
DB 1241 AAGTTGTAACACCTCAGTCATTACACAGGCCCTGTCCAAAGGTATCTTTAGCCCAATCC 1300
QY 666 CATACATTATTTGTGTCGGCTGGGTTCGCGATGCTAAAGTGAACAATAAGCATTTCAA 725
DB 1301 CATACATTATTTGTGTCGGCTGGGTTCGCGATGCTAAAGTGAACAATAAGCATTTCAA 1360

QY 726 TGGATCAGGACCATGSCACAAATGTGACACACAGTACAATGTACACATGGAATTAGGCCAGT 785
DB 1361 TGGAAAAGGACCATGTACAAATGTGACACACAGTACAATGTACACATGGAATTAGGCCAGT 1420
QY 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAACATAGTAATTAGATC 845
DB 1421 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGAGGTAGTAATTAGATC 1480
QY 846 TGAATAATTTACACACAAATGCTAAACCATATAGTACAGCTAAATGAATCTGTAGTAAT 905
DB 1481 CGCAATTTTCGGGACCAATGCTAAAGTCATATATAGTACAGCTGAATGAATCTGTAGTAAT 1540
QY 906 TAAATGTACAGAGCCCAACCAATACAGAGAGAGAGGTATCTATAGGACAGGAGAGC 965
DB 1541 TAAATGTACAGAGCCCAACCAATACAGAGAGAGAGGTATCTATAGGACAGGAGAGC 1600
QY 966 ATTTTATGCAAGAGAAACATATATAGGAGATATAGAGCAAGCAATTTGTAACATAGTAG 1025
DB 1601 ATTTTATGCAAGAGAAATATATAGGAGATATAGAGCAAGCAATTTGTAACATAGTAG 1660
QY 1026 AGCAAAATGGAAATACACTTTTACACACAGATAGTTTATAAATTTAGAGAAATTTAGGAA 1085
DB 1661 AGCAAAATGGAAATACACTTTTAAATAAGATAGTTTATAAATTTAGAGAAATTTAGGAA 1720
QY 1086 TAAACCAATAGCTTTTAAATCAATCTCAGGAGGAGGCCAGAAAATTTGTAATGACAGTTT 1145
DB 1721 TAAACCAATAGCTTTTAAAGCACTCTCAGGAGGAGGCCAGAAAATTTGTAATGACAGTTT 1780
QY 1146 TAAATGTGGAGGAAATCTTCTACTGTATAACAGCAACTGTTTAAATAGTACTTTGAA 1205
DB 1781 TAAATGTGGAGGAAATTTTCTACTGTATAACAGCAACTGTTTAAATAGTACTTTGAA 1840
QY 1206 TGTTACTGGAGGAGCAATGCACTGAGGAAATGACATATACATCCCAATGCAAGAT 1265
DB 1841 TGTTACTGAGAGTCAAAATAACACTGTAGAAAATAACAAATCAACATCCCAATGCAAGAT 1900
QY 1266 AAAACAAATTAATAATATGTCAGAGAAATAGTAAAGCAATGTATGCCCTCCCATCAC 1325
DB 1901 AAAACAAATTAATAATATGTCAGAGAAATAGTAAAGCAATGTATGCCCTCCCATCAC 1960
QY 1326 AGGACAAATTAATGTTTCAATCAAAATATTAAGGGTGTCTACTAAAGAGATGAGAGTAA 1385
DB 1961 AGGACAAATTAATGTTTCAATCAAAATATTAAGGGTGTCTACTAAAGAGATGAGAGTAA 2017
QY 1386 TAGTACTGAGACTGAGACTGAGATCTTACAGACCTGAGGAGGAGATATGAGGACAAATTG 1445
DB 2018 TCCTGAGGACAAAGAGCCGAGGTCTTACAGACCTGAGGAGGAGATATGAGGAGTAATIG 2077
QY 1446 GAGAAAGTAAATATATAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCCAC 1505
DB 2078 GAGAAAGTAAATATATAATAATAAGTAGTAAGAAATTTGAACCAATAGGAGTAGCACCCAC 2137
QY 1506 CAGGCAAGAGAGAGAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1546
DB 2138 CAGGCAAGAGAGAGAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2178

RESULT 4

US-08-417-210A-78/c
; Sequence 78, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: FIOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUPTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-78

Query Match 57.9%; Score 1174.2; DB 2; Length 3807;
Best Local Similarity 88.1%; Pred. NO. 1.2e-291;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

QY 52 TGGATCTCGGCTTCAGATCCATGCTCTCGGATATTGATCATCTGTAGTGTACAGAA 111
DB 1668 TGGGGGTGGAGATGGGGCACCATGCTCTCTGGGATGTTGATGATCTGTAGTGTACAGAA 1609

QY 112 AAATGTGGGTACACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTA 171
DB 1608 AAATGTGGGTACACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTA 1549

QY 172 TTTTGTGCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACAT 231
DB 1548 TTTTGTGCATCAGATGCTAAAGCCTTATGATACAGAGGTACATAATGTTTGGGCCACAT 1489

QY 232 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTCACAGAAAT 291
DB 1488 GCCTGTGTACCCACAGACCCCAACCAAGAGTAGTATTGGTAAATGTCACAGAAAT 1429

QY 292 TTTAACTGTGAAAAATAACATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGG 351
DB 1428 TTTAACTGTGAAAAATAACATGCTAGATCAGATGCATGAGGATATAATCAGTTTATGG 1369

QY 352 GATGAAAGCCTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATGCACT 411
DB 1368 GATCAAGCCTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTTACTTTAAATGCACT 1309

QY 412 AATTTG-----AATATCACTAAGAAATACCTACTACTATCCCACTAGTAGCAGTGG 459
DB 1308 GATTTGAGGAATACCTACTAATACCAATATAGTACTGCTTAACAAATAGTAATACGAG 1249

QY 460 GGAATGATGAGAGAGAGAGAAATAAAAAATTCCTCTTTCTATATCAACCAAGACATAAGA 519
DB 1248 GGAACATAAAGGAGAGAGAAATGAAAACTGCTCTTTCAATATATCCCAAGACATAAGA 1189

QY 520 AATAAGGTAAAGAAAGATATGCACTTTTAAATAGACTTGTATGTATACCAATAGAAAAAT 579
DB 1188 GATAAGATGCAGAAAGATATGCACTCTCTTTATAAACTTGATATAGTATCAAT--AAAT 1132

QY 580 ACTAATAATCTAAGTATAGTTAATAGTTGTTAACTCAGCTCAGTCAATACACAGCCCTGT 639
DB 1131 AATGATAGTACCAGCTATAGTTGATAGTTGTTAACTCAGTCAATACACAGCTTGT 1072

QY 640 CCAAGGTATCTTTTCAGCCCAATCCCATACATATTGTGTCGCGCTGGGTTTCGCGATG 699
DB 1071 CCAAGATATCTTTTGAGCCCAATCCCATACATATTGTGTCGCGCTGGGTTTCGCGAT 1012

QY 700 CTTAAGTGTAAACAATAAGACATTTCAATCGATCAGGACCATGCACAAATGTCAGCACAGTA 759
DB 1011 CTTAAGTGTAAACAATAAGATTTAGTGGAAAGAGATCATGTAAATATGTCAGCACAGTA 952

QY 760 CAATGTACACATGGAATTTAGGCCAGTGTGTCACATCAACTCACTGCTGTTAAATGGCAGTCTA 819
DB 951 CAATGTACACATGGAATTTAGGCCAGTGTATCAACTCACTGCTGTTAAATGGCAGTCTA 892

QY 820 GCAGAAGAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATATA 879
DB 891 GCAGAAGAAGAGGTAGTAATTTAGATCTGAGAATTTCAATGATAATGCTTAAACCATATA 832

QY 880 GTACAGCTTAATGAATCTGTAGTAATTTAATTTGTACAAGACCCCAACAATACAGAGA 939
DB 831 GTACATCTGAATGAATCTGTACAATTTAATTTGTACAAGACCCCAACAATACAGAGA 772

QY 940 AGTTTATCTATAGGACAGGAGAGACATTTTATGCAAGAAGAAACATATATAGGAGATATA 999
DB 771 AGGATACATATAGGACAGGAGAGACATTTTATACACAAAAAATATATATAGGAACTATA 712

QY 1000 AGACAAGCACATTTGTAACATTTAGTAGACAAAAATGGAATAACACATTTTCAACAGATGTT 1059
DB 711 AGACAAGCACATTTGTAACATTTAGTAGACAAAAATGGAATAACACATTTTAAAGACAGATGTT 652

QY 1060 ATAAATTTAAGAGAAAAATTTAGGAATAAACAATAGCTTTTAAATCAATCTCAGGAGGG 1119
DB 651 AGCAAAATTTAAAGAAACAATTTAAGAATAAACAATAGCTTTTAAATCAATCTCAGGAGGG 592

QY 1120 GACCAGAAAAATTTGTAATGTCACAGTTTAAATTTGTGGAGGGAAATCTTCTACTGTAAATACA 1179
DB 591 GACCAGAAAAATTTGTAATGTCACAGTTTAAATTTGTGGAGGGAAATCTTCTACTGTAAATACA 532

QY 1180 GCACAACCTGTTTAAATAGTACTTGGAAATTTACTGGAGGGAACAATGGCACTGAAGG---A 1236
DB 531 TCACCCTGTTTAAATAGTACTTGGAAATTTACTGGAAATAATACTACAGGGTCA 472

QY 1237 AATGACATATACACATCCATGCAAGTAAACAAATATATAATATGTCGACAGAAAGTA 1296
DB 471 AATGACATATACACATCCATGCAAGTAAACAAATATATAATATGTCGACAGAAAGTA 412

QY 1297 GGAAGAACAATGTTATGCCCTCCCATCACAGACAATTAGATGTTCAATCAATATTACA 1356
DB 411 GGAAGAACAATATATGCCCTCCCATCACAGACAATTAGATGTTCAATCAATATTACA 352

QY 1357 GGGCTGCTACTAACAGAGATGGAGTAAATAGTACTGA--GACTGAGACTGAGATCTTC 1413
DB 351 GGGCTGCTACTAACAGAGATGGTGGTAAAGACACGGACACGACACCGAGATCTTC 292

QY 1414 AGACCTGGAGGAGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAGTA 1473
DB 291 AGACCTGGAGGAGAGATATGAGGACAAATTTGGAGAGTGAATTTATATAATATAAGTA 232

QY 1474 GTAAGAATTGAACCAATAGGAGTAGCCACCCAGGGCAAGAGAGAAAGACAGTGCAGAGA 1533
DB 231 GTAAGAATTGAACCAATAGGAGTAGCCACCCAGGGCAAGAGAGAGAGTGGTGCAGAGA 172

QY 1534 GAAAAAAGA 1542
DB 171 GAAAAAAGA 163

RESULT 5
US-09-136-159A-78/c
; Sequence 78, Application US/09136159A
; Patent No. 6596279
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136,159A

;
; CURRENT FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-09-136-159A-78

Query Match 57.9%; Score 1174.2; DB 4; Length 3807;
Beat Local Similarity 88.1%; Pred. No. 1.2e-291;
Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

QY 52 TGGATCTCGGCTTCAGATCCATGCTCTGGGATTTGATGATCTGTAGTGTACAGAA 111
DB 1668 TGGGGGTGGAGATGGGGCACCATGCTCTTGGGATGTTGATGATCTGTAGTGTACAGAA 1609

QY 112 AAAATTGGGGTCCAGATCTTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 171
DB 1608 AAAATTGGGGTCCAGATCTTATTATGGGGTACCTGTGTGGAGAGAGCAACCACTCTA 1549

QY 172 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTGGGCCACACAT 231
DB 1548 TTTTGTGATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTGGGCCACACAT 1489

QY 232 GCCTGTGTACCCACAGACCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAAT 291
DB 1488 GCCTGTGTACCCACAGACCCCAACCCACAGAGGTAGTATTGGGAAATGTGACAGAAAT 1429

QY 292 TTTTAACTGTGGAAAAATAACAATGTGTAGATCAGATGCAATGAGGATATTAATCAGTTTATGG 351
DB 1428 TTTTAACTGTGGAAAAATAACAATGTGTAGATCAGATGCAATGAGGATATTAATCAGTTTATGG 1369

QY 352 GATGAAAGCCTTAAGCCATGTGTAAAATTTAACCCCACTCTGTGTACTTTAAATTTGCACT 411
DB 1368 GATGAAAGCCTTAAGCCATGTGTAAAATTTAACCCCACTCTGTGTACTTTAAATTTGCACT 1309

QY 412 AATTG-----AATATCTAAGATATCTTAATCCCACTAGTAGCAGCTGG 459
DB 1308 GATTTGAGGAATACTACTAATACCATATATGCTGCTTAATTAACCAATAGTATAGCGAG 1249

QY 460 GGAATGATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCATAGA 519
DB 1248 GGAACAAATAAGGGAGGAGAAATGAANAATCTCTCTTCAATATCACCACAGCATAGA 1189

QY 520 AATAAGGTAAGAAAGATATGCACCTTTTAAATAGACTGTGTAGTACCATAAGAAAT 579
DB 1188 GATAAGATGCAAGAAAGATATGCACCTTTTAAATAGACTGTGTAGTACCATAAGAAAT 1132

QY 580 ACTAATAATACATAGTATAGGTTAATAGTGTGACCTCAGTCACTATACAGAGCCTGT 639
DB 1131 AATGATAGTACCAGCTATAGGTTGATAGTGTGATACCTCAGTCACTATACAGAGCCTGT 1072

QY 640 CCAAGAGGTATCTTTTTCAGGCAATTCCTCATACATATTGTCCTCCGCTGGGTTTCGATG 699

DB 1071 CCAAAGATATCTTTTGAGCCAAATCCCATACACATTAATGTCGCCCGGTGGTTTGGCGATT 1012
QY 700 CTAAGTGTAAACAATAAGACATTCATGATGATGAGGACCATGACAAATGTCAGACACAGTA 759
DB 1011 CTAAGTGTAAACAATAAGAGTTCAAGTGGAAAGATCATGTAAATGTCAGACACAGTA 952
QY 760 CAATGTACACATGGAATTTAGGCCAGTGGTCAACTCAACTGCTTTAAATGGCAGTCTA 819
DB 951 CAATGTACACATGGAATTTAGGCCAGTGGTCAACTCAACTGCTTTAAATGGCAGTCTA 892
QY 820 GCAGAAGAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATATA 879
DB 891 GCAGAAGAAGAGGTAGTAATTTAGATCTGAGAATTTCAATGTAATGCTTAAACCATATA 832
QY 880 GTACAGCTAAATGAATCTGTAGTAATTAATTTGTCAAGACCCCAACAATACAGAGA 939
DB 831 GTACATCTGAATGAATCTGTACAAATTAATTTGTCAAGACCCCAACTCAATTAAGAAAA 772
QY 940 AGGTTATCTATAGGACCGAGGAGAGCATTTTATGCAAGAGAAAAATATAGGAGATATA 999
DB 771 AGGATACATATAGGACCGAGGAGAGCATTTTATACACAAAAAATATATAGGAACATA 712
QY 1000 AGACAAGCACAATTGTAACATTTAGTAGACAAAATGGAATAACACTTTTACACAGATGTT 1059
DB 711 AGACAAGCACAATTGTAACATTTAGTAGACAAAATGGAATAACACTTTTAAAGACAGATGTT 652
QY 1060 ATAAAAATTAAGAGAAAAATTTAGGAATAAAAAACAATAGCTTTTAATCAATCTCAGAGGG 1119
DB 651 AGCAAAATTAAGAGAAACAATTTAAGAAATAAACAATAGTCTTTTAATCAATCTCAGAGGG 592
QY 1120 GACCCAGAAAAATGTAATGACACAGTTTAAATTTGTGGAGGGAATTTCTTCTACTGTAATA 1179
DB 591 GACCCAGAAAAATGTAATGACACAGTTTAAATTTGTGGAGGGAATTTCTTCTACTGTAATA 532
QY 1180 GCACAACCTGTTTATAGTACTTTGGAAATGTTACTGGAGGGAACAATGCGCACTGAAGG---A 1236
DB 531 TCACCACCTGTTTAAATAGTACTTTGGAAATGTTAAATTAATTAATTAATTAATTAATTA 472
QY 1237 AATGACATAATCAACACTCCAAATGACAGATAAAAAACAATTAATAATTAATTAATTAATTA 1296
DB 471 AATGACATAATCAACACTCCAAATGACAGATAAAAAACAATTAATAATTAATTAATTAATTA 412
QY 1297 GGAAGAAGCAATGTATGCCCTCCCATCAAGGACAAATTTAGATGTTCTCAAAATTAATTA 1356
DB 411 GGAAGAAGCAATGTATGCCCTCCCATCAAGGACAAATTTAGATGTTCTCAAAATTAATTA 352
QY 1357 GGGTGTCTACTAAACAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTC 1413
DB 351 GGGTGTCTACTAAACAGAGATGGTAAAGGACACGGAACGACACGAGATCTTC 292
QY 1414 AGACTGGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAATAATAATA 1473
DB 291 AGACTGGAGGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATAATAATAATAATA 232
QY 1474 GTAAGAATTGAACCAATAGGAGTAGCACCACCGGCAAGAGAGAGAGAGAGAGAGAGAGAG 1533
DB 231 GTAAGAATTGAACCAATAGGAGTAGCACCACCGGCAAGAGAGAGAGAGAGAGAGAGAG 172
QY 1534 GAAAAAAGA 1542
DB 171 GAAAAAAGA 163

RESULT 6
US-08-448-603A-27
; Sequence 27, Application US/08448603A
; Patent No. 5864027
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fast-Seq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,603A

FILING DATE: 07-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/072,833

FILING DATE: 07-JUN-93

ATTORNEY/AGENT INFORMATION:

NAME: Haliday, Emily

REGISTRATION NUMBER: 38903

REFERENCE/DOCKET NUMBER: 14918-704

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-393-2000

TELEFAX: 415-393-2286

TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 2552 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2552

US-08-448-603A-27

Query Match 57.8%; Score 1172.6; DB 2; Length 2552;

Best Local Similarity 89.2%; Pred. No. 2.6e-291;

Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

Qy	64	TCGAGATCCATGCTCTTGGGATATTTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTC	123
Db	46	TGGGACCATGCTCTTGGGATTTGATGATCTGTAGTGTCTACAGAAAAATTTGGGTC	105
Qy	124	ACAGTCTATTATGGGTACCTGTGGGAGAGCAACCACTCTATTTTTGGCATCA	183
Db	106	ACAGTCTATTATGGGTACCTGTGGGAGAGCAACCACTCTATTTTTGGCATCA	165
Qy	184	GATGCTAAAGCTATGATACAGAGTACATATTTTGGGCCACACATGCTGTGTACCC	243
Db	166	GATGCTAAAGCATATGATACAGAGTACATATTTTGGGCCACACATGCTGTGTACCC	225
Qy	244	ACAGACCCCAACCCCAAGAGAGTATTTGGGAAATGTGACAGAAAAATTTTAAATGTGG	303
Db	226	ACAGACCCCAACCCCAAGAGAAATAGGATTTGGGAAATGTGACAGAAAAATTTTAAATGTGG	285
Qy	304	AAAAATACATGTTAGTACAGTACATGATGATATTAATCAGTTTATGGATGAAGCCTA	363
Db	286	AAAAATACATGTTAGTACAGTACATGATGATATTAATCAGTTTATGGATGAAGCCTA	345
Qy	364	AAGCCATGTGAAAAATTAACCCCACTCTGTGTTACTTTTAAATTTGCAATATC	423
Db	346	AAGCCATGTGAAAAATTAACCCCACTATGTGTTACTTTTAAATTTGCAATATG	399
Qy	424	ACTAAGAAATCTACTTAATCCCACTAGTAGCAGCTGGGAAATGTAGGAAAGGAGAAATA	483
Db	400	---AAAAATGCTACTTAATACCACCTAGTAGCAGCTGGGAAAGATGTAGGAGAGGAGAAATA	456
Qy	484	AAAAATTCCTCTTCTATATACCAACAGCATAGAAATAGGTAAGAAAGAAATATGCA	543
Db	457	AAAAACTGCTCTTCTCAATGTCCCAACAGTATAGAGATAAGATGAAGATGAATATGCA	516

RESULT 7

US-09-134-075-27

; Sequence 27, Application US/09134075

Qy	544	CTTTTAAATAGACTTGTAGTACCAATAGAAATACTAATAATCTAATAGTATAGGTTA	603
Db	517	CTTTTAAATAGACTTGTAGTACCAATAG--ATAATGATAATCTAGCTATAGGTTG	573
Qy	604	ATAAGTTGTACACCTCAGTCATTACACAGCCCTGTCACAAAGGTATCTTTTCAGCCAATT	663
Db	574	ATAAGTTGTACACCTCAGTCATTACACAGCCCTGTCACAAAGGTATCTTTTCAGCCAATT	633
Qy	664	CCCATACATTATTGTGTCGCCGCTGGGTTTCGGATGCTTAAAGTGTAAACAATAAGACATTC	723
Db	634	CCCATACATTATTGTGTCGCCGCTGGGTTTCGGATGCTTAAAGTGTAGAGATAAAAAGTTC	693
Qy	724	AATGGATCAGACCATGTGACAAATGTGACGACAGTACAATGTACACATGGAATTAGGCCA	783
Db	694	AACGGAACAGACCATGTACAAATGTGACGACAGTACAATGTACACATGGAATTAGGCCA	753
Qy	784	GTGGTGTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATAGA	843
Db	754	GTAGTATCACTCACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGAGATAGTAATAGA	813
Qy	844	TCTGAAAATTTTCACAGACAAATGCTTAAACCAATAATAGTACAGCTAAATGAAATCTGTAGTA	903
Db	814	TCTGCCAATTTCTCGGACATGCTTAAACCAATAATAGTACAGCTGAACGAATCTGTAGAA	873
Qy	904	ATTAATTTGTACAGACCCCAACAAATACAAGAGAGAGTTTATCTATAGGACCAAGGGAGA	963
Db	874	ATTAATTTGTACAGACCCCAACAAATACAAGAGAGAGTATACATATAGGACCAAGGGAGA	933
Qy	964	GCATTTTATGCAAGAGAAACATATAGGAGATATAGACAGACATGTTGAACATTAAT	1023
Db	934	GCATTTTATGCAAGAGAGAAATATAGGAGATATAGACAGACATGTTGAACATTAAT	993
Qy	1024	AGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAATTAAGAGAGAAAAATTTAGG	1083
Db	994	AGCAAAATGGAATATATCTTTTAAACAGATAGTTACAAATTTAGAGAACATTTT---	1050
Qy	1084	AATAAAACAATPAGCCTTTAATCAATCTCAGAGGGGACCCAGAAATTTGTAATGCACAGT	1143
Db	1051	AATAAAACAATPAGTCTTTTAAATCACTCTCAGAGGGGACCCAGAAATTTGTAATGCACAGT	1110
Qy	1144	TTTAAATTTGGAGGGGAAATTTCTCTACTGTAATACAGACACACTGTTTAAATAGTACTTGG	1203
Db	1111	TTTAAATTTGGAGGGGAAATTTTCTACTGTAATACACACCACTGTTTAAATAGTACTTGG	1170
Qy	1204	AATGTTACTGGAGGGAACAAATGGCACTGAAGGAAATGA-----CATATACACA	1251
Db	1171	AATTTACTTTATCTTGGATATATCTGAGGGTCAATGACACTGGAGAAATATACACA	1230
Qy	1252	CTCCAATGCAGAAATAAAAATTAATAATGTGGCAGAAAGTAGGAAAAAGCAATGTAT	1311
Db	1231	CTCCAATGCAGAAATAAAAATTAATAATGTGGCAGAAAGTAGGAAAAAGCAATGTAT	1290
Qy	1312	GCCCTCCCATCAGACAGCAAAATTAGATGTTCAATATATACAGGCTGCTACTACA	1371
Db	1291	GCCCTCCCATCAGAGCAAAATTAGATGTTCAATATATACAGGCTGCTACTACA	1350
Qy	1372	AGAGATGGAGTAAATAGTACTGAGACTGAGACTCTTTCAGACCTTGGAGGAGAGAT	1431
Db	1351	AGAGATGGTGAATA-----ACAGGGAACCGAGATCTTCAGACCTTGGAGGAGAGAT	1404
Qy	1432	ATGAGGACAAATTTGGAGAGTGAATATATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1491
Db	1405	ATGAGGACAAATTTGGAGAGTGAATATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1464
Qy	1492	GGAGTAGACCCACAGGGCAAGAGAGAAACAGTGCACAGAGAAAAAGACCCG	1546
Db	1465	GGAGTAGACCCCAAGGCAAGAGAGAGTGTATGCAGAGAGAAAAAGAGCAG	1519

; Patent No. 6042836
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,603
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hallday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2552
US-09-134-075-27

Query Match 57.8%; Score 1172.6; DB 3; Length 2552;
Best Local Similarity 89.2%; Pred. No. 2.6e-291;
Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

Qy	64	TCGAGATCCATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGGGGTC	123
Db	46	TGGGGCACATGCTCTCTGGGATATTGATGATCTGTAGTGTACAGAAAAATTGGGGTC	105
Qy	124	ACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACACACCTCTATTTTGTGCATCA	183
Db	106	ACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACACACCTCTATTTTGTGCATCA	165
Qy	184	GATGCTAAAGCCATGATACAGAGTACATAATGTGTGGGCCACACATGCCTGTGTACCC	243
Db	166	GATGCTAAAGCATATGATACAGAGTACATAATGTGTGGGCCACACATGCCTGTGTACCC	225
Qy	244	ACAGACCCCAACCCACAGAGTACTGTTGGGAATGTGACAGAAAAATTTTAAACATGGG	303
Db	226	ACAGACCCCAACCCACAGAGTACTGTTGGGAATGTGACAGAAAAATTTTAAACATGGG	285
Qy	304	AAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGCCTA	363
Db	286	AAAAATAACATGGTAGAGACAGATGATGAGGATATAATCAGTTTATGGGATCAAAAGCTTA	345
Qy	364	AAGCCATGTGTAATAATTAACCCACCTCTGTGTTACTTTTAAATGGACACTAAATTTGAATATC	423
Db	346	AAGCCATGTGTAATAATTAACCCACCTCTGTGTTACTTTTAAATGGACACTGATTTG	399

Qy	424	ACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAAATGATGGAGAAAGGAGAATA	483
Db	400	---AAAAATGCTACTAATACCACCTAGTAGCAGCTGGGGAAAGATGGAGAGGAGAAATA	456
Qy	484	AAAAATTGCTCTTCTATATACCCACAAGCATAAGAAATAGGTTAAAGAAAGATATATGCA	543
Db	457	AAAAACTGCTCTTTCAATGTACCCACAAGTATAAGAGATAGATGAAGAATATATGCA	516
Qy	544	CTTTTAAATAGACITTAGTAGTACCATAAGAAATACTATAATATCTAACTTAAGTATAGGTTA	603
Db	517	CTTTTAAATAGACITTAGTAGTACCATAAG---ATAATGATATATCTAGCTATAGGTTG	573
Qy	604	ATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTATCCTTTACGCCAATT	663
Db	574	ATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAGGTGTCCTTTGAGCCAATT	633
Qy	664	CCCATACATTATTGTGTCCTGGCTGGGTTTTCGGATGCTAAAGTGTAAACAATAAGACATTC	723
Db	634	CCCATACATTATTGTGTCCTGGCTGGGTTTTCGGATGCTAAAGTGTAAACAATAAGACATTC	693
Qy	724	AATGGATCAGGACCATGCACAAATGTCAGCACAGTACAAATGTCACACATGGAATTAGGCCA	783
Db	694	AACGGAACAGGACCATGTACAAATGTCAGCACAGTACAAATGTCACACATGGAATTAGGCCA	753
Qy	784	GTGGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA	843
Db	754	GTAGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAAGACATAGTAATTAGA	813
Qy	844	TCTGAAATTTTCACAGACAATGCTAAACCAATATAGTACAGCTAAATGAATCTGTAGTA	903
Db	814	TCTGCAATTTCTCGGCAATGCTAAACCAATATAGTACAGCTAAATGAATCTGTAGTA	873
Qy	904	ATTAATTTGTCAAGACCCCAACAATACRAGAAAGGTTTCTATAGGACCAAGGAGA	963
Db	874	ATTAATTTGTCAAGACCCCAACAATACRAGAAAGGTTTCTATAGGACCAAGGAGA	933
Qy	964	GCATTTTATGCAAGAAGAAACATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGT	1023
Db	934	GCATTTTATGCAAGAGAAATATAGGAGACATAGACAAGCACATTTGTAACATTAGT	993
Qy	1024	AGAGCAAAATGGAAATACACTTTTACACAGATAGTTATAAAATTAAGGAAAAATTTAGG	1083
Db	994	AGCAAAATGGAAATATACTTTTAAACAGATAGTTTACAAATTAAGGAAAAATTTAGG	1050
Qy	1084	AATAAAACAATAGCTTTTAATCAATCTCAGAGGGGACCCAGAGAAATTTGTAATGCACAGT	1143
Db	1051	AATAAAACAATAGCTTTTAATCACTCTCAGAGGGGACCCAGAGAAATTTGTAATGCACAGT	1110
Qy	1144	TTTAATTGTGGAGGGGAATCTCTTACTGTATAACAGACAACCTGTTTAAATAGTACTTGG	1203
Db	1111	TTTAATTGTGGAGGGGAATTTTCTACTGTATAACACACCACCTGTTTAAATAGTACTTGG	1170
Qy	1204	AATGTTACTGGAGGACAAATGGGCACCTGAAGAAATGA-----CATTAATCACA	1251
Db	1171	AATTATCTTATCTTGGAAATAACTGGAAGGCTCAATATGACCTGGAAGAAATATCACA	1230
Qy	1252	CTCCAAATGCAATAAACAATTTATAATATGTGGCAGAAAGTAGGAAAAAGCAATGTAT	1311
Db	1231	CTCCAAATGCAATAAACAATTTATAAACAATGTGGCAGAAAGTAGGAAAAAGCAATGTAT	1290
Qy	1312	GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATTTATACAGGCTGCTACTAACA	1371
Db	1291	GCCCTCCCATACAGGACAAATTAGATGCTCATCAAAATTTATACAGGCTGCTACTAACA	1350
Qy	1372	AGAGATGAGGATATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAT	1431
Db	1351	AGAGATGAGGATATAGTACTGAGACTGAGACTGAGACTTTCAGACCTGGAGGAGGAT	1404
Qy	1432	ATGAGGACAAATTTGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1491
Db	1405	ATGAGGACAAATTTGAGAAAGTGAATTATATAAATATAAAGTAGTAAGAAATTTGAACCAATA	1464
Qy	1492	GGAGTAGCACCCACGAGGGCAAGAGAGAAACAGTGCACAAAGAGAAAAAAGACCGG	1546

Db 1465 GGAGTAGCACCACCAAGCAAGAGAGAGTGTGCGAGAGAGAGAGAGCAG 1519
|||||
RESULT 8
US-09-492-739-27
; Sequence 27, Application US/09492739
; Patent No. 6331404
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,739
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,075
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2552
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-492-739-27
Query Match 57.8%; Score 1172.6; DB 3; Length 2552;
Best Local Similarity 89.2%; Pred. No. 2.6e-291;
Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;
Qy 64 TCGAGATCCATGCTCTTGGGATTTGATCTGTAGTGTCTACAGAGAAATTTGGGTC 123
Db 46 TGGGCGACCATGCTCCTTGGGATTTGATCTGTAGTGTCTACAGAGAAATTTGGGTC 105
Qy 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGCAACACCACTCTATTATTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGCAACCACTCTATTATTTGTGCATCA 165
Qy 184 GATGCTAAAGCCTATGATACAGAGTACATAATTTGGGCAACACATGCTGTGTACC 243
Db 166 GATGCTAAAGCATATGATACAGAGTACATAATTTGGGCAACACATGCTGTGTACC 225
Qy 244 ACAGACCCCAACCCACAGAAAGTAGTATTTGGAAATGTGACAGAAATTTTAACATGTGG 303
Db 226 ACAGACCCCAACCCACAGAAATAGGATTTGGAAATGTAAACAGAAATTTTAAACATGTGG 285

Qy 304 AAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAGAGCCTA 363
Db 286 AAAATAACATGGTAGAGACAGATGCATGAGGATATAATCAGTTTATGGATGAGAGCCTA 345
Qy 364 AAGCATGTGTAATAAATTAACCCCACTCTGTGTGTACTTTAAATTTGACATTAATTTGAATATC 423
Db 346 AAGCATGTGTAATAAATTAACCCCACTATGTGTGTACTTTAAATTTGACATTAATTTGAATATC 399
Qy 424 ACTAAGAAATACCTAATCCCACTAGTAGAGCTGGGAATGATGGAGAAAGAGAAATA 483
Db 400 --AAATAATGCTACTAATACCACCTAGTAGAGCTGGGAAGATGGAGAGAGAGAAATA 456
Qy 484 AAAAATTCCTCTTCTATATCACCACAGCATAAGAAATAGGTAAAGAAAGAAATATGCA 543
Db 457 AAAAATTCCTCTTCTATATCACCACAGCATAAGAAATAGGTAAAGAAAGAAATATGCA 516
Qy 544 CTTTTTAATAGACTTGTAGTAGTACCAATAGAAAATACCTAAATACTAAAGTATAGTTA 603
Db 517 CTTTTTAATAGACTTGTAGTAGTACCAATAG---ATAATGATTAATCTAGCTATAGTTG 573
Qy 604 ATAAAGTTGTAACACCTCAGTCAATTAACAGAGCCTGTCCAAAGGATATCCTTTTCAGCAAT 663
Db 574 ATAAAGTTGTAACACCTCAGTCAATTAACAGAGCCTGTCCAAAGGATATCCTTTTCAGCAAT 633
Qy 664 CCATACATATTTGTGTCCTGGGTTTGGGATGCTAAAGTGTAAACATTAAGACATTC 723
Db 634 CCATACATATTTGTGTCCTGGGTTTGGGATTTCTAAAGTTGTAGAGATAAAAGTTTC 693
Qy 724 AATGGATCAGGACCAATGCACAAATGTGCAGCAGTACAAATGTACACATGGAATTAGGCCA 783
Db 694 AATGGATCAGGACCAATGTACAAATGTGCAGCAGTACAAATGTACACATGGAATTAGGCCA 753
Qy 784 GTGGTGTCAACTCTGTTAAATGGCAGTCTAGCAGAGAAAGACATAGTAATTAAGA 843
Db 754 GTGGTGTCAACTCTGTTAAATGGCAGTCTAGCAGAGAAAGACATAGTAATTAAGA 813
Qy 844 TCTGAAATTTTCAAGACAAATGCTAAACCATATATAGTACAGCTAAATGAATCTGTAGTA 903
Db 814 TCTGCAATTTCTCGGACAAATGCTAAACCATATATAGTACAGCTGAACGAATCTGTAGAA 873
Qy 904 ATTAATTTGTACAGACCCCAACAAATACAGAGAGGTTTATCTATAGGACCGAGAGA 963
Db 874 ATTAATTTGTACAGACCCCAACAAATACAGAGAGTATACATATAGGACCGAGAGA 933
Qy 964 GCATTTTATGCAACAGGAGAAATTAAGAGACATATAAGACAGCATTTGTAACTTAGT 1023
Db 934 GCATTTTATGCAACAGGAGAAATTAAGAGACATATAAGACAGCATTTGTAACTTAGT 993
Qy 1024 AGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAATTAAGAGAAAAATTTAGG 1083
Db 994 AGACAAAAATGGAATAATACCTTTAAACAGATAGTTACAAAAATTAAGAGAACATTTT 1050
Qy 1084 AATAAACAATAGCCTTTAATCAATCTTCAGAGGGGACCCAGAAATTTGTATGACAGT 1143
Db 1051 AATAAACAATAGTCTTTAATCACTCTTCAGAGGGGACCCAGAAATTTGTATGACAGT 1110
Qy 1144 TTTAATTTGTGAGGGGAATTTCTTCTACTGTATAACAGACACTGTTTAAATAGTACTGG 1203
Db 1111 TTTAATTTGTGAGGGGAATTTTCTACTGTATAACACCACTGTTTAAATAGTACTGG 1170
Qy 1204 AATGTTACTGGAGGACAAATGGCACTGAAAGAAATGA-----CATATACACA 1251
Db 1171 AATTATCTTATCTTGGAAATAATCTGAAGGGTCAATAGACATGGAAGAAATATACACA 1230
Qy 1252 CTCCAAATCGAATAAATAAATTAATAATGTGGCAGAAAGTAGGAAAGCAATGTAT 1311
Db 1231 CTCCAAATCGAATAAATAAATTAATAAATGTGGCAGAAAGTAGGAAAGCAATGTAT 1290
Qy 1312 GCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACAGGCTGCTACTAACA 1371
Db 1291 GCCCTCCCATTAAGAGGACAAATTAGATGCTCATCAATATTATACAGGCTGCTATTACA 1350
Qy 1372 AGAGATGGAGGTAATAGTACTGAGACTGAGACTGAGACTCTTCAGACCTGGAGGAGAGAT 1431

Db 1351 AGAGATGGTGAATA-----ACAGCGAAACCGAGATCTTCAGACCTGGAGGAGGAGAT 1404
Qy 1432 ATGAGGACAATTGGAGAGTGAATTATATAAATAAAGTAGTAAGAAATTGAACCAATA 1491
Db 1405 ATGAGGACAATTGGAGAGTGAATTATATAAATAAAGTAGTAAGAAATTGAACCAATA 1464
Qy 1492 GGAGTAGCACCCACCAGGCGCAAGAGAGAACAGAGTGCAGAAAGAGAAAGACCGG 1546
Db 1465 GGAGTAGCACCCACCAGGCGCAAGAGAGAGTGCAGAGAGAGAGAGAGAGAGAG 1519

RESULT 9

US-08-254-358-3
; Sequence 3, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254.358
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658785and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-254-358-3

Query Match 57.8%; Score 1172.2; DB 1; Length 2571;
Best Local Similarity 87.9%; Pred. No. 3.2e-291;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCAGATCCATGCTCCTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGATGGGCGACGATGCTCCTGGGTTATTAATGATCTGTAGTGTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACACATCCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCACAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCCACAGAGTAGAATTGGTAAATGTGACAGAAAAATTTAAC 279

Qy 298 ATGTGGAAAAATAACATGGTAGATCAGATGCATGAGGATATAAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGGTAGAACAGATGCATGAGGATATAAATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTGTACTTTAAATGACACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAATAATTAACCCCACTCTGTGTGTACTTTAAATGACACTAATTG 399
Qy 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATAACCAATAATAGTAGTCTCTAATAAACAATAGTAAGCGAGGAACA 459
Qy 466 ATGGAGAAAGGAGAAAAATTAATAAATTTGCTCTTTCTATATCACCACAAGCATAAAGAAATAG 525
Db 460 ATAAAGGGAGAGAAATGAAAAAATCTGCTCTTTCAATATCACCACAAGCATAAAGATAAG 519
Qy 526 GTAAAGAAAGAAATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCACCTTTCTTTATAAACTTGATATAGTATCAATAG--ATAATGAT 576
Qy 586 AATACTAAGTATAGTTTAATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAG 645
Db 577 AGTACCAGCTATAGGTTGATAGTTGTAATACCTCAGTCATTACACAAGCTTGTCCAAG 636
Qy 646 GTATCCTTTTCAGCCAAATTCCTCATACATTTATTTGTGCCGGCTGGGTTTTCGATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATTCCTCATACATTTATTTGTGCCCGGCTGGTTTTCGATGCTAATA 696
Qy 706 TGTAAACAATAAGACATTTCAATGGATCAGGACATGCAACAATGTCCAGACAGTACATGT 765
Db 697 TGTAAACGATAAAAAAGTTTCAGTGGAAAAAGGATCATGTAAAAATGTCCAGACAGTACAAATGT 756
Qy 766 ACACATGGAATTAGGCCAGTGTGTCACTCAACTGCTGTAAATGCGAGTCTACAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGTGTCACTCAACTGCTGTAAATGCGAGTCTACAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAAAATTTTCACAGACATGCTAAACCATTAATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAGAAATTTTCACTGATATGCTAAACCATCATAGTACAT 876
Qy 886 CTAATGAATCTGTAGTAATTTAATTTGTACAAAGCCCAACAACAATACAAAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTTAATTTGTACAAAGCCCAACTCAATAAAGAAAAAGGATA 936
Qy 946 TCTATAGCACCGGAGAGAGCAATTTATGCAAGAGAGAAACAATAAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCCAGGAGAGAGCAATTTTATACAAACAAAAATAATAATAGGAACCTATAAGACAA 996
Qy 1006 GCACATTTGTAACATTTAGTAGAGCAAAATGGAATAACACTTTTCAACAGATAGTTTAAAA 1065
Db 997 GCACATTTGTAACATTTAGTAGAGCAAAATGGAATGACACTTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAACAATAGCTTTTAATCAATCTCCTAGGAGGGAGCCCA 1125
Db 1057 TTAAGAGAACCAATTTAAGATAAAAAACAATAGTCTTTTAATCAATCTCCTAGGAGGGAGCCCA 1116
Qy 1126 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGAAATTTCTTCTACTGTAAATACACACAA 1185
Db 1117 GAAATTTGTAATGCACAGTTTAAATTTGTGGAGGGAAATTTTCTACTGTAAATACATACCA 1176
Qy 1186 CTGTTTAAATAGTACTTGGAAATG--TTACTGGAGGGACAAATGGCACTGAAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGTAATAATTTCTTGGAAATAATCTACAGGGTCAATAAAC 1236
Qy 1243 ATAATCACATCTCAATAGCAGAAATAAACAATAATATAAATATGTGCGACAGAGTAGGAAA 1302
Db 1237 AATATCACATCTCAATAGCAGAAATAAACAATAATATAAATATGTGCGAGGAGTAGGAAA 1296
Qy 1303 GCATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATAATTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCAATAATTTACAGGGCTA 1356

Qy	1363	CTACTAACAGAGATGAGAGGTAAATGATCTGA---GACTCAGACTGAGATCTTTCAGACCT	1419
Db	1357	CTATTAAACAAGAGATGGTGGTAAAGGACACGGACACGAAACGACACCGAGATCTTTCAGACCT	1416
Qy	1420	GGAGGGAGGAGATATGACGGACAATTGCGAGAAGTGCAATTATATAAATAAAGTAGTGAAGA	1479
Db	1417	GGAGGGAGGAGATATGAGGGACAATTGCGAGAAGTGCAATTATATAAATAAAGTAGTGAACA	1476
Qy	1480	ATTGGAACCAATAGGAGTAGCACCCACCGGGCAAGAGAAAGAACAGTGCAGAGAGAAAAA	1539
Db	1477	ATTGAACCAATTAGGAGTAGCACCCACCGCAAGAGAGAGTGGTGCAGAGAGAAAAA-1536	
Qy	1540	AGACCGGATCCAGAA	1554
Db	1537	AGACGCGGATAGGA	1551

RESULT 10

```

US-08-475-391-3
; Sequence 3, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786211and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-475-391-3

```

	Query Match	57.8%;	Score 1172.2;	DB 1;	Length 2571;
	Best Local Similarity	87.9%;	Pred. No. 3.2e-291;		
	Matches 1331;	Conservative	0;	Mismatches 163;	Indels 21; Gaps 4;
Qy	58	TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATTG	117		
Db	40	TGGGGATGGGGCACGATGCTCCTTGGGTTATTATGATCTGTAGTGTCTACAGAAAAATTG	99		
Qy	118	TGGGTCACTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGT	177		
Db	100	TGGGTCACTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACCTCTATTTTGT	159		

Qy	178	GCATCAGATGCTAAAGCCTATGATACAGAGGTTACATAA	TGTTTGGGCCACACATGCGCTGT	237
Db	160	GCATCAGATGCTAAAGCATATGATACAGAGGTTACATAA	TGTTTGGGCCACACAAAGCCTGT	219
Qy	238	GTACCCACAGACCCCAACCCCAAGAGTAGTATTTGGAA	TGTGACAGAAAAATTTTAAAC	297
Db	220	GTACCCACAGNCCCAACCCCAAGAGTAGAATTTGGTA	ATGTCAGAAAAATTTTAAAC	279
Qy	298	ATGTGGAAAAATAACATGTGTAGATTCAGATGCATGAG	GATATAATATCATGTTTATCGGATGAA	357
Db	280	ATGTGGAAAAATAACATGTGTAGAACAGATGCATGAG	GATATAATATCATGTTTATCGGATCAA	339
Qy	358	AGCCTAAGCCATGCTGTAAAAATTAACCCCACTCTGT	GTGTACTTTTAAATTCGCACCTAAATTCG	417
Db	340	AGCCTAAGCCATGCTGTAAAAATTAACCCCACTCTGT	GTGTACTTTTAAATTCGCACCTGATTTG	399
Qy	418	-----AATATCACTAAGAAATACATAAATCCCACT	AGTACAGCTGGGAATG	465
Db	400	AGGAATACTACTAATACCAATAATAGTACTGCTAA	TAAACAATAGTAATACGGAGGAAACA	459
Qy	466	ATGGAGAAAGGAGAAATAAAAAATTCGCTCTTATAT	CACCAAGCATAAGAAATTAAG	525
Db	460	ATAAAGGGAGGAGAAATGAAAAAATCGCTCTTCA	ATATCACCAAGCATAAGAGATAAG	519
Qy	526	GTAAGAGAAAGAAATATGCACATCTTTTAAATAGA	CTTTTATAGTAGTACCAATAGAAAAATCACTAAT	585
Db	520	ATGCAGAAAGAAATATGCACATCTTTTAAACTTTG	ATATGATATAGTATCAATAG---ATAATGAT	576
Qy	586	AATACTAAGTATAGGTTTAATAAGTTGTAACACCT	CAGTCAATTAACAGGGCCTGTCCAAAG	645
Db	577	AGTACCAGCTATAGGTTGATAAGTTGTAATACCT	CAGTCAATTAACAGAACTTGTCCAAAG	636
Qy	646	GTATCCTTTTCAGGCCAATTCCCATACATATTGT	TGTGCCGCTGGTTTGGATGCTCAATAG	705
Db	637	ATATCCTTTTCAGGCCAATTCCCATACATATTGT	TGTGCCGCTGGTTTGGATCTCTAAAA	696
Qy	706	TGTAACAATTAAGACATTTCAATTGGATCAGGACCA	TCAGCAAAATGTCAGCAGACATCAATGT	765
Db	697	TGTAACGATAAAAAGTTTCAGTGGAAAAAGGAT	CATGTAAAAAATGTCAGCAGACATCAATGT	756
Qy	766	ACACATGGAAATTAGCGCAGTGGTGCNACTCACT	CGTGTAAATGGCAGTCTCAGCAA	825
Db	757	ACACATGGAAATTAGCGCAGTAGTATCAACTCA	ATCTGTTTAAATGGCAGTCTCAGCAA	816
Qy	826	GAAGACATAGTAATTAGATCTGAAAAATTTCA	CAGACAATGCTAAAAACCAATAATAGTACAG	885
Db	817	GAAGAGTAGTAATTAGATCTGAGAAATTTCACT	GTGTAATGCTAAAAACCATCATAGTATCAT	876
Qy	886	CTAAATGAATCTGTAGTAATTAATTGTAACAAG	ACCAACAAATTAACAAGAAAGGTTA	945
Db	877	CTGAATGAATCTGTACAAAATTAATTGTAACA	AGCAACCACTACAAATAAAGAAAGGATA	936
Qy	946	TCTATAGGACCGGGAGGCAATTTATGCAAGAA	GAACAATATAGGAGATATAAGACAA	1005
Db	937	CATATAGGACCGGGAGGAGCATTTTATACAA	AAAAAATATAATATAGAACTATAAGACAA	996
Qy	1006	GCATTTGTAACTATTAGTAGACAAAATGGAAT	TAACAATTTTAAACAGATAGTTATAAAA	1065
Db	997	GCATTTGTAACTATTAGTAGACAAAATGGAAT	TAACAATTTTAAAGACAGATAGTTAGCAA	1056
Qy	1066	TTAAGAGAAAAATTTAGGAATAAAACNATAG	CCCTTTAATCAATCCTCAGAGGGGACCCA	1125
Db	1057	TTAAGAGAACAAATTTAAGAAATAAAACAAT	AGTCTTTTAAATCAATCTCAGAGGGGACCCA	1116
Qy	1126	GAATTTGTAATGCACAGTTTAAATTTGAGAG	GGGAATTTCTTACTGTATAACAGACAA	1185
Db	1117	GAATTTGTAATGCACAGTTTAAATTTGAGAG	GGGAATTTTCTTACTGTATAATCATCACA	1176
Qy	1186	CTGTTTAAATAGTACTTGGAAATG---TTACT	GTGGAGGACAAATGGCACTGAAGGAATGAC	1242
Db	1177	CTGTTTAAATAGTACTTGGAAATGTAATAAT	ACTTGTGAAATAATACTACTACAGGTCAAATAAC	1236


```
Qy 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAAGGCAAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGGAATAATTAATCTTGGAAATAATCTACAGGGTCAAAATAAC 1236
Qy 1243 ATAATCACACTCCCAATGAGATTAACAAATTAATAATATGTCGCGAAGATGAGGAAA 1302
Db 1237 AATATCACACTTCAATGCAAAATAAAACAAATTAATAACATGTGCGAAGATGAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCATCAATATTACAGGGCTA 1356
Qy 1363 CTACTCAACAGAGATGGAGTAAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGGACACCGACACGAAACGACACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATCGGGGCAATTTGGAGAGTGAATTTATATAATAATAAATAGTAAAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGGCAATTTGGAGAGTGAATTTATATAATAATAAATAGTAAAGTAAGA 1476
Qy 1480 ATTGAACCAATAGGATAGTACCCACAGGCGCAAGAGAGAAACAGTGCACAAAGAGAGAAAA 1539
Db 1477 ATTGAACCAATAGGATAGTACCCACAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAAAA 1536
Qy 1540 AGACCGGATCCAGAA 1554
Db 1537 AGACGAGCGATAGGA 1551
```

RESULT 12

```
US-09-552-950-3
; Sequence 3, Application US/09552950
; Patent No. 6541248
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/09/552,950
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-552-950-3
```

```
Query Match 57.8%; Score 1172.2; DB 4; Length 2571;
Best Local Similarity 87.9%; Pred. No. 3.2e-291;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCTCTGGGATATTGATCTCTAGTGTCTACAGAGAAAATTG 117
Db 40 TGGGGATGGGCGACGATGCTCTCTGGGTTATTAATGATCTGTAGTGTCTACAGAGAAAATTG 99
Qy 118 TGGGTTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 177
Db 100 TGGGTTCACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCACAGAGTGTATTTGGAAATGTGCAGAGAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTGAATTTGGTAAATGTGCAGAGAAATTTTAAAC 279
Qy 298 ATGTGGAAAAATAACATGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATGAA 357
Db 280 ATGTGGAAAAATAACATGTAGATCAGATGCATGAGGATATAATCAGTTTATGGATCAA 339
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTCACACTAATTTG 417
```

```
Db 340 AGCCTAAAGCCATGTGTAAAAATTAACCCCACTCTGTGTACTTTTAAATTCACACTAATTTG 399
Qy 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTACTGCTAATAACAATAGTAATATAGCGAGGAACA 459
Qy 466 ATGGAGAAAGAGAGAAATAAAAAATTTGCTCTTTTATATATCACCACAGCATTAAGAAATAG 525
Db 460 ATAAAGGGAGAGAGAAATGAAAAAATCTGCTCTTTCAATATCACCACAGCATTAAGAGATAG 519
Qy 526 GTAAGAGAAAGATATGACATTTTAAATAGACTTCAATGTAGTACCAATAGAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGACATCTTTTATAAACTTGATATAGTATCAATAG---ATANTGAT 576
Qy 586 AATACTAAGTATAGTTTAAATAAGTTTGAACACCTCAGTCATTACACAGCCCTGTCACAAAG 645
Db 577 AGTACCAGCTATAGTTTGAATAAGTTTGAATACTCAGTCATTACACAGCTTGTCCAAAG 636
Qy 646 GTATCCTTTCCAGCAATTTCCCATACATTTATGTGTCCCGCTGGGTTTGCATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACACTATTGTGCCCGCTGGTTTTCGATTTCTAAAA 696
Qy 706 TGTAAACAATAAGACATTTCAATGGATCAGGACCATGCAAAATGTACAGCACAGTACAAATGT 765
Db 697 TGTAAACGATAAAAAGTTTCAGTGGAAAAGGATCATGTAAAAATGTACAGCACAGTACAAATGT 756
Qy 766 ACACATGGAATTTAGGCCAGTGTCTCAACTCAACTGCTGTTTAAATGGCAGCTAGCAGAA 825
Db 757 ACACATGGAATTTAGGCCAGTGTATCACTCACTGCTGTTTAAATGGCAGCTAGCAGAA 816
Qy 826 GAAGACATAGTAATAGATCTGAAAAATTTACAGACAAATGTCTAAAAACCATTAATAGTACAG 885
Db 817 GAAGAGGTAGTAATTAGATCTGAGAAATTTCACTGATAATGTCTAAAAACCATCATAGTACAT 876
Qy 886 CTAAATGAATCTGTAGTAATTAATTTGTACAGAGCCCAACACATATACAGAGAGAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTTAATTTGTACAGAGCCCACTCAATAAAGAAAAAGGATA 936
Qy 946 TCTATAGGACCCAGGAGAGCATTTTATGCAAGAGAGAAACATAATAGGAGATATTAAGACAA 1005
Db 937 CATATAGGACCCAGGAGAGCATTTTATACACAAANAATAATAATAGGAACTATTAAGACAA 996
Qy 1006 GCACATTTGAACATTAGTAGCAAAATGGAATTAACACTTTTACACAGATAGTTTATAAAA 1065
Db 997 GCACATTTGAACATTAGTAGCAAAATGGAATGACACTTTTAAAGACATAGTTAGCAAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGATTAACCAATAGCCCTTTAATCAATCTCAGGAGGGAGCCCA 1125
Db 1057 TTAAGAGAACAAATTTAAGAAATAAAACAATAGTCTTTAATCAATCTCAGGAGGGAGCCCA 1116
Qy 1126 GAAATTTGTAATGACAGTTTTAAATTTGTGGAGGGAAATTTCTTCTACTGTAAATACAGCACA 1185
Db 1117 GAAATTTGTAATGACAGTTTTAAATTTGTGGAGGGAAATTTTCTACTGTAAATACATCACA 1176
Qy 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAAGGCAAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGTAATAATCTTTGGAATAATACTACAGGGTCAAAATAAC 1236
Qy 1243 ATAATCACACTCCAATGCAGNAATAAACAATTAATAATATGTGCGAAGATAGGAAAA 1302
Db 1237 AATATCACACTTCAATGCAAAATAAACAATTAATAACATGTGCGAGGAATAGGAAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGCAAAATTTAGATGTTTCATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTTCATCAATATTACAGGGCTA 1356
Qy 1363 CTACTAAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGTTGGTAAAGGACACGACACGAAACGACACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGAGATATGAGGGAACAATTTGGAAGATGAATTTATATAATAATAAAGTAGTAGA 1479
```

Db 1417 GGAGGAGGATATGAGGACAAATTGGAGAAGTGAATTTATATAATATAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGAGTAGCACCCACAGGCAAGAGAGAAACAGTGCAAGAGAAAA 1539
Db 1477 ATTGAACCAATTAGAGTAGCACCCACCAAGCAAGAGAGAGAGTGGTGACAGAGAAAA 1536
Qy 1540 AGACCGGATCCAGAA 1554
Db 1537 AGAGCAGGATAGGA 1551

RESULT 13

US-09-936-572-3

; Sequence 3, Application US/09936572

; Patent No. 6783981

; GENERAL INFORMATION:

; APPLICANT: UDEN, MARK

; APPLICANT: MITROPHANOUS, KYRIACOS

; TITLE OF INVENTION: ANTI-VIRAL VECTORS

; FILE REFERENCE: 078883/0137

; CURRENT APPLICATION NUMBER: US/09/936,572

; CURRENT FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: PCT/GB00/01002

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: GB 9906177.2

; PRIOR FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2571

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus type 1

US-09-936-572-3

Query Match 57.8%; Score 1172.2; DB 4; Length 2571;

Best Local Similarity 87.9%; Pred. No. 3.2e-291;

Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGTTTCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGATGGGCGCAGATCTCTTGGGTATTAAATGATCTGTAGTGTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGTACTCTGTGGAGAGAACCAACCACTCTATTGTGT 177
Db 100 TGGGTACAGTCTATTATGGGTACTCTGTGGAGAGAACCAACCACTCTATTGTGT 159
Qy 178 GCATCAGATGCTAAGCCTATGATACAGAGGTACATAATGTTGGGCCACACATGCCCTGT 237
Db 160 GCATCAGATGCTAAGCATATGATACAGAGGTACATAATGTTGGGCCACACAGCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCACAGAGTATGTTGGGAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCCACAGAGTATGTTGGGAATGTGACAGAAAAATTTAAC 279
Qy 298 ATGTGGAAAAATACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATACATGGTAGAAGATGATGAGGATATAATCAGTTTATGGGATGAA 339
Qy 358 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTG 417
Db 340 AGCCTAAAGCCATGTGTAATAATTAACCCCACTCTGTGTACTTTAAATTTGCACTAAATTG 399
Qy 418 -----AATATCACTAAGAAATCTACTAATCCACTAGTAGCAGCTGGGGATG 465
Db 400 AGGAATACTACTAATACCAATAATAGTAGTCTGCTAATAACAAATAGTAATAGCGAGGAAACA 459
Qy 466 ATGGAGAAAGAGAAATAAAAATTCCTTTCTATATACACCAAGCATAAAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAAAACTCTCTTTCAATATACCAACGATATAGAGTAAG 519
Qy 526 GTAAAGAAAGAAATATGCATCTTTTAAATAGACTGTGATGATACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCATCTTTTAAATAGACTGTGATGATACCAATAGTAATAGTAATAGT 576

RESULT 14

PCT-US95-07178-3

; Sequence 3, Application PC/TUS9507178

RESULT 15
US-08-651-472-66/c
; Sequence 66, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651.472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pselP-gp160MN
US-08-651-472-66
Query Match 57.8%; Score 1172.2; DB 3; Length 6474;
Best Local Similarity 87.9%; Pred. No. 4.7e-291;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCCATGCTCTCGGATATTGATGATCTGAGTGTGAGAGAGCAACCAACCACTCTATTTTGT 117
Db 3877 TGGGATGGGACGATGCTCTCGGTTATTATGATCTGAGTGTGAGAGAGCAACCAACCACTCTATTTTGT 3818
Qy 118 TGGGTACAGTCTATTATGGGTACCTGTGTGAGAGAGCAACCAACCACTCTATTTTGT 177
Db 3817 TGGGTACAGTCTATTATGGGTACCTGTGTGAGAGAGCAACCAACCACTCTATTTTGT 3758
Qy 178 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 237
Db 3757 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 3698
Qy 238 GTACCCACAGACCCCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAGAAATTTTAAC 297

Db 3697 GTACCCACAGACCCCCCAACCAAGAGTAGTATTGGTAAATGTGACAGAGAAATTTTAAC 3638
Qy 298 ATGTGGAAAAATAACATGCTAGATCAGATCAGATGAGGATATAATCAGTTTATGGATGAA 357
Db 3637 ATGTGGAAAAATAACATGCTAGATCAGATCAGATGAGGATATAATCAGTTTATGGATCAA 3578
Qy 358 AGCCTAAAGCCATGCTGTAATAATTAACCCCTCTGTGTGTACTTTTAAATTTGACACTAATTG 417
Db 3577 AGCCTAAAGCCATGCTGTAATAATTAACCCCTCTGTGTGTACTTTTAAATTTGACACTAATTG 3518
Qy 418 -----AATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 3517 AGGAATACTACTAATACCAATAATAGTACTCTAATAACAATAGTAAATAGCGAGGGAACA 3458
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTCTTTCTATATCACCACAGCATAAAGAAATAG 525
Db 3457 ATAAAGGAGAGAGAAATGAAAACTGCTCTTTCAATATCACCACAGCATAAAGAGATAG 3398
Qy 526 GTAAGAGAAAGAAATATGCACATTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAAT 585
Db 3397 ATGCAGAAAGAAATATGCACATTTTAAATAGACTTGTATGTAGTACCAATAGAAAAATACTAAT 3341
Qy 586 AATACTAAGTATAGGTTAATAAGTTGTAACACCTCAGTCATTACACAGCCCTGTCCAAAG 645
Db 3340 AGTACCAGCTATAGTTGATAAGTTGTAATACCTCAGTCATTACACAGCTTGTCCAAAG 3281
Qy 646 GTATCCTTTAGCCCAATTTCCCATACATTTTGTGTCCCGCTGGGTTTGGCATGTAAAG 705
Db 3280 ATATCCTTTAGCCCAATTTCCCATACATTTTGTGTCCCGCTGGGTTTGGCATGTAAAG 3221
Qy 706 TGTAAACATAAGACATTCAAATGGATCAGGACCATGACAAATGTCAGCACAGTACAATGT 765
Db 3220 TGTAAACATAAGAAAGTTTCAGTGGAAAGGATCATGTAATAAATGTCAGCACAGTACAATGT 3161
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCACTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 825
Db 3160 ACACATGGAATTAGGCCAGTGGTGTCACTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 3101
Qy 826 GAAGACATAGTAATTAGTCTGAAATAATTTACAGACAAATGCTAAACCATTAATAGTACAG 885
Db 3100 GAAGAGGTAGTAATTAGTCTGAGAAATTTCACTGATATGCTAAACCATCATAGTACAT 3041
Qy 886 CTAAATGAATCTGTAGTAATTAATTTGTACAAGACCCAAACAATAACAAGAGAGGTTA 945
Db 3040 CTGAATGAATCTGTACAAATTAATTTGACAGACCCAACTACATTAAGAAAAAGGATA 2981
Qy 946 TCTATAGGACCCAGGAGAGCAATTTTATGCAAGAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 2980 CATATAGGACCCAGGAGAGCAATTTTATACAACAAAAATAATAAGGAACTATAAGACAA 2921
Qy 1006 GCACATTTGTAACATTAGTAGACAAATGGAATTAACATTTTACACACAGATAGTTATAAA 1065
Db 2801 TTAAGAAACAAATTTAAGAAATAAACAATAGTCTTTAATCAATCTCTAGGAGGAGCCCA 2801
Qy 1126 GAAATTTGTAATGCACAGTTTTAAATTTGTGGAGGGGAAATTTCTTACTGTAAATACACACAA 1185
Db 2800 GAAATTTGTAATGCACAGTTTTAAATTTGTGGAGGGGAAATTTTCTACTGTAAATACACACCA 2741
Qy 1186 CTGTTTAAATAGTACTTGGAAATG-----TTACTGGAGGACAAATGGCAGCTGAAGGAATGAC 1242
Db 2740 CTGTTTAAATAGTACTTGGAAATGAAATAATACTTTGAAATAATACTACAGGGTCAATAATAC 2681
Qy 1243 ATAATCACATCCCAATGAGAAATAAACAATAATATAATATGTGCGAGAGAGTAGGAAAA 1302
Db 2680 AATATCACATTTCAATGCAAAAATAAACAATAATATAACATGTGCGAGAGAGTAGGAAAA 2621
Qy 1303 GCAATGTATGCCCTCCCATCAGGACAAATTTAGATGTTTCATCAAAATATTACAGGGCTG 1362

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 07:54:46 ; Search time 705.358 Seconds
(without alignments)
15528.563 Million cell updates/sec

Title: US-09-687-864A-15

Perfect score: 2028

Sequence: 1 aagcttgccgcgcgtctgta.....aactcgagtataatctaga 2028

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1221.8	60.2	9540	17	US-10-325-468-46
2	1198.8	59.1	2612	15	US-10-414-692-20
3	1197	59.0	1512	9	US-09-759-841-3
4	1179.8	58.2	1422	18	US-10-728-195-7
5	1174.2	57.9	3807	15	US-10-441-788-78
6	1172.6	57.8	2552	10	US-09-966-931-27
7	1172.6	57.8	2552	17	US-10-459-121-27
8	1172.2	57.8	2571	9	US-09-999-183-3
9	1172.2	57.8	2571	13	US-10-077-294-3
10	1172.2	57.8	2571	13	US-10-163-886-3
11	1172.2	57.8	2571	14	US-10-263-127-3
12	1172.2	57.8	2571	15	US-10-375-777-3

13	1172.2	57.8	2571	16	US-10-351-938-3	Sequence 3, Appli
14	1169.4	57.7	2573	10	US-09-966-931-29	Sequence 29, Appl
15	1169.4	57.7	2573	17	US-10-459-121-29	Sequence 29, Appl
16	1166.4	57.5	9706	17	US-10-325-468-45	Sequence 45, Appl
17	1166.2	57.5	9704	17	US-10-325-468-40	Sequence 40, Appl
18	1164.6	57.4	9715	17	US-10-325-468-44	Sequence 44, Appl
19	1164.6	57.4	9942	17	US-10-325-468-5	Sequence 5, Appli
20	1164.6	57.4	9942	17	US-10-325-468-54	Sequence 54, Appl
21	1164.2	57.4	2627	15	US-10-177-390-9	Sequence 9, Appli
22	1163	57.3	9942	17	US-10-325-468-1	Sequence 1, Appli
23	1163	57.3	9942	17	US-10-325-468-2	Sequence 2, Appli
24	1163	57.3	9942	17	US-10-325-468-7	Sequence 7, Appli
25	1163	57.3	9942	17	US-10-325-468-50	Sequence 50, Appl
26	1163	57.3	9942	17	US-10-325-468-51	Sequence 51, Appl
27	1163	57.3	9942	17	US-10-325-468-56	Sequence 56, Appl
28	1161.8	57.3	1932	15	US-10-387-336-31	Sequence 31, Appl
29	1161.8	57.3	2457	15	US-10-387-336-32	Sequence 32, Appl
30	1161.4	57.3	9942	17	US-10-325-468-3	Sequence 3, Appli
31	1161.4	57.3	9942	17	US-10-325-468-52	Sequence 52, Appl
32	1161.2	57.3	2570	10	US-09-966-931-31	Sequence 31, Appl
33	1161.2	57.3	2570	17	US-10-459-121-31	Sequence 31, Appl
34	1161	57.2	1419	15	US-10-387-336-30	Sequence 30, Appl
35	1160.8	57.2	9737	10	US-09-827-688-12	Sequence 12, Appl
36	1160	57.2	1530	15	US-10-361-849-13	Sequence 13, Appl
37	1160	57.2	1929	14	US-10-032-162-12	Sequence 12, Appl
38	1159.8	57.2	9942	17	US-10-325-468-6	Sequence 6, Appli
39	1159.8	57.2	9942	17	US-10-325-468-55	Sequence 55, Appl
40	1148.6	56.6	2214	15	US-10-336-566-85	Sequence 85, Appl
41	1148.6	56.6	9505	15	US-10-336-566-9	Sequence 9, Appli
42	1148.6	56.6	9506	15	US-10-336-566-8	Sequence 8, Appli
43	1148.6	56.6	9544	9	US-09-798-675-4	Sequence 7, Appli
44	1148.6	56.6	9544	15	US-10-336-566-7	Sequence 7, Appli
45	1148.6	56.6	9545	17	US-10-093-953A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-325-468-46
; Sequence 46, Application US/10325468
; Publication No. US20040101823A1
; GENERAL INFORMATION:
; APPLICANT: Soong, Nay Wei
; APPLICANT: Pekrun, Katja
; APPLICANT: Shibata, Riri
; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; FILE REFERENCE: 0166.210US
; CURRENT APPLICATION NUMBER: US/10/325.468
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,524
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 9540
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
; FEATURE:
; OTHER INFORMATION: parent JRCSEF DNA (GenBank Accession No. M38429)
US-10-325-468-46

Query Match	60.2%	Score 1221.8;	DB 17;	Length 9540;
Best Local Similarity	90.4%	Pred. No. 3.8e-273;	Indels 15;	Gaps 2;
Matches 1333;	Conservative	0;	Mismatches 127;	
Qy	72	CATGCTCTTGGGATATTGATGATCTGTAGTGCTACAGAAAATTTGGTGCACAGTCTA	131	
Db	6289	CTTGCTCTTGGGACATTAAATGATCTGTAGTGCTAGAAAAGTTGGTGCACAGTCTA	6348	
Qy	132	TTATGGGTACTGTGTGGAGAGAACCACTCTATTGTCATCAGATGCTTAA	191	

Db 6349 TTATGGGTACCTGTGTGGAAAGAAACAAACACCACCTCTATTTTGTGCATCAGATGCTAA 6408
QY 192 AGCTATGATACAGAGGTACATAATGTTTGGGCGACACATCGCTGTGTACCCACAGACCC 251
Db 6409 AGCATATGATACAGAGGTACATAATGTTTGGGCGACACATCGCTGTGTACCCACAGACCC 6468
QY 252 CAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAATTTTAAACATGTGGAAAAATAA 311
Db 6469 CAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAATTTTAAACATGTGGAAAAATAA 6528
QY 312 CATGTTAGATCAGATGCAATAGGATATAATCAGTTTATGGATGAAGCCCTAAAGCCCATG 371
Db 6529 CATGTTAGATCAGATGCAATAGGATATAATCAGTTTATGGATGAAGCCCTAAAGCCCATG 6588
QY 372 TGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCACTAATTTGAATATCACTAAGAA 431
Db 6589 TGTAATAATTAACCCCACTCTGTGTACTTTTAAATGGCAAGATGT-----GAA 6636
QY 432 TACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAAATAAAAAATTG 491
Db 6637 TGCTACTAATACCCTAGTAGTAGTGAGGGGAATGATGGAGAGAGAGAAATAAAAACTG 6696
QY 492 CTCCTTTCTATATCACCAACAGCATAAGAAATAAGGTAAAGAAAGAAATATGCATTTTAA 551
Db 6697 CTCCTTTCTAATATCACCAAAAGCATAAGAGATAAGGTGCAGAAAGAAATATGCTCTTTTAA 6756
QY 552 TAGACTTGATGTAGTACCAATAGAAAATCTAATAATCTAAGTATAGTTTAAATAGTTG 611
Db 6757 TAAACTGATGTAGTACCAATAGAAAATCTAATAATCTAAGTATAGTTTAAATAGTTG 6816
QY 612 TAACACCTCAGTCATATACACAGGCTGTCCAAAGGTATCTTTCAAGCCAAATCCCATACA 671
Db 6817 TAACACCTCAGTCATATACACAGGCTGTCCAAAGGTATCTTTGACCAATCCCATACA 6876
QY 672 TTATTTGTCGCGGTGGGTTTGGCATGCTTAAAGTGTAAACAATAAGACATTCATTTGGATC 731
Db 6877 TTATTTGTCGCGGTGGGTTTGGCATGCTTAAAGTGTAAACAATAAGACATTCATTTGGAAA 6936
QY 732 AGGACCATGCACAAATGTCAGCACAGTACATATGATACATCGAATTAGGCCAGTGGTGC 791
Db 6937 AGGACCATGTAAAAATGTCAGCACAGTACATATGATACATCGAATTAGGCCAGTATATC 6996
QY 792 AACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGACATAGTAAATTAGATCTGAAA 851
Db 6997 AACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAAAGAGTGTGTAATAGATCTGACAA 7056
QY 852 TTTCACAGCAATGCTAAAAACCATATAATAGTACAGCTAAATGAATCTGTAGTAATTAATG 911
Db 7057 TTTTACGGCAATGCTAAAAACCATATAATAGTACAGCTGAATGAATCTGTAAAAATTAATG 7116
QY 912 TACAAGCCCAACAAATACAGAGAAAGGTTTATCTATAGACAGGAGAGCAATTTTA 971
Db 7117 TACAAGGCCCAACAAATACAGAGAAAGGTTTATCTATAGACAGGAGAGCAATTTTA 7176
QY 972 TGCAAGAGAAACATAATAGGAGATATAAGCAAGCACAATTGTAACTTAGTAGACAAA 1031
Db 7177 TACAAGCGAGAAATAATAGGAGATATAAGCAAGCACAATTGTAACTTAGTAGACACA 7236
QY 1032 ATGGAATAACACTTTTACACAGATAGTTTATAAAATTAAGAGAAAATTTAGGAATAAAAC 1091
Db 7237 ATGGAATAACACTTTTAAACAGATAGTTTGAAGAAATTAAGAGAAACAAATTAATAAATAAC 7296
QY 1092 AATAGCCTTTAATCAATCCTCAGAGGGGACCCAGAAAATGTAATGACAGTTTAAATG 1151
Db 7297 AATAGCTTTTACTCACTCCTCAGAGGGGATCCAGAAAATGTAATGACAGTTTAAATG 7356
QY 1152 TGGAGGGGAATTTCTCTACTGTGTAATACAGCAACACTGTTTAAATAGTACTTGGAAATGTAC 1211
Db 7357 TGGAGGGGAATTTTCTACTGTGTAATTAACACACTGTTTAAATAGTACTTGGAAATGTAC 7416
QY 1212 TGGAGGGCAAAATGGCACTGAAGGAAATGACATATCACTCCCAATGCAGAAATAAACA 1271
Db 7417 TGAAAAGTCAAGTGGCACTGAAGGAAATGACACCATCATCTCCCATGCAGAAATAAACA 7476

RESULT 2

US-10-414-692-20
; Sequence 20, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-ceptor Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2612
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-414-692-20

Query Match 59.1%; Score 1198.8; DB 15; Length 2612;
Best Local Similarity 90.5%; Pred. No. 4.8e-268;
Matches 1343; Conservative 0; Mismatches 117; Indels 24; Gaps 5;

QY 66 GAGATCCATGCTCCTTGGGATATTGATCATCTGTAGTGTCTACAGAAAAATTTGGGTCCAC 125
Db 442 GGGCACCTTGCTCCTTGGGATATTAAATGATCTGTAGTGTCTAGAAAAAGTTTGGGTCCAC 501
QY 126 AGTCTATTATGGGTACTCTGTGTGGAGAGAACCAACCACTCTATTTTTGTGCATCAGA 185
Db 502 AGTCTATTATGGGTACTCTGTGTGGAAAAAGAACCAACCACTCTATTTTTGTGCATCAGA 561
QY 186 TGCTAAAGCCCTATCATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCAC 245
Db 562 TGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCAC 621
QY 246 AGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAA 305
Db 622 AGACCCCAACCCCAAGAAAGTAGTATTGGGAAATGTGACAGAAAATTTTAACTGTGGAA 681
QY 306 AAATAACATGTTAGATCGATGAGGATATAATCGATTATGGGATGAAGCCTAAA 365
Db 682 AAATAACATGTTAGACAGATGAGGAGGATATAATCGATTATGGGATGAAGCCTAAA 741
QY 366 GCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAATATCAC 425
Db 742 GCCATGTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCAAGGATGT----- 792
QY 426 TAAGAACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGAGAAATAAAA 485

Db 793 ---GAATGCTACTAATACCACTAATGATGCGAGGAACGATGGAGAGAGAGAAATAAA 849
Qy 486 AAATTGCTCTTTCTATATACCAAGCATAGAAATAAGGTAAAGAAAGAAATATGCACT 545
Db 850 AAATGCTCTTTCTAATATACCAAGCATAGAGATGAGGTGCGAGAAAGAAATATGCTCT 909
Qy 546 TTTTAAATAGACTTGATGTAGTACCAATAGAAAATACTAATACTAAGTATAGTTAAT 605
Db 910 TTTTATAAATCTTGATGTAGTACCAATAG---ATAATAATAATACCACTATAGTTGAT 966
Qy 606 AAGTTGTAACACTCAGTCATTACACAGCCTGTCCAAAGGTATCTTTTCAGCCCAATTC 665
Db 967 AAGTTGTGACACCTCAGTCATTACACAGCCTGTCCAAAGATATCTTTTGAGCCCAATTC 1026
Qy 666 CATACATTATTGTGTCCCGCTGGGTTTTCGATGCTAAAGTGTAAACAATAAGACATTCAA 725
Db 1027 CATACATTATTGTGCCCCCGCTGGTTCGCGATTCTAAAGTGTAAATGATAAGACGTTCAA 1086
Qy 726 TGGATCAGGACCATGCACAAATGTGACACAGTACAAATGTACACATGGAATTAGGCCAGT 785
Db 1087 TGGAAAGGACCATGTAAATAATGTGACACAGTACAAATGTACACATGGAATTAGGCCAGT 1146
Qy 786 GGTGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGACATAGTAATTTAGATC 845
Db 1147 AGTATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAGGAGTAAATTTAGATC 1206
Qy 846 TGAATAATTTACAGACAATGCTAAACCATATAGTACAGCTAAATGAATCTGTAGTAAT 905
Db 1207 TGACAATTTACGAAACAATGCTAAACCATATAGTACAGCTGAAAGAAATCTGTAGAAAT 1266
Qy 906 TAAATTGTACAGACCAACAATACAAAGAAAGGTTATCTATAGACACAGGAGAGC 965
Db 1267 TAAATTGTACAGACCAACAATACAAAGAAAGTATACATATAGGACACAGGAGAGC 1326
Qy 966 ATTTTATCAAGAAACAATAATAGGAGATATAGACAAGACACATTTGTAACATTTAGTAG 1025
Db 1327 ATTTTATCAAGAGAAATAATAGGAGATATAGACAAGACACATTTGTAACATTTAGTAG 1386
Qy 1026 AGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAATTAAGAGAAAAATTTAGGAA 1085
Db 1387 AGCAAAATGGAATGACACTTTTAAACACAGATAGTTATAAAATTAAGAGAAACAATTTAGAA 1446
Qy 1086 TAAACAATAGCCTTTAATCAATCTCTAGGAGGAGCCAGAAATTTGTAATGACAGTTT 1145
Db 1447 TAAACAATAGTCTTTAATCACTCTCTAGGAGGAGCCAGAAATTTGTAATGACAGTTT 1506
Qy 1146 TAAATTGTGAGGGAATTTCTTCTACTGTAATACACACAACTGTTTAAATAGTACTTGG-- 1203
Db 1507 TAAATTGTGAGGAGAAATTTTCTACTGTAATTTCAACAACTGTTTAAATAGTACTTGGAA 1566
Qy 1204 -AATGTTTACTGGAGGACAAATGGCACTGAAAGGAAATGACATTAATCACTCCCAATGCAG 1262
Db 1567 TAAATAATCTGAGGGTCAATTAACATGGAAGAAAT---ACTATCACTCCCATGCAG 1623
Qy 1263 AATAAAACAATTTAATAATATGTGCGAGAAAGTAGGAAAGCAATGTATGCCCTCCCAT 1322
Db 1624 AATAAAACAATTTAATAATATGTGCGAGAAAGTAGGAAAGCAATGTATGCCCTCCCAT 1683
Qy 1323 CACAGGACAAATTAGATGCTCATCAATATTTACAGGCTGCTACTTAAACAAGATGGAGG 1382
Db 1684 CAGAGGACAAATTTAGATGTTTATCAATATTTACAGGCTGCTACTTAAACAAGATGGAGG 1743
Qy 1383 TAATAGTACTGAGACTGAGATCTTTCAGACTCTGGAGGAGAGATATAGAGGACAA 1442
Db 1744 ---TATTAAATGGAATGGACCGAGATCTTCAGACCTGAGGAGGAGATATAGGGACAA 1800
Qy 1443 TTGAGAGAGTGAATTTATATAATATAAGTATAGTAAGAAATTTGAACCAATAGAGTAGCAC 1502
Db 1801 TTGAGAGAGTGAATTTATATAATATAAGTATAGTAAGAAATTTGAACCAATAGAGTAGCAC 1860
Qy 1503 CACAGGCGCAAGAGAGAAACAGTGCCTCAAGAGCAAGAAAGACCGG 1546
Db 1861 CACCAAGGCAAGAGAGAGTGGTGTCAAGAGCAAGAAAGAGCAG 1904

RESULT 3

US-09-759-841-3
; Sequence 3, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manoussos
; FILE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-759-841-3

Query Match 59.0%; Score 1197; DB 9; Length 1512;
Best Local Similarity 89.2%; Pred. No. 9.8e-268;
Matches 1316; Conservative 0; Mismatches 150; Indels 9; Gaps 2;
Qy 74 TGCTCCTTGGGATATGATGATCTGTAGTGTCTGACAGAAAAAATTTGGGTTCACAGTCTATT 133
Db 38 TGCTGTGTGGAGCAGTCTTCGTTTCGGCTAGCGTAGAAAAATTTGGGTTCACAGTCTATT 97
Qy 134 ATGGGGTACCTGTGTGGAGAGCAACCACTCTATTTTGTGTCATCAGATGCTAAAG 193
Db 98 ATGGGGTACCTGTGTGGAGAGCAACCACTCTATTTTGTGTCATCAGATGCTAAAG 157
Qy 194 CCTATGATACAGAGTACATAATGTTTGGGCCACACACCTGCTGTATCCCAAGCCCA 253
Db 158 CATATGATACAGAGTACATAATGTTTGGGCCACACACCTGCTGTATCCCAAGCCCA 217
Qy 254 ACCCAAGAAGTAGTATTTGGGAAATGTGACAGAAAAATTTTAAACATGTGGAATAAACA 313
Db 218 ACCCAAGAAGTAGAATTTGAAAAATGTGACAGAAAAATTTTAAACATGTGGAATAAACA 277
Qy 314 TGGTAGATCAGATGATGAGGATATATATCAGTTTATGGGATGAAAGCCCTAAAGCCATGTG 373
Db 278 TGGTAGAACAGATGATGAGGATATATATCAGTTTATGGGATCAAAGCCCTAAAGCCATGTG 337
Qy 374 TAAATTAACCCCACTCTGTGTTACTTTAAATTCACCTAAATTTGA-----ATATCACTA 427
Db 338 TAAATTAACCTCCACTCTGTGTTACTTTAAATTCACCTAAATTTGAGGAATGCTACTAATG 397
Qy 428 AGAATACTACTTAATCCCACTAGTAGCAGCTGGGAAATGATGGAGAAAGGAGAAATAAAAA 487
Db 398 GGAATGACACTAATACCCTAGTAGTAGCAGGAAATGATGGGGGAGGAGAAATGAAAA 457
Qy 488 ATTGCTCTTTCTATATACCAAGAGATAGAAATATAGGTAAAGAAAGATATGACATTT 547
Db 458 ATTGCTCTTTCAAATCAACCAACATAGAGGTGAAGGTGAGAGGATATGACATTT 517
Qy 548 TTAATAGACTTGATGTAGTACCAATAGAAATATCTAATAATAGTATAGTTAGTTAATAA 607
Db 518 TTTATGAACTTGATGTAGTACCAATAGATAATAATAGTAATAATAGTATAGTTAGTTAATA 577
Qy 608 GTTGTAAACCTCAGTCATTACACAGGCTGTCCAAAGGTATCTTTTCAGGCCAATTTCCA 667
Db 578 GTTGTAAACCTCAGTCATTACACAGGCTGTCCAAAGATATCTTTTCAGGCCAATTTCCA 637
Qy 668 TACATTAATTTGTCCCGGCTGGGTTTGGGATGCTGCTAAAGGTGTAACAATAAGACATTCATG 727

```

|||||
638 TACATATTGTCGCCGCTGGTTTTCGATTCTAAAGTGTAAGAGATAAGAAGTTCRAATG 697
|||
728 GATCAGGACCAATGCACAAATGTACAGCAGTACAAATGTACACATGGAATTTAGGCCAGTGG 787
|||
698 GAAAGGACCATGTTCAAATGTACAGCAGTACAAATGTACACATGGGATTTAGGCCAGTAG 757
|||
788 TGTCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGACATAGTAATTAGATCTG 847
|||||
758 TATCAACTCAACTGCTGTTAAATGGCAGTCTAGCAGAGAGAGAGAGATAGTAATTAGATCCG 817
|||||
848 AAAATTTTCACAGACAAATGCTAAACCAATAATAGTACAGCTAAATGAATCTGTAGTAATTA 907
|||||
818 AAAATTTTCGCGACAAATGCTAAACCAATAATAGTACAGCTGAATGAATCTGTAGAAATTA 877
|||||
908 ATTGTACAAGACCCCAACAAATCAAGAAAGAGTTATCTATAGGACCGAGGAGAGCAT 967
|||||
878 ATTGTACAAGACCCCAACAAATCAAGAAAGAGTATACATATAGGACCGAGGAGAGCAT 937
|||||
968 TTTATGCAAGAGAAACATAATAGGAGATATAAGACAGACATTTGTAACATTTAGTAGAG 1027
|||||
938 TATATACAAGAGGAGAAATATAGGAGATATAAGACAGACATTTGTAACCTTTAGTAGAG 997
|||||
1028 CAAAATGGAATACACTTTTACAACAGATAGTTTATAAAATTAAAGAGAAAAATTTTAGGAATA 1087
|||||
998 CAAAATGGAATGACACTTTTAAATAGATAGTTTATAAAATTAAAGAGAAACAATTTGGGAATA 1057
|||||
1088 AAACAAATAGCCTTTAATCAATCTCAGAGGGGACCCAGAAATTTGTAATGCACAGTTTTTA 1147
|||||
1058 AAACAAATAGTCTTTAAGCATTTCTCAGAGGGGACCCAGAAATTTGTGACGCACAGTTTTTA 1117
|||||
1148 ATTGTGGAGGGGAATTTCTTACTGTAATACAGACACACTGTTTAAATAGTACTTTGGAAATG 1207
|||||
1118 ATTGTGGAGGGGAATTTTCTACTGTAATCAACAACTGTTTAAATAGTACTTTGGAAATG 1177
|||||
1208 TTACTGAGGAGGACAAATGGCACTGAAGGAAATGACATAATCACACTCCCAATGCAGAAATA 1267
|||||
1178 TTACTGAGAGAGTCAAAATAACACTGTAGAAATAACACAATCACACTCCATGCAGAAATA 1237
|||||
1268 AACAAATTTAATAATATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1327
|||||
1238 AACAAATTTAACAATGTGGCAGAAAGTAGGAAAGCAATGTATGCCCTCCCATCACAG 1297
|||||
1328 GACAAATTAGATGTTTCATCAATAATTTACAGGCTCTACTAACAGAGATGCAGTAATA 1387
|||||
1298 GACAAATTAGATGTTTCATCAATAATTTACAGGCTGCTATTTAACAGAGATGTTGTTCCCG 1357
|||||
1388 GTACTGAGACTGAGACTGAGATCTTTACAGCCTGGAGGAGGAGATATGAGGGACAAATTGGA 1447
|||||
1358 AGGCCAACAA---AGACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAAATTGGA 1414
|||||
1448 GAAGTGAATTTATATAAATATAAGTAGTAAGAAATTGAACCAATAGGAGTAGCAGCCACCA 1507
|||||
1415 GAAGTGAATTTATATAAATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCAGCCACCA 1474
|||||
1508 GGGCAAGAGAGAACACGTGCAAGAGAGAAAAAGA 1542
|||||
1475 AGGCAAGAGAGAGTGTGTGCAGAGAGAAAAAGA 1509
|||||
```

RESULT 4

```

US-10-728-195-7
; Sequence 7, Application US/10728195
; Publication No. US20040191269A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Shan
; APPLICANT: Pal, Ranajit
; APPLICANT: Kalyanaraman, V.S.
; APPLICANT: Whitney, Stephen Charles
; APPLICANT: Keen, Jim
; TITLE OF INVENTION: POLYVALENT, PRIMARY HIV-1 GLYCOPROTEIN
; TITLE OF INVENTION: DNA VACCINES AND VACCINATION METHODS
; FILE REFERENCE: 07917-269001
```

```

; CURRENT APPLICATION NUMBER: US/10728,195
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/430,732
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-728-195-7

Query Match      58.2%; Score 1179.8; DB 18; Length 1422;
Best Local SImilarity 90.4%; Pred. No. 9.5e-264;
Matches 1285; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

QY 115 TTGTGGGTCAAGTCTATTTATTTGGGGTACCTGTGTGGAGAGAAAGCAACCCACACTCTATTT 174
DB 1 TTGTGGGTCAAGTCTATTTATTTGGGGTACCTGTGTGGAGAGAAAGCAACCCACACTCTATTT 60

QY 175 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATATGTTTGGGCCACACATGCC 234
DB 61 TGTGCATCAGATGCTAAAGCCTATGATACAGAGGTACATATGTTTGGGCCACACATGCC 120

QY 235 TGTGTACCCACAGACACCCCAACCCCAAGAGTAGTATTTGGGAAATGTGACAGAAAAATTTT 294
DB 121 TGTGTACCCACAGACACCCCAACCCCAAGAGTAGAATTTGGAANAATGTGACAGAAAAATTTT 180

QY 295 AACATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGAT 354
DB 181 AACATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGAT 240

QY 355 GAAAGCCTTAAGCCATGTTAAANAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAAT 414
DB 241 CAAAGCCTTAAGCCATGTTTAAANAATTAACCTCCTCTGTGTACTTTTAAATTTGCACTGAT 300

QY 415 TTGA-----ATATCACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATG 468
DB 301 TTGAGGAATGCTACTAATGGGAATGACACTAATACCCTAGTAGCAGGGAATGATG 360

QY 469 GAGAAAGAGAGAAATAAAAAATTTGCTCTTTATATATCACCACCAAGCATTAAGAAATAAGGTA 528
DB 361 GGGGAGAGAGAAATGAAAAATTTGCTCTTTCAAAAATCACAACAAACATAAAGAGGTAAGGTG 420

QY 529 AAGAAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCCTAGTACCCTAGTACCCTAGT 588
DB 421 CAGAAAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCCTAGTACCCTAGTACCCTAGT 480

QY 589 ACTAAGTATAGGTTTAAATAAGTTGTAACACCTCAGTCAATTTACACAGGCTGTCCAAAGGTA 648
DB 481 AATAGATATAGGTTTAAATAAGTTGTAACACCTCAGTCAATTTACACAGGCTGTCCAAAGGTA 540

QY 649 TCCCTTCAGCCAAATCCCATACATTTTGTGTCCCGCTGGGTTTGCATGCTTAAAGTGT 708
DB 541 TCCCTTCAGCCAAATCCCATACATTTTGTGTCCCGCTGGGTTTGCATGCTTAAAGTGT 600

QY 709 AACATAAGACATTTCAATGGATCAGGACCATGACAAATGTACAGACATGACATGACATGACATG 768
DB 601 AAAGTAAAGAGTTCAATGGAAAGAGGACCATGTTTCAATATGTACCAATGACATGACATGACATG 660

QY 769 CATGGAATTAGGCCAGGCTGTCAACTCAACTGCTGTTTAAATGGCAGTCTTAGCAGAGAA 828
DB 661 CATGGAATTAGGCCAGGCTGTCAACTCAACTGCTGTTTAAATGGCAGTCTTAGCAGAGAA 720

QY 829 GACATAGTAATTAGATCTGAAAAATTTTACAGACAAATGCTTAAACCAATTAATAGTACAGTGA 888
DB 721 GAGGTAGTAATTAGATCTGAAAAATTTTCCGCGACAAATGCTTAAACCAATTAATAGTACAGTGA 780

QY 889 AATGAATCTGTAGTAATTTAAATTTGTACAGAGCCCAACCAATACAAAGAGAGGTTTATCT 948
DB 781 AATGAATCTGTAGTAATTTAAATTTGTACAGAGCCCAACCAATACAAAGAGAGGTTTATCT 840

QY 949 ATAGGACCCAGGAGAGCATTTTATGCAAGAGAAACATAATATAGGAGATATATAGCAACGA 1008
```

```
Db 841 ATAGGACCGGAGGAGCATTATATACACAGGAGAAATATAGGAGATATATAGCAAGCA 900
Qy 1009 CATTGTAACTAGTAGACAAAATGGAATAACACTTTTACAACAGATAGTTATAAAATTA 1068
Db 901 CATTGTAACTAGTAGACAAAATGGAATGACACTTTTAAATAAGATAGTTATAAAATTA 960
Qy 1069 AGAGAAAATTTAGGAATAAACAATAGCCTTTTAAATCAATCTCAGGAGGGAGCCAGAA 1128
Db 961 AGAGAACAAATTTGGGAATAAACAATAGTCTTTTAAAGCATTCCTCAGGAGGGAGCCAGAA 1020
Qy 1129 ATTGTAAATGCACAGTTTAAATTTGGAGGGGAATCTTCTACTGTAAATACAGCAAACTG 1188
Db 1021 ATTGTAGCCACAGTTTAAATTTGGAGGGGAATTTTCTACTGTAAATCAACACAACATG 1080
Qy 1189 TTTTAAATAGTACTTGAATCTTACTCGAGGGAACAAATGGCACTGGAAGGAAATGACATAATC 1248
Db 1081 TTTTAAATAGTACTTGAATCTTACTCGAGGGAACAAATGACAGTCAATACACCAATC 1140
Qy 1249 ACATCCCAATGAGAAATAAACAATTTAATATATGTGGCAGAAAGTAGGAAAAGCAATG 1308
Db 1141 ACATCCCAATGAGAAATAAACAATTTAATATATGTGGCAGAAAGTAGGAAAAGCAATG 1200
Qy 1309 TATGCCCTCCCATCACGAGCAAAATTTAGATGTTTATCAATATTTACAGGGCTGCTACTA 1368
Db 1201 TATGCCCTCCCATCACGAGCAAAATTTAGATGTTTATCAATATTTACAGGGCTGCTACTA 1260
Qy 1369 ACAAGAGATGGAGGTAATAGTACTCGAGACTGAGACTGAGATCTTCAGACCTCGAGGAGGA 1428
Db 1261 ACAAGAGATGGAGGTAATAGTACTCGAGGCAACA---AGACCGAGGCTTCAGACCTCGAGGAGGA 1317
Qy 1429 GATATGAGGACAATTTGGAGAGTGAATTTATATAATATAAATGATAGTAAAGTAAGCA 1488
Db 1318 GATATGAGGACAATTTGGAGAGTGAATTTATATAATATAAATGATAGTAAAGTAAGCA 1377
Qy 1489 ATAGAGTAGACCCACCGGCAAGAGAGAAACAGTGCA 1529
Db 1378 TTAGAGTAGACCCACCGGCAAGAGAGAGAGTGGTGA 1418
```

RESULT 5

```
US-10-441-788-78/c
; Sequence 78, Application US/10441788
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/10/441,788
; PRIORITY FILING DATE: 2003-05-20
; PRIORITY FILING DATE: 1998-08-14
; PRIORITY FILING DATE: 1995-04-05
; PRIORITY FILING DATE: 1995-04-05
; PRIORITY FILING DATE: 1994-04-06
; PRIORITY FILING DATE: 1997/897,382
; PRIORITY FILING DATE: 1992-06-11
; PRIORITY FILING DATE: 1997/715,921
; PRIORITY FILING DATE: 1991-06-14
; PRIORITY FILING DATE: 1991-06-14
; PRIORITY FILING DATE: 1993-08-12
; PRIORITY FILING DATE: 1997/847,951
; PRIORITY FILING DATE: 1992-03-06
; PRIORITY FILING DATE: 1997/713,967
; PRIORITY FILING DATE: 1991-06-11
; PRIORITY FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 78
; LENGTH: 3807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32, coding strand
US-10-441-788-78
```

Query Match 57.9%; Score 1174.2; DB 15; Length 3807;

Best Local Similarity 88.1%; Pred. No. 3e-262;

Matches 1330; Conservative 0; Mismatches 158; Indels 21; Gaps 4;

```
Qy 52 TGGATCTCGGCTTCGAGATCCATGCTCCTTGGGATATTTGATGATCTGTAGTCTCAGAA 111
Db 1668 TGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTCTCAGAA 1609
Qy 112 AAATTTGGGTTCACAGTCTTATTTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 171
Db 1608 AAATTTGGGTTCACAGTCTTATTTATGGGTACCTGTGTGGAGAGAGCAACCACTCTTA 1549
Qy 172 TTTTGTGATCAGATGCTTAAAGCCTTATGATACAGAGGTACATAATTTTGGGCCACACAT 231
Db 1548 TTTTGTGATCAGATGCTTAAAGCCTTATGATACAGAGGTACATAATTTTGGGCCACACAT 1489
Qy 232 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAT 291
Db 1488 GCCTGTGTACCCACAGACCCCAACCCCAAGAGTAGAATTTGGTAAATGTGACAGAAAT 1429
Qy 292 TTTTAACTGTGAAAAATAACATGCTAGATCAGATGATGAGGATATATCAATTTTATGG 351
Db 1428 TTTTAACTGTGAAAAATAACATGCTAGATGATGAGGATATATCAATTTTATGG 1369
Qy 352 GATGAAAGCCTTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTTAAATTTGCACT 411
Db 1368 GATGAAAGCCTTAAAGCCATGTGTAAATTTAAACCCCACTCTGTGTACTTTTAAATTTGCACT 1309
Qy 412 AATTGT-----AATATCACTAAGAAATCTACTAATCCCACTAGTACAGAGCTGG 459
Db 1308 GATTGTGAGGAATCTACTAATTAACCAATTAATAGTACTGCTAATAACATAGTAATAGCGAG 1249
Qy 460 GGAATGATGGAGAGAGGAGAAATAAAAATTTGCTCTTTCTATATCACCAAGCATAGA 519
Db 1248 GGAACATTAAGGGAGGAGAAATGAAATCTGCTCTTTCAATATCACCAAGCATAGA 1189
Qy 520 AATAAGGTAAAGAGAAATATGCACTTTTAAATAGACTTGTATGTAGTACCAATAGAAAT 579
Db 1188 GATAAGATGCAAGAGAAATATGCACTTCTTTATAACTTTGATATAGTATCAAT---AAAT 1132
Qy 580 ACTAATAATCTAAGTATAGTATAGTTTAAATAGTGTAAACCTCAGTCACTACAGAGCTGT 639
Db 1131 AATGATAGTACCAGCTATAGTTTGAATAAGTTGTAATACCTCAGTCACTTACACAAGCTGT 1072
Qy 640 CCAAGGTATCTTTTCAGCCCAATTTCCCATACATATTGTTGTCCTGCTGGGTTTCCGATG 699
Db 1071 CCAAGATATCTTTTGAGCCCAATTTCCCATACATATTGTTGTCCTGCTGGGTTTCCGATG 1012
Qy 700 CTAAGGTAAACAAATAGACATTTCAATGGATCAGGACCATGCAACAAATGTTCAGACAGTA 759
Db 1011 CTAAGGTAAACAAATAGACATTTCAATGGATCAGGACCATGCAATGTAAGATGTTCAGACAGTA 952
Qy 760 CAATGTACATGGAATTTAGGCCAGTGTGTCACTCACTCACTGCTGTTTAAATGGCAGTCTA 819
Db 951 CAATGTACATGGAATTTAGGCCAGTGTGTCACTCACTCACTGCTGTTTAAATGGCAGTCTA 892
Qy 820 GCAGAGAGACATAGTAAATTTAGATCTGAAATTTTACAGACCAATGCTTAAACCAATATA 879
Db 891 GCAGAGAGAGAGGTAGTAAATTTAGATCTGAGAAATTTCAATGATATGCTTAAACCAATATA 832
Qy 880 GTACAGCTTAAATGATCTGTAGTAAATTTTGTACAGAGCCCAACCAATATACAGAGAA 939
Db 831 GTACATCTGATGATCTGTACAAATTTAATTTGTACAGAGCCCACTACATTAAGAGAAA 772
Qy 940 AGGTTATCTATAGGACCGAGGAGAGCATTTTATGCAAGAGAAACATATATAGGAGATATA 999
```

Db	771	AGGATACATATAGGACAGGAGGAGCATTTTATACAAACAAAATATAATAGGAACATATA	712
Qy	1000	AGACAAACGACATTTGTAAACATTTAGTAGAGCAAAATGGGAATAACACTTTTACAAACAGATAGTT	1059
Db	711	AGACAAAGCACATTTGTAAACATTTAGTAGAGCAAAATGGGAATGCACACTTTAAGACAGATAGTT	652
Qy	1060	ATAAAAATTAGAGAGAAAAATTTAGGAATAAACAAATAGCCTTTAACTCAATCCTCAGGAGGG	1119
Db	651	AGCAAAATTTAAAGAGAACAAATTTAAGAAATAAACCAATAGTCTTTAATCAATCCTCAGGAGGG	592
Qy	1120	GACCCGAAATTTGAATGCGACAGTTTTAAATTTGTGGAGGGGAATCTTCTACTGTAAATACA	1179
Db	591	GACCCGAAATTTGAATGCGACAGTTTTAAATTTGTGGAGGGGAATCTTCTACTGTAAATACA	532
Qy	1180	GCACAACTGTTTAAATAGTACTTTGGAATGTTTACTGGAGGGGACAAATGGCACTGAAGG--A	1236
Db	531	TCACCACCTGTTTAAATAGTACTTTGGAATGTTTAAATGGAATATACTACAGGCGTCA	472
Qy	1237	AATGACATAATCACACCTCCAATGCAGAAATAAACAAATTTAAATATGTGGCAGAAAAGTA	1296
Db	471	AATAACAAATATCACACTTCAATGCAGAAATAAACAAATTTAAACATGTGGCAGGAAGTA	412
Qy	1297	GGAAAAAGCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTTCATCAAAATATTACA	1356
Db	411	GGAAAAAGCAATATATGCCCTCCCATTTGAAGGACAAATTAGATGTTTCATCAAAATATTACA	352
Qy	1357	GGGCTGCTACTTACAAGAGATGGAAGTAAATAGTACTGA--GACTGAGACTGAGATCTTC	1413
Db	351	GGGCTACTTTAACAAGAGATGGTGGTTAAGGACACGACACGACACGAGATCTTC	292
Qy	1414	AGACCTGGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAAATATAAAGTA	1473
Db	291	AGACCTGGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAAATATAAAGTA	232
Qy	1474	GTAAGAAATTCGACCAATATGAGGTAGCACCCACGAGGGCAAGAGAGACACAGTGCRAAGA	1533
Db	231	GTAACAATTTGAACCTTTAGGAGTAGCACCCACGAGGGCAAGAGAGAGTGGTCAGAGA	172
Qy	1534	GAACAAAAGA	1542
Db	171	GAACAAAAGA	163

RESULT 6

US-09-966-931-27	346	AGCCATGTGTAAAAATTAACCCCACTATGTGTTACTTTAAATGCACTGATTTG	399
Sequence 27, Application US/09966931	QY		
Publication No. US20030064361A1	Db		
GENERAL INFORMATION:			
APPLICANT: Berman, Phillip W.	QY		
TITLE OF INVENTION: HIV Envelope Polypeptides	Db		
NUMBER OF SEQUENCES: 33			
CORRESPONDENCE ADDRESS:	QY		
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP	Db		
STREET: 3 Embarcadero Center	QY		
CITY: San Francisco	Db		
STATE: CA	QY		
COUNTRY: USA	Db		
ZIP: 94111	QY		
COMPUTER READABLE FORM:	Db		
MEDIUM TYPE: Diskette	QY		
COMPUTER: IBM Compatible	Db		
OPERATING SYSTEM: DOS	QY		
SOFTWARE: FastSeq for Windows Version 2.0	Db		
CURRENT APPLICATION DATA:	QY		
APPLICATION NUMBER: US/09/966,931	Db		
FILING DATE: 27-Sep-2001	QY		
CLASSIFICATION: <Unknown>	Db		
PRIOR APPLICATION DATA:	QY		
APPLICATION NUMBER: 09/492,739	Db		
FILING DATE: 2000-01-27	QY		
ATTORNEY/AGENT INFORMATION:	Db		


```
Db 754 GTAGTATCAACTCACTGCTGTTAAATGGCAGTTTAGCAGAGAGAGAGTAGTAATTAGA 813
Qy 844 TCTGAAATTTTACAGACAATCTCTAAACCATTAATAGTACAGCTAAATGAATCTGTAGTA 903
Db 814 TCTGCCAATTTCTCGGACATGCTAAACCATTAATAGTACAGCTGAACGAATCTGTAGAA 873
Qy 904 ATTAATTTGTAAGACCCCAACCAATTAACAGAGAGAGTTTATCTATAGGACCGAGGAGA 963
Db 874 ATTAATTTGTAAGACCCCAACCAATTAACAGAGAGAGTTTATCTATAGGACCGAGGAGA 933
Qy 964 GCATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
Db 934 GCATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993
Qy 1024 AGAGCAAAATGGAATTAACACTTTTCAACACAGATAGTTTATAAATTAAGAGAGAGAGAG 1083
Db 994 AGCACAATGGAATTAATCTTTTAAACAGATAGTTTACAAATTAAGAGAGAGAGAGAG 1050
Qy 1084 AATAAAACAATAGCCTTTTAAATCAATCTCTCAGGAGGAGCCCAAGAAATTTGTAATGACAGT 1143
Db 1051 AATAAAACAATAGTCTTTTAAATCAATCTCTCAGGAGGAGCCCAAGAAATTTGTAATGACAGT 1110
Qy 1144 TTTAATTTGAGGGGAGATTTCTTCTACTGTATACAGCAGCAGTCTTTAATAGTACTTGG 1203
Db 1111 TTTAATTTGAGGGGAGATTTTCTACTGTATACAGCAGCAGTCTTTAATAGTACTTGG 1170
Qy 1204 AATGTTACTGAGGAGCAATGGCACTGAAGGAAATGA-----CATATATCA 1251
Db 1171 AATATATCTTACTTGGAGATTAATCTGAAGGTCAATGACACTGGAGAGAGATATCA 1230
Qy 1252 CTCCAATGAGATTAATAAATAATTAATATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAT 1311
Db 1231 CTCCAATGAGATTAATAAATAATTAATATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAT 1290
Qy 1312 GCCCTCCCATCAGGAGCAATTAATAGATGTTTCATCAATATTAACAGGCTGCTACTTACA 1371
Db 1291 GCCCTCCCATTAAGAGGCAATTAATAGATGTTTCATCAATATTAACAGGCTGCTACTTACA 1350
Qy 1372 AGAGATGAGGATTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1431
Db 1351 AGAGATGAGGATTAATAGTACTGAGACTGAGACTGAGATCTTCAGACCTGGAGGAGAGAT 1404
Qy 1432 ATGAGGAGCAATTTGAGAGAGTGAATTAATAATAAAGTAGTAAAGTAATGAACCAATA 1491
Db 1405 ATGAGGAGCAATTTGAGAGAGTGAATTAATAATAAAGTAGTAAAGTAATGAACCAATA 1464
Qy 1492 GGAGTAGCACCCACAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1546
Db 1465 GGAGTAGCACCCACAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
```

RESULT 7

```
US-10-459-121-27
; Sequence 27, Application US/10459121
; Publication No. US20040121317A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/459,121
; FILING DATE: 10-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/448,603
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2552
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-459-121-27

Query Match 57.8%; Score 1172.6; DB 17; Length 2552;
Best Local Similarity 89.2%; Pred. No. 5.8e-262;
Matches 1333; Conservative 0; Mismatches 129; Indels 33; Gaps 5;

Qy 64 TCGAGATCCATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAGAAAATTTGGGTC 123
Db 46 TGGGGACCATGCTCTTGGGATATTGATGATCTGTAGTGTCTACAGAGAAAATTTGGGTC 105
Qy 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGTGCATCA 165
Qy 184 GATGCTAAAGCCTATGATACAGAGTACATTAATGTTTGGGCCACACATGCTGTGTACCC 243
Db 166 GATGCTAAAGCATATGATACAGAGTACATTAATGTTTGGGCCACACATGCTGTGTACCC 225
Qy 244 ACAGACCCCAACCCACAGAGAGTATTGGGAATGTGACAGAGAAAATTTTAAACATGTGG 303
Db 226 ACAGACCCCAACCCACAGAGAGTATTGGGAATGTGACAGAGAAAATTTTAAACATGTGG 285
Qy 304 AAAAATAACATGGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAAGCCTTA 363
Db 286 AAAAATAACATGGTAGACAGATGCATGAGGATATAATCAGTTTATGGGATCANAGCTTA 345
Qy 364 AAGCCATGTGAAAATTAACCCCACTCTGTGTACTTTAAATTTGACATAATTTGTAATATC 423
Db 346 AAGCCATGTGAAAATTAACCCCACTATGTGTACTTTTAAATTTGACATAATTTGTAATATC 399
Qy 424 ACTAAGATATCTACTTAATCCCACTAGTAGCAGCTGGGGAATGTGAGAGAGAGAGAGATA 483
Db 400 ---AAAAATGCTACTAATACCACCTAGTAGCAGCTGGGGAATGTGAGAGAGAGAGAGATA 456
Qy 484 AAAAATTTGCTCTTTCTATATCAACCAAGCATAAGAAAATAAGGTAAAGAGAGAGATATGCA 543
Db 457 AAAAATTTGCTCTTTCTATATCAACCAAGCATAAGAAAATAAGGTAAAGAGAGAGATATGCA 516
Qy 544 CTTTAAATAGATCTGTAGTACCAATAGAAAATACTAATAATCTAATAGTATAGTTA 603
Db 517 CTTTAAATAGATCTGTAGTACCAATAGAAAATACTAATAATCTAATAGTATAGTTA 573
Qy 604 ATAAGTTGTAACACCTCAGTATTACAGAGCCTGTCCAAAGGTATCTTTTACAGCAATT 663
Db 574 ATAAGTTGTAACACCTCAGTATTACAGAGCCTGTCCAAAGGTATCTTTTACAGCAATT 633
```


Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAGACCCCACTCAATAAAGAAAGGATA 936
Qy 946 TCTATAGGACCGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGGACCGGAGAGCAATTTTATACAAACAAATAATATAAGAACTATAAGACAA 996
Qy 1006 GCACATTCTACATTAGTAGCAAAATGGAATACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTCTACATTAGTAGCAAAATGGAATGACACTTTTAAGACAGATAGTTAGCAAA 1056
Qy 1066 TTAAGAGAAATTTAGGAATAAAACAATAGCTTTTAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAATTTAGGAATAAAACAATAGCTTTTAATCAATCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGACAGATTTTAAATTTGTGGAGGGAAATTTCTTACTCTGTAATACAGACAA 1185
Db 1117 GAAATTTGTAATGACAGATTTTAAATTTGTGGAGGGAAATTTTCTACTCTGTAATACATCACCA 1176
Qy 1186 CTGTTTAATAGTACTTGAATG---TTACTGGAGGACAAATGGCACTGAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGAATGTAATAATCTTGGAAATAATCTACAGGGTCAAAATAAC 1236
Qy 1243 ATAATCACACTCCCAATGAGATTAACAAACAAATTAATAATATGTCGACAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCCCAATGAGATTAACAAACAAATTAATAATATGTCGACAGAAAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATGGAAGGACAAATTAGATGTTCAATCAAAATATTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGGACACGGACACGACACGACCGAGATCTTCAGACCT 1416
Qy 1420 GGAGGAGGATATCAGGACAAATTTGGAGAGTGAATTAATATAATATAAAGTACTAAGA 1479
Db 1417 GGAGGAGGATATCAGGACAAATTTGGAGAGTGAATTAATATAATATAAAGTACTAAGA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCCACAGGGCAAGAGAGAAACAGTGCAAAGAGAAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCCACAGGGCAAGAGAGAGAGTGGTGCAGAGAGAAAA 1536
Qy 1540 AGACGGATCCAGAA 1554
Db 1537 AGACGAGCATAGGA 1551

RESULT 9

US-10-077-294-3
; Sequence 3, Application US/10077294
; Publication No. US20020159979A1

GENERAL INFORMATION:

; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,294

; FILING DATE: 15-Feb-2002

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/691,604
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020159979A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-077-294-3

Query Match 57.8%; Score 1172.2; DB 13; Length 2571;
Best Local Similarity 87.9%; Pred. No. 7.2e-262;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTCTACAGAAAAATG 117
Db 40 TGGGGATGGGCGAGATGCTCCTTTGGGTTATTAAATGATCTGTAGTGTCTACAGAAAAATG 99
Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 177
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAACCAACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGCAGAGAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGAATTGGTAAATGTGCAGAGAAATTTTAAAC 279
Qy 298 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 339
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTGCACTAATTG 399
Qy 418 -----ATATCACTAAGATTAATACTACTTCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATAACCAATAATAGTACTGCTAATAACAATAGTAATAGCGAGGAAACA 459
Qy 466 ATGGAGAGAGAGAAATAAAAAATTTGCTTTCTATATCACCACAGCATAGAAATAG 525
Db 460 ATAAAGGGAGAGAAATGAAAAACTGCTCTTTCAATATACCAAGCATAGAGATAG 519
Qy 526 GTAAAGAGAGAAATATGCACCTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAAT 585
Db 520 ATGCAGAGAGAAATATGCACCTTTTAAATAGACTTGATGTAGTATAGTATCAATAG--ATAATGAT 576
Qy 586 AATACTAAGTATAGGTTAAATAGTTGTAAACCTCAGTCATTACAGAGCTGTCCAAG 645
Db 577 AGTACCAGCTATAGGTTGATAAGTTGTAATACCTCAGTCATTATACAAAGCTTGTCCAAG 636
Qy 646 GTATCCTTTACGCAATTTCCCATACATTTTGTGTCCCGGTGGTTCGATGCTTAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACATTTTGTGCCCCGGCTGGTTTTCGAGTTCTAATA 696
Qy 706 TGTAAACAAATAGACATTTCAATGGATCAGGACCATGCAAAAATGTGAGCAGACAGTACAATGT 765
Db 697 TGTAAACGATAAAAGTTTCAGTGGAAAGGATCATGTAAAAATGTGAGCAGACAGTACAATGT 756
Qy 766 ACACATGGAATTAGGCCAGTGGTGTCAACTCAACTGCTGTTTAAATGGCAGTCTAGCAGAA 825

Db 757 ACACATGGAATAGGCGAGTAGTATCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATAGATCTGAAATTTTCACAGCAATGTCTAAACCATATAGTACAG 885
Db 817 GAAGAGGTAGTAATAGATCTGAGAAATTTCTAGTAAATGTCTAAACCATATAGTACAT 876
Qy 886 CTAATGAAATCTAGTATGTAATTTGTACAGACCCCAACCAATACACAGAGAGGTTA 945
Db 877 CTGAATGAAATCTGACAAATTAATTTGTACAGACCCCACTCAATAAAGAAAGGATA 936
Qy 946 TCTATAGGACGAGGAGAGCACTTTTATCCAAAGAGAAACATAATAGGAGATATAAGCAA 1005
Db 937 CATATAGGACGAGGAGAGCACTTTTATACACAAATAATATATAGGAACTATAGACAA 996
Qy 1006 GCACATTGTAACTAGTAGAGCAAAATGGAATAACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTGTAACTAGTAGAGCAAAATGGAATGACACTTTTAAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAATTTAGGAATTAACATAGCTTAAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAAATTTAGGAATTAACATAGCTTAAATCAATCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGTAATGACAGCTTTTAAATTTGAGAGGGAAATTTCTTACTGTAAATACAGCAA 1185
Db 1117 GAAATTTGTAATGACAGCTTTTAAATTTGAGAGGGAAATTTTCTTACTGTAAATACACCA 1176
Qy 1186 CTGTTTAAATAGTACTTGGAAATG---TTACTGGAGGACAAATGGCACTGGAAGGAAATGAC 1242
Db 1177 CTGTTTAAATAGTACTTGGAAATGGAATTAATCTTGGAAATTAATCTACAGGGTCAAATAAC 1236
Qy 1243 ATAATCACACTCCCAATGAGATTAACAAATTAATATATGCGCAGAAAGTAGGAAA 1302
Db 1237 AATATCACACTCAATGCAAAATAAACAATTTATAAAACATGTGGCAGGAAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGACAAATTTAGATGTTCAATAATTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATGGAAGGACAAATTTAGATGTTCAATAATTTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGGACACGGACACGACGACCGAGATCTTCAGACCT 1416
Qy 1420 CGAGAGAGGATATGAGGACAAATTTGGAGAGTGAATTAATATATAAATATAAGTAGTAAGA 1479
Db 1417 GGAGAGGAGATATGAGGACAAATTTGGAGAGTGAATTAATATAAATATAAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGATAGCACCACCGGCAAGAGAGAAACAGTGCACAAAGAGAAAAA 1539
Db 1477 ATTGAACCAATAGGATAGCACCACCGGCAAGAGAGAAAGGAGAGAGAGAGAGAAAA 1536
Qy 1540 AGACCGGATCCAGAA 1554
Db 1537 AGAGCAGCGATAGGA 1551

RESULT 10

US-10-163-886-3
; Sequence 3, Application US/10163886
; Publication No. US20020187129A1

GENERAL INFORMATION:

; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/163.886
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020187129A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-163-886-3

Query Match 57.8%; Score 1172.2; DB 13; Length 2571;
Best Local Similarity 87.9%; Pred. No. 7.2e-262;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;

Qy 58 TCGGCTTCGAGATCCATGCTCCTTGGGGATATTGATGATCTGTAGTGCCTACAGAAAAATTG 117
Db 40 TGGGGATGGGACGATGCTCCTTGGGTTATTAATGATCTGTAGTGCCTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTATGGGGTACCTGTGGGAGAGCAACCAACCACTCTATTTTGT 177
Db 100 TGGGTACAGTCTATTATGGGGTACCTGTGGGAGAGCAACCAACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCCTATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATCCCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTATGTTGGGAATGTGACAGAAAAATTTTAAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTATGTTGGGAATGTGACAGAAAAATTTTAAAC 279
Qy 298 ATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGAAAAATAACATGCTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 339
Qy 358 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTG 417
Db 340 AGCCTAAAGCCATGTGTAAAAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTG 399
Qy 418 -----ATATCACTAAGATACTACTATAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTATAACCAATAATAGTACTGCTATAATAAAGTAGGAGGGAACA 459
Qy 466 ATGGAGAAAGGAGAAATAAAAAATTTGCTTCTATATCACCACAGCATTAAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAAAAAATGCTCTCTTCAATATACCAACAGCATAGAGATAG 519
Qy 526 GTAAAGAAAGAAATATGCACCTTTTAAATAGACTGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCACCTTTTAAATAGACTGTAGTACCAATAGAAAAATACTAAT 576
Qy 586 AATACTAAGTATAGGTTAATAGTTTGAACACCTCAGTCATTACACAGCCCTGTCARAAG 645
Db 577 AGTACCAGCTATAGGTTGATAAGTTTGAATACCTCAGTCATTACACAGCTTTGTCCAAAG 636

Db 460 ATAAAGGAGGAGAAATGAAAACTGCTCTTCAATATCACCAAGCATAGAGATAAG 519
Qy 526 GTAAAGAAAGATATGCACTTTTAAATAGACTTGATGTAGTACCAATAGAAAAATCTAAT 585
Db 520 ATGCAGAAAGAAATATGCACTCTTTATATAAATTGATATAGTATCAATAG---ATAATGAT 576
Qy 586 AATACTAGTATAGTTAATAGTTTAACTGTTAACTCAGTCAATACACAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTTGTAATACCTCAGTCAATACACAGCTGTGCCAAAG 636
Qy 646 GTATCCTTTAGCCAAATCCCATACATATTTGTGTCGCCGCTGGGTTTGGCATGCTAAAG 705
Db 637 ATATCCTTTAGCCAAATCCCATACATATTTGTGCCCGCTGGTGTTCGATCTTAAAA 696
Qy 706 TGTAAACAATAAGACATTCOAATGGATCAGGACCAATGCAAAATGTCAGCACAGTCAATGT 765
Db 697 TGTAAAGATAAAAGTTTCAAGTGAAGAAAGGATCATGTAAATAATGTCAGCACAGTCAATGT 756
Qy 766 ACACATGGAATTAGCCAGTGGTGTCACTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGCCAGTGGTGTCACTCACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAATTTTCAGACAAATGCTAAACCATATATAGTACAG 885
Db 817 GAAGAGGTAGTAATTTAGATCTGAGAAATTTCTGATATGCTAAACCATATAGTACAT 876
Qy 886 CTAATAGATCTGTAGTAAATTAATTTGTAACAAGACCAACAATATACAGATAGTTATAAAA 945
Db 877 CTGAATGAATCTGTACAAATTAATTTGTACAAGACCAACTCAATAAAAGAAAGGATA 936
Qy 946 TCTATAGACACGAGGAGACATTTTATCGAAGAGAAACATAATAGGAGATATAGACAA 1005
Db 937 CATATAGACACGAGGAGACATTTTATACAAACAAAAATATAATAGGAACTATAGACAA 996
Qy 1006 GCACATTTGAATTTAGTAGACAAATGGAATACTTTTCAACAGATAGTTATAAAA 1065
Db 997 GCACATTTGAATTTAGTAGACAAATGGAATGACATTTTAAAGACATAGTTAGCAAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAACTCAATCTCAGGAGGGACCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAACTCAATCTCAGGAGGGACCA 1116
Qy 1126 GAATTTGTAATGACAGTTTTAAATTTGAGGAGGAAATTTCTTACTGTAAATACACACAA 1185
Db 1117 GAATTTGTAATGACAGTTTTAAATTTGAGGAGGAAATTTTCTACTGTAAATACATCACA 1176
Qy 1186 CTGTTTAATAGTACTTGAATG---TTACTGGAGGACAAATGACCTGAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGAATGTTAATTAATCTTGAATATACTACAGGGTCAATTAAC 1236
Qy 1243 ATAAATCACATCTCAATGAGGAGATAAAACAATTAATAATATGTGCGAGAAAGTAGGAAA 1302
Db 1237 AATATCACATCTCAATGAGGAGATAAAACAATTAATAATGTCGAGGAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTCCCATCACAGACAAATTAGATGTTCAATCAATATTTACAGGGCTG 1362
Db 1287 GCAATGTATGCCCTCCCATTAAGAGGACAAATTTAGATGTTCAATCAATATTTACAGGGCTA 1356
Qy 1363 CTACTAAACAAGAGATGGAGGTAAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACT 1419
Db 1357 CTATTAAACAAGAGATGGTGGTAGACACCGGACACGAGACACCGAGATCTTTCAGACT 1416
Qy 1420 GGAGGAGGAGATATGAGGAGCAATTTGGAGAGTGAATTAATAATAAAGTAGTAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGAGCAATTTGGAGAGTGAATTAATAATAAAGTAGTAACA 1476
Qy 1480 ATTGAACCAATAGGAGTAGCACCCACCGGCAAGAGAGACAGTGTCCAAAGAGAAA 1539
Db 1477 ATTGAACCAATAGGAGTAGCACCCACCGGCAAGAGAGAGAGTGTCCAAAGAGAAA 1536
Qy 1540 AGACCGGATCCAGAA 1554

Db 1537 AGACGAGCGATAGGA 1551
RESULT 12
US-10-375-777-3
; Sequence 3, Application US/10375777
; Publication No. US20030147912A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,777
; FILING DATE: 26-Feb-2003
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,886
; FILING DATE: 04-Jun-2002
; APPLICATION NUMBER: 09/292,703
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030147912A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-375-777-3
Query Match 57.8%; Score 1172.2; DB 15; Length 2571;
Best Local Similarity 87.9%; Pred. No. 7.2e-262;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCCATCTCTCTGGGATATTTGATGATCTGTAGTGCTACAGAAAAATTG 117
Db 40 TGGGATGGGACCATGCTCTCTGGGTTATTAATGATCTGTAGTGCTACAGAAAAATTG 99
Qy 118 TGGGTACAGTCTATTTATGGGTACCTGTGTGGAGAGCAACCACTCTATTTGT 177
Db 100 TGGGTACAGTCTATTTATGGGTACCTGTGTGGAGAGCAACCACTCTATTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGGATACATATGTTGGGCCACACATCCCTGT 237
Db 160 GCATCAGATGCTAAAGCCTATGATACAGGATACATATGTTGGGCCACACATCCCTGT 219
Qy 238 GTACCCACAGACCCCAACCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTAAC 297
Db 220 GTACCCACAGACCCCAACCAAGAGTAGTATTGGTAAATGTGACAGAAAAATTTAAC 279
Qy 298 ATGTGAAAAAATAACATGCTAGATCAGATGATGATGATATATATCAGTTTATGGATGAA 357

Db 280 ATGTCGAAAAATAACATGCTGTGAGAACAGATGCTGATGAGGATATATAATCAGTTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTTG 417
Db 340 AGCCTAAAGCCATGTTGTAATAATTAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTTG 399
Qy 418 -----AATATCACTAAGAAATCTACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATATAGTAGCTGCTTAATAACATAGTAATAGCGAGGGAACA 459
Qy 466 ATGGAGAAAGGAGAAATTAATAATTTGCTTTCTATATCACCACAAGCATAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAATGAATACTGCTTTCTTAATATCACCAAGCATAGAGATAAG 519
Qy 526 GTAAAGAAGAATATGCATTTTAAATAGACTGTAGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGCATTTTAAACTTTGATATAGTATCAATAG---ATAATGAT 576
Qy 586 AATACTAAGTATAGTTAATAAGTTGTAACACCTCAGTCATTAACAGCCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGGTTGTAAGTTGTAATACCTCAGTCATTAACAAAGCTTGTCCAAAG 636
Qy 646 GTATCCTTTAGCCCAATTTCCCATACATATTGTTGTCGCGCTGGGTTTGGCATGCTAAAG 705
Db 637 ATATCCTTTGAGCCAAATTTCCCATACATATTGTTGCCCGCTGGTTTGGCATTTCTAAA 696
Qy 706 TGTAAACAATAGACATTCATAGGATCAGGACCATGCACAAATGTGAGCACAGTACAATGT 765
Db 697 TGTAACGATAAAAGTTTCAGTGGAAGAGATCATGTAAATAATGTGAGCACAGTACAATGT 756
Qy 766 ACACATGGAATTAGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGCCAGTGTGTCAACTCACTGCTGTTAAATGGCAGTCTAGCAGAA 816
Qy 826 GAAGACATAGTAATTTAGATCTGAAATTTTCAGACAAATGCTTAAACCATATAGTACAG 885
Db 817 GAAGAGTAGTAATTTAGATCTGAGAAATTTCTGTAATGCTTAAACCATATAGTACT 876
Qy 886 CTAATAGATCTGTAGTAAATTAATGTACAAGACCCCAACAATATACAAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAATTAATTTGTACAAGACCCCAACTACAATAAAGAAAGGATA 936
Qy 946 TCTATAGCACAGGAGAGATTTTATGCAAGAGAAACATAAATAGGAGATATAGACAA 1005
Db 937 CATATAGCACAGGAGAGATTTTATACAACAAAAATATAATAGGAACTATAAGACAA 996
Qy 1006 GCACATTTGAACATTTAGTAGCAAAATGGGAATACACTTTTACACAGATAGTTATRAAA 1065
Db 997 GCACATTTGAACATTTAGTAGCAAAATGGGAATGACACTTTTAAGACAGATAGTTAGCAA 1056
Qy 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCCTTTTAATCAATCTCAGGAGGGACCCA 1125
Db 1057 TTAAGAGAACAAATTTAAGAAATAAACATAGTCTTTAATCAATCTCAGGAGGGACCCA 1116
Qy 1126 GAAATTTGAATGCACAGTTTAAATTTGGAGGGGAATTTCTTCTACTGTAATACAGACAA 1185
Db 1117 GAAATTTGAATGCACAGTTTAAATTTGGAGGGGAATTTTCTACTGTAATACATCACCA 1176
Qy 1186 CTGTTTAATAGTACTTTGGAATG---TTACTGGAGGACAAATGGCAGCTGAAGGAATGAC 1242
Db 1177 CTGTTTAATAGTACTTTGGAATGTAATTAATTTACTTTGGAATAATACTTACAGGGTCAAAATAC 1236
Qy 1243 ATAATCACATCCCAATGCAGAAATAAAACAAATTAATAATATGTGGCAGAAAGTAGGAAA 1302
Db 1237 AATATCACATTTCAATGCAGAAATAAAACAAATTAATAACATGTGGCAGAAAGTAGGAAA 1296
Qy 1303 GCAATGTATGCCCTTCCCATCACAGGACAAATTAGATGTTTATCAAAATTTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTTCCCATTTGAAGGACAAATTAGATGTTTATCAAAATTTTACAGGGCTA 1356
Qy 1363 CTACTAACAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 CTATTAAACAGAGATGGTGGTAAGGACACGGACACGAAACGACCGAGATCTTCAGACCT 1416

Qy 1420 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATATAAAGTAGTAAAGA 1479
Db 1417 GGAGGAGGAGATATGAGGACAAATTTGGAGAAAGTGAATTTATATAATATAAAGTAGTAAACA 1476
Qy 1480 ATTGAACCAATAGAGTAGACCCCAAGCCAGGAGGAGAGAAAGCAAGTCTCAAGAGAAAAA 1539
Db 1477 ATTGAACCAATAGAGTAGACCCCAAGCCAGGAGGAGAGAAAGTCTGTCAGAGAGAAAAA 1536
Qy 1540 AGACCGATCCAGAA 1554
Db 1537 AGACGAGCGATAGGA 1551

RESULT 13

US-10-351-938-3
; Sequence 3, Application US/10351938
; Publication No. US20040009603A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Anti-Viral Vectors
; FILE REFERENCE: 674524-2004
; CURRENT APPLICATION NUMBER: US/10/351,938
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US/09/552,950
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 2571
; ORGANISM: Human immunodeficiency virus type 1
US-10-351-938-3

Query Match 57.8%; Score 1172.2; DB 16; Length 2571;
Best Local Similarity 87.9%; Pred. No. 7.2e-262;
Matches 1331; Conservative 0; Mismatches 163; Indels 21; Gaps 4;
Qy 58 TCGGCTTCGAGATCCATGCTCTCTTGGGATATTGATGATCTCTGTAGTGTACAGAAAAATTG 117
Db 40 TGGGATGGGACGATGCTCTTGGGTTATTATGATCTCTGTAGTGTACAGAAAAATTG 99
Qy 118 TGGGTCAAGTCTATTATATGGGTTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 177
Db 100 TGGGTCAAGTCTATTATGGGTTACCTGTGTGGAGAGAGCAACCACTCTATTTTGT 159
Qy 178 GCATCAGATGCTAAAGCCTATGATACAGAGTACATATGTTTGGGCCACACATGCTCTGT 237
Db 160 GCATCAGATGCTAAAGCATATGATACAGAGTACATATGTTTGGGCCACACATGCTCTGT 219
Qy 238 GTACCCACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAC 297
Db 220 GTACCCACAGACCCCAACCCCAAGAGTAGATAGTTGGTAATGTGACAGAAAAATTTTAAC 279
Qy 298 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAA 357
Db 280 ATGTGGAAAAATAACATGTTAGATCAGATGATGAGGATATAATCAGTTTATGGGATCAA 339
Qy 358 AGCCTAAAGCCATGTTAATAATTAACCCCACTCTGTGTTTACTTTTAAATTTGCACTAATTTG 417
Db 340 AGCCTAAAGCCATGTTAATAATTAACCCCACTCTGTGTTTACTTTTAAATTTGCACTAATTTG 399
Qy 418 -----AATATCACTAAGAATACTACTAATCCCACTAGTAGCAGCTGGGGAATG 465
Db 400 AGGAATACTACTAATACCAATATAGTACTGCTTAATAACATAGTAATAGCGAGGGAACA 459
Qy 466 ATGGAGAAAGGAGAAAAATAAAAAATTTGCTTTTCTTATATCACCAAGCATTAAGAAATAAG 525
Db 460 ATAAAGGAGGAGAAAAATGAATACTGCTCTTTCAATATCACCAAGCATTAAGAGATAAG 519
Qy 526 GTAAAGAAGAATATGACATTTTAAATAGACTTGTAGTACCAATAGAAAAATACTAAT 585
Db 520 ATGCAGAAAGAAATATGACATTTTCTTTTATAAACTTGTATATAGTATCAATAG---ATAATGAT 576


```
QY 586 AATACTAGTATAGTAAATAGTTGTAAACACCTCAGTCATTACACAGGCCTGTCCAAAG 645
Db 577 AGTACCAGCTATAGTTGATAGTTGTAATACCTCAGTCATTACACAAGCTTGCCAAAG 636
QY 646 GTATCTCTTTAGCCAAATTTCCCATACATTAATTGTGTCCCGGCTGGGTGTTCGATGCTAAAG 705
Db 637 ATATCTTTGAGCCAAATTTCCCATACATTAATTGTGTCCCGGCTGGGTGTTCGATGCTAAAG 696
QY 706 TGTAAACAATAGACATTCOAATGGATCAGGACCATGCACAAAATGTCAGCACAGTACAATGT 765
Db 697 TGTAAACGATAAAAGTTTCAGTGGAAAAGGATCATGTAAATAATGTCAGCACAGTACAATGT 756
QY 766 ACACATGCAATTTAGCCAGTGGTGTCACTCAATCTGCTTAAATGGCAGTCTACGAAA 825
Db 757 ACACATGCAATTTAGCCAGTGGTGTCACTCAATCTGCTTAAATGGCAGTCTACGAAA 816
QY 826 GAAGACATAGTAATTTAGATCTGAAATTTTCACAGACAATGCTTAAACCATTAATAGTACAG 885
Db 817 GAAGNGGTAGTAATTTAGATCTGAGNAATTTCACTGATAATGCTTAAACCATCATAGTACAT 876
QY 886 CTAATAGTAATCTGTAGTAAATTAATTGTGTAACAAGCCCAACAATACAAAGAAAGGTTA 945
Db 877 CTGAATGAATCTGTACAAATTAATTGTGTAACAAGCCCAACAATACAAAGAAAGGTTA 936
QY 946 TCTATAGCACAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CATATAGCACAGGAGAGCAATTTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 996
QY 1006 GCACATTTGAATTTAGTAGAGCAAAATGGAATTAACACTTTTACACAGATAGTTATAAAA 1065
Db 997 GCACATTTGAATTTAGTAGAGCAAAATGGAATTAACACTTTTAAAGACATAGTTAGCAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAATCAATCTCAGGAGGGAGCCCA 1125
Db 1057 TTAAGAGAAAAATTTAGGAATAAAACAATAGCTTTTAATCAATCTCAGGAGGGAGCCCA 1116
QY 1126 GAAATTTGAATTCACAGTTTAAATTTGTGAGGGGAATTTCTCTAGTGAATACAGCACAA 1185
Db 1117 GAAATTTGAATTCACAGTTTAAATTTGTGAGGGGAATTTTCTCTAGTGAATACATACCA 1176
QY 1186 CTGTTTAATAGTACTTGGAAATG---TTACTGGAGGGCAAAATGGCACTGAAAGGAAATGAC 1242
Db 1177 CTGTTTAATAGTACTTGGAAATGTTAATAATCTTGGAAATAATCTACAGGGTCAAATAAC 1236
QY 1243 ATAATCACACTCAATGCAGATAAAACAATTAATAATATATGTCGCAAGAAAGTAGGAAAA 1302
Db 1237 AATATCACACTTCAATGCAGATAAAACAATTAATAATATATGTCGCAAGAAAGTAGGAAAA 1296
QY 1303 GCATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTCAATCAATATTTACAGGGCTG 1362
Db 1297 GCAATGTATGCCCTCCCATTTGAAGGACAAATTTAGATGTTCAATCAATATTTACAGGGCTA 1356
QY 1363 CTACTAAACAAGAGATGGAGGTAATAGTACTGA---GACTGAGACTGAGATCTTTCAGACCT 1419
Db 1357 CTATTTAAACAAGATGGTGGTAAGGACACGGACACGACGACACCGAGATCTTTCAGACCT 1416
QY 1420 GGAGGAGAGATATGAGGGAACAATTTGGAGAAGTGAATTAATAATAATAAGTAGTAAGA 1479
Db 1417 GGAGGAGAGATATGAGGGAACAATTTGGAGAAGTGAATTAATAATAATAAGTAGTAAGA 1476
QY 1480 ATTTGAACCAATAGGAGTAGCCACCCAGGCGAAGAGAGAACAGTGCAAAGAGAAAAA 1539
Db 1477 ATTTGAACCAATAGGAGTAGCCACCCAGGCGAAGAGAGAGAGTGGTCAGAGAGAAAAA 1536
QY 1540 AGACCGGATCCAGAA 1554
Db 1537 AGAGCAGCGATAGGA 1551
```

RESULT 14
US-09-966-931-29
; Sequence 29, Application US/09966931

```
; Publication No. US20030064361A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; ; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: 2000-01-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2573
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-966-931-29
```

```
Query Match 57.7%; Score 1169.4; DB 10; Length 2573;
Best Local Similarity 88.3%; Pred. No. 3.2e-261;
Matches 1330; Conservative 0; Mismatches 141; Indels 36; Gaps 4;

QY 64 TCGAGATCCATGCTCCTTGGGATATTGATGATCTGTAGTGTACAGAGAAAAATTTGGGTC 123
Db 46 TGGGCGACCATGCTCCTTGGGATATTGATGATCTGTAGTGTGAGGAAATTTGGGTC 105
QY 124 ACAGTCTATTATGGGTACCTGTGTGGAGAGCAAGCAACACCTCTATTTTTGTGCATCA 183
Db 106 ACAGTCTATTATGGGTACCTGTGTGGAGAGCAAGCAACACCTCTATTTTTGTGCATCA 165
QY 184 GATGCTAAAGCCTATGATACAGAGTACATTAATGTTTTGGGCCACACATGCTGTGTACCC 243
Db 166 GATGCTAAAGCATATGATACAGAGATACATAATGTTTTGGGCCACACATGCTGTGTACCC 225
QY 244 ACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 303
Db 226 ACAGACCCCAACCCCAAGAGTAGTATTGGGAAATGTGACAGAAAAATTTTAAACATGTGG 285
QY 304 AAAAAATAACATGGTAGATCAGATGATGAGGATATAATCAGTTTATGGGATGAAAGCCTTA 363
Db 286 AAAAAATAACATGGTAGGACAGATGATGAGGATATAATCAGTTTATGGGATCAAAGTTTA 345
QY 364 AAGCCATGTGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTAATTTGAATATC 423
Db 346 AAGCCATGTGTAATAATTAAACCCCACTCTGTGTACTTTTAAATTTGCACTGAT----- 396
```


Db 166 GATGCTAAGCATATGATACAGAGATACATATGTTGGGCCACACATGCTGTGTACCC 225
QY 244 ACAGACCCCAACCCCAAGAAGTAGTAGTTGGGAAATGTGACAGAAAATTTTAAACATGTGG 303
Db 226 ACAGACCCCAACCCCAAGAAGTAGTAGTTGGGAAATGTGACAGAAAATTTTAAACATGTGG 285
QY 304 AAAAATACATGCTGTAGATCAGATGCATGAGGATATAATCAGTTTATGGGATGAAGCCCTA 363
Db 286 AAAAATAACATGCTGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAGTTTAA 345
QY 364 AAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATGTGACCTAAATTTGAATATC 423
Db 346 AAGCCATGTGTAAATTAACCCCACTCTGTGTACTTTTAAATGTGACCTGTAT- 396
QY 424 ACTAAGAAATACTACTAATCCCACTAGTAGCAGCTGGGGAATGATGGAGAAAGGAGAAATA 483
Db 397 GCGGGGAATACTACTAATACCAATAGTAGTAGCAGGGGAAAGCTGGGAGAAAGGAGAAATA 456
QY 484 AAAAATTGCTCTTCTATATCACCACAGCATAGAAATAGGTAAGGTAAGAAAGAAATATGCA 543
Db 457 AAAAATGCTCTTCTCAATATCACCACAAAGCTGAGAGATAAGATGCAGAAAGAAACTGCA 516
QY 544 CTTTTTAATAGACTTGTAGTAGTACCAATAGA- 585
Db 517 CTTTTTAATAACTTGTATAGTAGTACCAATAGATGATGATAGTAGAATAGTAGTAGGAAT 576
QY 586 AATACTAAGTAGTAGGTTAATAGTTGTAAACACCTCAGTCATTATACAGAGCCTGTCCAAAG 645
Db 577 AGTACTAATATAGGTTGATAAGTTGTAAACACCTCAGTCATTATACAGAGCCTGTCCAAAG 636
QY 646 GTATCCTTTTCAGCCAAATTTCCCATACATTTATGTGTCCCGCTGGGTTTTCGATGCTAAAG 705
Db 637 GTATCATTTGAGCCAAATTTCCCATACATTTCTGTACCCCGCTGGTTTTCGCTTCTAAAG 696
QY 706 TGTAAACAATAAGACATTTCAATGGATCAGGACCATGCACAAATGTGAGCACAGTACAATGT 765
Db 697 TGTAAATAATAGACGTTCAATGGATCAGGACCATGCACAAATGTGAGCACAGTACAATGT 756
QY 766 ACACATGGAATTAGGCCAGTGGTGCAACTCAACTGTGTTAAATGGCAGTCTAGCAGAA 825
Db 757 ACACATGGAATTAGGCCAGTGGTGCAACTCAACTGTGTTAAATGGCAGTCTAGCAGAA 816
QY 826 GAAGCATAGTAATTTAGATCTGAAATTTTCACAGCAATGCTTAAACCATTAATAGTACAG 885
Db 817 GGAGAGGTAGTAATTTAGATCTGAAATTTTCAGAACAATGCTTAAACCATTAATAGTACAG 876
QY 886 CTAATGAATCTGTAGTAATTAATTTGTACAAGACCCCAACAATAACAAGAAAGGTTA 945
Db 877 CTGACAGAACCAAGTAATAATTAATTTGTACAGACCCCAACAATAACAAGAAAGTATA 936
QY 946 TCTATAGACACGGAGAGCAATTTATGCAAGAGAAACATAATAGGAGATATAAGACAA 1005
Db 937 CCTATAGGACCCGAGAGCAATTTATGCAACAGGAGACATAATAGGAAATATAAGACAA 996
QY 1006 GCACATTTCACTAGTAGAGCAAAATGGATACACTTTTACACAGATAGTTTATAAAA 1065
Db 997 GCACATTTGAACCTTAGTAGAACAGACTGGAAATAACCTTTAGGACAGATAGTTGAAAAA 1056
QY 1066 TTAAGAGAAAAATTTAGGAATAAAAACAATAGCCTTTTAATCAATCCTCAGGAGGGGACCCA 1125
Db 1057 TTAAGAGAACAAATTTGGGAAATAAAACATAATCTTTAATCACTCCTCAGGAGGGGACCCA 1116
QY 1126 GAAATTTGAATGCAACAGTTTAAATTTGTGGAGGGGAATTTCTTCTACTGTAAATACAGCAAA 1185
Db 1117 GAAATTTGAATGCAACAGTTTAAATTTGTAGAGGGGAATTTTCTACTGTAAATACAGCAAA 1176
QY 1186 CTGTTTAAATAGTACTTGGAAATGTTACTGGAGGGCAAAATG- 1239
Db 1177 TGTGTTGACAGTACTTGGGAATAATTAAGTGTCAAATGGCAGCTAGCAGCTGAAGGAAT 1236
QY 1240 GACATAATCACACTCCAATGCAGAAATAAAACAAATTTATAAATATGTGGCAGAAAGTAGGA 1299

Db 1237 AGCACAATCACACTCCCATGCAGAAATAAAGCAAAATTTGTAACATGTGCGAGGAAGTAGGA 1296
QY 1300 AAAGCAATGTATGCCCTCCCATCACAGGACAAATTTAGATGTTTCATCAAAATATTACAGGG 1359
Db 1297 AAAGCAATGTATGCCCTCCCATCAGAGGACAAATTTAGATGTTTCATCAAAATATTACAGGG 1356
QY 1360 CTGCTACTTAACAAGAGATGGAGGTAATAGTAGTCTGAGACTGAGACTGAGATCTTCAGACCT 1419
Db 1357 TTGCTATTACAGAGATGGAGG---TAGTAAACAACAGCATGAATGAGACCTTCAGACCT 1413
QY 1420 GGAGGAGAGATATGAGGGACAATTGGAGAAAGTGAATATATAAATATAAAGTAGTAGA 1479
Db 1414 GGAGGAGAGATATGAGGGACAATTGGAGAAAGTGAATATATAAATATAAAGTAGTAGA 1473
QY 1480 ATTGAACCAATAGGAGTAGCACCCACAGGGGCAAGAGAGAAACAGTGCAGAGAGAAAAA 1539
Db 1474 ATTGAACCAATAGGAGTAGCACCCACCAAGGCAAGAGAGAGAGTGGTGCAGAGAGAAAAA 1533
QY 1540 AGACCGG 1546
Db 1534 AGAGCAG 1540

Search completed: November 12, 2004, 19:50:40
Job time : 712.358 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	464.8	22.9	786	9	AY416061	AY416061 Homo sapi
2	464.8	22.9	786	9	AY416062	AY416062 Pan trogl
3	392	19.3	767	6	CD638712	CD638712 AGENCOURT
4	332.2	16.4	783	9	AY416063	AY416063 Mus muscu
5	327	16.1	806	6	CD521613	CD521613 AGENCOURT
6	286.4	14.1	571	7	CNT94193	CNT94193 4129335 B
7	240	11.8	628	7	CNT86611	CNT86611 4120632 B
8	221.4	10.9	702	6	CD640741	CD640741 AGENCOURT
9	217.2	10.7	690	6	CD642064	CD642064 AGENCOURT
10	211	10.4	796	6	CD520208	CD520208 AGENCOURT
C 11	176.4	8.7	527	8	BH886550	BH886550 LB00861a
C 12	108.4	5.3	847	7	CK777858	CK777858 965004 MA
13	105.2	5.2	740	7	CK834247	CK834247 4058618 B
14	103.2	5.1	492	2	BF599437	BF599437 263218 MA
C 15	85	4.2	1843	9	AG435185	AG435185 Mus muscu
C 16	83	4.1	1786	8	CG307208	CG307208 TAM32-34F
C 17	82.6	4.1	1811	9	CG753732	CG753732 P048-4-GO
18	81.4	4.0	1491	9	CL071740	CL071740 Ch2116-122
C 19	81.2	4.0	1453	9	AJ591978	AJ591978 Arabidops
C 20	81.2	4.0	1491	9	CG753221	P048-2-A0
C 21	81.2	4.0	1654	9	CL118709	CL118709 ISB1-721I
C 22	80.8	4.0	1104	6	CF264382	CF264382 AGENCOURT
C 23	80.6	4.0	1373	9	CG750869	P045-2-E1
C 24	80.6	4.0	1785	9	CL082738	CL082738 Ch2116-170

FEATURES	High quality sequence stop: 564.	
	Location/Qualifiers	
source	1..767	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:30416146"	
	/issue_type="Pooled"	
	/lab_host="DH10B (T1 phage-resistant)"	
	/clone_lib="NIH_MGC_191"	
	/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);	
	Site 2: SfiI (ggccgcttcggcc); Library is oligo-dT primed	
	and directionally cloned. PMK - Peripheral Blood	
	Mononuclear Cells. RNA was pooled from 3/6hour stimulation	
	with PMA and Ionomycin. 5' and 3' adaptors were used in	
	cloning as follows: 5' adaptor sequence:	
	5'-ATTCTAGAGCGGCGCGCCGACATG-DT(30)BN-3' (where B = A,	
	C, or G and N = A, C, G, or T). Average insert size 1.69	
	Kb (range 0.70-5.0 Kb). 15/15 colonies contained inserts	
	by PCR. This library was enriched for full-length clones	
	and was constructed by Clontech Laboratories (Palo Alto,	
	CA). Note: this is a NIH_MGC Library."	
ORIGIN		
Query Match	19.3%; Score 392; DB 6; Length 767;	
	Best Local Similarity 93.7%; Pred. No. 6.3e-86;	
Matches	418; Conservative 0; Mismatches 27; Indels 1; Gaps 1;	
Qy	1522	ACAGTGCAGAGAAAAGACCGATCCAGAAACACAGCTTTGAATGCAAAAGGTGAT 1581
Db	181	ATAATGTTAAACAAGAGGAGAGCAAGAAAGAAAACAGCTTTGAATGCAAAAGGTGAT 240
Qy	1582	CAGAACTCCTCAAAATTCGCGCCATGTCATAAGTGAGGCGCAGGTAAACCAACATCTGTG 1641
Db	241	CAGAACTCCTCAAAATTCGCGCCATGTCATAAGTGAGGCGCAGGTAAACCAACATCTGTG 300
Qy	1642	TTACAGTGGGTGAAAAAGGATATACACCATGAGCAACAACTTGGTAAACCTTGAAAAAT 1701
Db	301	TTACAGTGGGTGAAAAAGGATATACACCATGAGCAACAACTTGGTAAACCTTGAAAAAT 360
Qy	1702	GGGAAACAGCTGACCGTTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC 1761
Db	361	GGGAAACAGCTGACCGTTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTC 420
Qy	1762	TGTTCCAAATCGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTTAAAGTCC 1821
Db	421	TGTTCCAAATCGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTTAAAGTCC 480
Qy	1822	CCCGGTAGATTGAGAGAACTTTACTCAGAGCTGCAAAATACCCAGTTCGCCCAAACTT 1881
Db	481	CCCGGTAGATTGAGAGAACTTTACTCAGAGCTGCAAAATACCCAGTTCGCCCAAACTT 540
Qy	1882	TGCGGGCAACATCCATTCACCTTGGGAGGAGTATTGAAATTCACACAGGTGCTTCGGTG 1941
Db	541	TGCGGGCAACATCCATTCACCTTGGGAGGAGTATTGAAATTCACACAGGTGCTTCGGTG 600
Qy	1942	TTTGTCAATGTGACTGATCCAGCCA 1967
Db	601	TTTGTGTC-ATGTGACTGATCCNAGCNA 625
RESULT 4		
AY416063		
LOCUS		
DEFINITION	783 bp DNA linear GSS 17-DEC-2003	
SOURCE	Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,	
	genomic survey sequence.	
ACCESSION	AY416063	
VERSION	AY416063.1	
KEYWORDS	GI:39772023	
SOURCE	GSS.	
	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
1 (bases 1 to 783)		
REFERENCE		
AUTHORS		
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,		
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,		
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,		
Adams, M.D. and Cargill, M.		
TITLE		
Inferring nonneutral evolution from human-chimp-mouse orthologous		
gene trios		
JOURNAL		
Science 302 (5652), 1960-1963 (2003)		
PUBMED		
14671302		
REFERENCE		
AUTHORS		
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,		
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,		
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,		
Adams, M.D. and Cargill, M.		
TITLE		
Direct Submission		
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		
Rockville, MD 20850, USA		
COMMENT		
This sequence was made by sequencing genomic exons and ordering		
them based on alignment.		
FEATURES		
Location/Qualifiers		
1..783		
/organism="Mus musculus"		
/mol_type="genomic DNA"		
/db_xref="taxon:10090"		
<1..>783		
/gene="TNFSF5"		
/locus_tag="HCM5765"		
ORIGIN		
Query Match	16.4%; Score 332.2; DB 9; Length 783;	
	Best Local Similarity 80.7%; Pred. No. 4.1e-71;	
Matches	388; Conservative 0; Mismatches 93; Indels 0; Gaps 0;	
Qy	1533	AGAAAAGACCGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCA 159
Db	300	AAACAAGAGAGAAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCA 359
Qy	1593	AATTGCGGCACATGTCAATAGTGAGGCGCAGCAAGTAAACAAACATCTGTGTACAGTGGGC 165
Db	360	AATTGCGGCACATGTGTAAAGCGAAGCAACAGTAAATGCAAGTCCGTTCTACAGTGGGC 419
Qy	1653	TGAAAAGAGATCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAGCT 171
Db	420	CAAGAAGAGATATTATACCATGAAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCT 479
Qy	1713	GACCGTTAAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAATCG 177
Db	480	GACCGTTAAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTGCTCTAATCG 539
Qy	1773	GGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGTAGATT 183
Db	540	GGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGTAGATC 599
Qy	1833	CGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTGGGGCAACA 189
Db	600	TGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCTCCAGCTTTGGCAGCAGCA 659
Qy	1893	ATCCATTACCTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTGTGTCAATCT 195
Db	660	GTCTGTTCATCTGGGCGGAGTGTGTTGAAATTAACAAGCTGGTGTCTTGTGTCAACGT 719
Qy	1953	GACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 201
Db	720	GACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 779
Qy	2013	C 2013
Db	780	C 780
RESULT 5		
CD521613		

LOCUS CD521613 806 bp mRNA linear EST 06-JUN-2003
DEFINITION AGSCOURT 14356206 NIH MGC 191 Homo sapiens cDNA clone IMAGE:30413128 5', mRNA sequence.

ACCESSION CD521613
VERSION CD521613.1 GI:31453331
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 806)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at:
<http://image.llnl.gov>
Plote: NDCM207 row: j column: 17
High quality sequence stop: 466.
Location/Qualifiers
1..806
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:30413128"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/note="Vector: pDONR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgctctggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 16.1%; Score 327; DB 6; Length 806;
Best Local Similarity 91.5%; Pred. No. 8.1e-70;
Matches 356; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 1592 ACAGTGCAGAGAAAAGACCGATCCAGAAAACAGCTTTGAATCAAAAAGTGTAT 1581
DB 386 ATAATGTTAAACAAAGAGGAGAGAGAGAAAGANAAACAGCTTTGAATCAAAAAGTGTAT 445
QY 1582 CAGAAATCCTCAAAATGGCGCACATGTCATAGTGAAGGCGAGAGTAAACACACATCTGTG 1641
DB 446 CAGAAATCCTCAAAATGGCGCACATGTCATAGTGAAGGCGAGAGTAAACACACATCTGTG 505
QY 1642 TTACAGTGGGCTGAAAAAGGATCTACACCATGAGCAACAATTGGTAACCCCTGGAATAT 1701
DB 506 TTACAGTGGGCTGAAAAAGGATCTACACCATGAGCAACAATTGGTAACCCCTGGAATAT 565
QY 1702 GGGAAACAGCTGACCGTTAAAGACAGGACTCTATTATCTATGCCCAAGTCACCTTC 1761
DB 566 GGGAAACAGCTGACCGTTAAAGACAGGACTCTATTATCTATGCCCAAGTCACCTTC 625
QY 1762 TGTTCCAATCGGGAAGCTTCGAGTCAAGTCTCCATTATAGCCAGCTCTGCTCAAAAGTCC 1821

DB 626 TGTTCCAATCGGGAAGCTTCGAGTCAAGTCCATTATAGCCAGCTCTGCTCAAAAGTCC 685
QY 1822 CCGGTAGATTCGAGAGAAATCTTACTCAGAGCTCAATATACCCACAGTTCGCGCAACCT 1881
DB 686 CCGGTAGATTCGAGAGAAATCTTACTCAGAGCTCAATATACCCACAGTTCGCGCAACCT 745
QY 1882 T-GGGGCAACAATCCATTCACTTGGGAG 1909
DB 746 TGGCGGGCAACATCCCTTTCCCTTGGGG 774

RESULT 6
LOCUS CN794193 571 bp mRNA linear EST 26-MAY-2004
DEFINITION CN794193 4129335 BARC 8BOV Bos taurus cDNA clone 8BOV_50H03 5', mRNA sequence.
ACCESSION CN794193
VERSION CN794193.1 GI:47690173
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 571)
AUTHORS Baumann, R.G.; Baldwin, R.L.; Sonstegard, T.S.; Van Tassell, C.P. and Matukumalli, L.K.
TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)
JOURNAL Contact: Richard G. Baumann
COMMENT Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred 0.000325 using options -trim_alt'' -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 18 Plate: 50 row: H column: 03
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 571.
Location/Qualifiers
1..571
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clones="8BOV_50H03"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1: NotI; Site 2: EcoRI; Normalized cow cDNA intestinal library in pCMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating from equimolar, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

ORIGIN
Query Match 14.1%; Score 286.4; DB 7; Length 571;
Best Local Similarity 89.5%; Pred. No. 8.7e-60;
Matches 308; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1670 CCATGAGCAACAACTTGTAACTCCCTGGAAATGGAAACAGCTGACCGTTAAAGACAAG 1729
DB 1 CCCTAAGCAACAACCTGTGTAACTCCCTGGAAACAGCTGCGCCGTGAAAGACAAG 60

with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 10.9%; Score 221.4; DB 6; Length 702;
Best Local Similarity 88.4%; Pred. No. 1.2e-43;
Matches 252; Conservative 0; Mismatches 31; Indels 2; Gaps 1;
Qy 1522 ACAGTGCAGAGAGAAAAGACCGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGAT 1581
Db 362 ATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGAT 421
Qy 1582 CAGATCTCTCAAAATTCGGCCACATGCTCATAGTGAGCGCAGCAGTAAACACACATCTGTG 1641
Db 422 CAGAATCTCTCAAAATTCGGCCACATGCTCATAGTGAGCGCAGCAGTAAACACACATCTGTG 481
Qy 1642 TTACAGTGGGCTGAAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAAT 1701
Db 482 TTACAGTGGGCTGAAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAAT 541
Qy 1702 GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTACACCTTC 1761
Db 542 GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTACACCTTC 601
Qy 1762 TGTTCATCGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGC 1806
Db 602 CTGTCCATCGGAGAGCTTCAGTCA--GCTCATTTATAGCCAGC 644

RESULT 9

CD642064 CD642064 690 bp mRNA linear EST 17-JUN-2003
LOCUS AGENCOURT_14538852 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30418744 5', mRNA sequence.

ACCESSION CD642064

VERSION CD642064.1 GI:31811566

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 690)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM222 row: d column: 17

High quality sequence stop: 536.

Location/Qualifiers

1..690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30418744"

/tissue_type="Pooled"

FEATURES

source

/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_191"
/note=vector: pDONR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctggcc); Library is oligo-dT primed
and directionally cloned. FMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 10.7%; Score 217.2; DB 6; Length 690;
Best Local Similarity 92.3%; Pred. No. 1.3e-42;
Matches 228; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1522 ACAGTGCAGAGAGAAAAGACCGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGAT 1581
Db 367 ATAATGTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGAT 426
Qy 1582 CAGAATCTCTCAAAATTCGGCCACATGCTCATAGTGAGCGCAGCAGTAAACACACATCTGTG 1641
Db 427 CAGAATCTCTCAAAATTCGGCCACATGCTCATAGTGAGCGCAGCAGTAAACACACATCTGTG 486
Qy 1642 TTACAGTGGGCTGAAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAAT 1701
Db 487 TTACAGTGGGCTGANAAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAAT 546
Qy 1702 GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTACACCTTC 1761
Db 547 GGGAAACAGCTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTACACCTTC 606
Qy 1762 TGTTCCTCA 1768
Db 607 TGTTCCTCA 613

RESULT 10

CD520208 CD520208 796 bp mRNA linear EST 06-JUN-2003
LOCUS AGENCOURT_14355767 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30412573 5', mRNA sequence.

ACCESSION CD520208

VERSION CD520208.1 GI:31451926

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM206 row: c column: 14

High quality sequence stop: 541.

Location/Qualifiers

FEATURES


```

cross_match v0.990329.
plate_33 row: N column: 5
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
1..847
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN
Query Match 5.3%; Score 108.4; DB 7; Length 847;
Best Local Similarity 91.3%; Pred. No. 1.2e-15;
Matches 115; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1888 CAACAATCCATTCACTTCGGAGGAGTATTGAATTGCAACGAGTGCTTCGGTGTTC 1947
Db |||||||
847 CAGCAATCCATTCACTTAGGAGGAGTCTTTGAAATTGCAATCGGGTGTTCGGTGTTC 788
Qy 1948 AATGTGACTGATCCAAAGCCAAAGTGCATGCGCTTCACGTCCCTTTGGCTTACTC 2007
Db |||||||
787 AATGTGACTGATCCAAAGTCAAGTGCACGAGCCAGGGGCTTCACATCAITTTGGCTTACTC 728
Qy 2008 AACTC 2013
Db |||||||
727 AACTC 722

RESULT 13
CK834247
LOCUS 740 bp mRNA linear EST 04-MAR-2004
DEFINITION 4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA
sequence.
ACCESSION CK834247
VERSION CK834247.1 GI:45064536
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 740)
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
Matukumalli,L.K.
TITLE Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '' -trim fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 2 row: M column: 16
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 740.
Location/Qualifiers
1..740
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_2M16"

FEATURES
source
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN
Query Match 5.2%; Score 105.2; DB 7; Length 740;
Best Local Similarity 79.1%; Pred. No. 7.3e-15;
Matches 125; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1522 ACAGTGCAGAGAAAAAGACCGGATCCAGAAACAGCTTTGAAATGCAAAAAGGTGAT 1581
Db |||||||
583 ATATGCACAAACAAAGAGTAAGAAGAAAAAATTTGAATGCACAAAGGTGAT 642
Qy 1582 CAGAAATCTCAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACTCTGTG 1641
Db |||||||
643 CAGGAGGCTCAGATAGGGGCACATGTCATCAGTGAGGCCAGTAGTAAACAACTCTGT 702
Qy 1642 TTACAGTGGGCTGAAAAGGATACATACACCATGAGCAA 1679
Db |||||||
703 CTCAGTGGGGCCCCCAAGGATACACCCCTTAAGCAA 740

RESULT 14
BF599437
LOCUS 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 492)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 33 row: N column: 5
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..492
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 2483.19 Seconds
(without alignments)
16453.933 Million cell updates/sec

Title: US-09-687-864A-17
Perfect score: 864
Sequence: 1 aagcttgcgcctatgctga.....aactcgagtataatctaga 864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642.8	74.4	786	6	187864 Sequence 3
2	642.8	74.4	786	6	B064000 Novel exp
3	642.8	74.4	786	6	B064003 Novel exp
4	642.8	74.4	786	6	B064005 Novel exp
5	642.8	74.4	786	6	B064006 Novel exp
6	642.8	74.4	840	6	AR044779 Sequence
7	642.8	74.4	840	6	AR076926 Sequence
8	642.8	74.4	840	6	AR078316 Sequence
9	642.8	74.4	840	6	AR085419 Sequence
10	642.8	74.4	840	6	AR103375 Sequence
11	642.8	74.4	840	6	AR106246 Sequence
12	642.8	74.4	840	6	AR169232 Sequence
13	642.8	74.4	840	6	AR171647 Sequence
14	642.8	74.4	840	6	BD190674 Method of
15	642.8	74.4	840	6	I23893 Sequence 1
16	642.8	74.4	840	6	I27345 Sequence 7
17	642.8	74.4	840	6	I67828 Sequence 1
18	642.8	74.4	840	6	AR216259 Sequence
19	642.8	74.4	840	6	AR267621 Sequence

20	642.8	74.4	870	9	BC074950	BC074950 Homo sapi
21	642.8	74.4	879	6	AR254616	AR254616 Sequence
22	642.8	74.4	879	6	AX090039	AX090039 Sequence
23	642.8	74.4	879	9	HSGP39MR	Z15017 H. sapiens m
24	642.8	74.4	1803	6	AR350226	AR350226 Sequence
25	642.8	74.4	1803	9	HSCD40	X67878 H. sapiens m
26	642.8	74.4	1816	6	BD187611	BD187611 Screening
27	642.8	74.4	1816	6	BD270930	BD270930 Use of CD
28	642.8	74.4	1816	6	AR254617	AR254617 Sequence
29	642.8	74.4	1816	9	HUMCD40L	L07414 Human CD40-
30	642.8	74.4	1859	9	BC071754	BC071754 Homo sapi
31	641.2	74.2	1798	6	CQ725625	CQ725625 Sequence
32	641.2	74.2	1822	9	HSTRAPA	X68550 H. sapiens T
33	638.4	73.9	1566	6	AX455878	AX455878 Sequence
34	636	73.6	929	6	AR076932	AR076932 Sequence
35	636	73.6	929	6	AR078322	AR078322 Sequence
36	636	73.6	929	6	AR085425	AR085425 Sequence
37	636	73.6	929	6	AR103381	AR103381 Sequence
38	636	73.6	929	6	AR169238	AR169238 Sequence
39	636	73.6	929	6	187867	187867 Sequence 10
40	636	73.6	929	6	AR216265	AR216265 Sequence
41	635.2	73.5	1425	6	AR076929	AR076929 Sequence
42	635.2	73.5	1425	6	AR078319	AR078319 Sequence
43	635.2	73.5	1425	6	AR085422	AR085422 Sequence
44	635.2	73.5	1425	6	AR103378	AR103378 Sequence
45	635.2	73.5	1425	6	AR169235	AR169235 Sequence

ALIGNMENTS

RESULT 1
LOCUS I87864 786 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 3 from patent US 5716805.
ACCESSION I87864
VERSION I87864.1 GI:3407804
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 786)
AUTHORS Srinivasan,S. and Spriggs,M.K.
TITLE Methods of preparing soluble, oligomeric proteins
JOURNAL Patent: US 5716805-A 3 10-FEB-1998;
FEATURES Location/Qualifiers
source 1..786
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match	74.4%;	Score 642.8;	DB 6;	Length 786;
Best Local Similarity	99.7%;	Pred. No. 5.1e-157;		
Matches	644;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
Qy	204	TCCAAGAGGTTGGCAAGATAGAAGATGAAGAAATCTTCATCAAGATTGTATTTCAT	263	
Db	138	TCATAGAAGGTTGGCAAGATAGAAGATGAAGAAATCTTCATCAAGATTGTATTTCAT	197	
Qy	264	GAACACATACAGATGCAACACAGGAGAAAGATCTTATCTTACTGAAGTGTGAGGA	323	
Db	198	GAACACATACAGATGCAACACAGGAGAAAGATCTTATCTTACTGAAGTGTGAGGA	257	
Qy	324	GATTTAAAGCCAGTTTCAAGGCTTTGTGAAGGATATATGTGTAAACAAAGAGGAGACGA	383	
Db	258	GATTTAAAGCCAGTTTCAAGGCTTTGTGAAGGATATATGTGTAAACAAAGAGGAGACGA	317	
Qy	384	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443	
Db	318	GAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	377	
Qy	444	CATTAAGTAGGCCAGCAGTAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA	503	

Db	378	CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGATCTA	437
Qy	504	CACCATGAGCAACAACTTGTTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGCA	563
Db	438	CACCATGAGCAACAACTTGTTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGCA	497
Qy	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGAGTCA	623
Db	498	AGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGAGTCA	557
Qy	624	AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	683
Db	558	AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	617
Qy	684	CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAACAATCCATTCACCTTGGG	743
Db	618	CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAACAATCCATTCACCTTGGG	677
Qy	744	AGGAGTATTTGAATGCAACACAGTGTTCGGTGTGTTGTCATATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTTGAATGCAACACAGTGTTCGGTGTGTTGTCATATGTGACTGATCCAAAGCCA	737
Qy	804	AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC	849
Db	738	AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC	783
RESULT 2			
BD064000			
LOCUS			
DEFINITION	BD064000	786 bp DNA linear	PAT 27-AUG-2002
		Novel expression vectors containing accessory molecule ligand genes	
		and their use for immuno-modulation and treatment of malignancies	
		and autoimmune disease.	
ACCESSION	BD064000		
VERSION	BD064000.1	GI:22609603	
KEYWORDS	JP 2001505782-A/1.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 786)		
AUTHORS	Kipps,T.J., Sharma,S. and Cantwell,M.		
TITLE	Novel expression vectors containing accessory molecule ligand genes		
	and their use for immuno-modulation and treatment of malignancies		
	and autoimmune disease		
JOURNAL	Patent: JP 2001505782-A 1 08-MAY-2001;		
COMMENT	UNIVERSITY OF CALIFORNIA		
	PN JP 2001505782-A/1		
	PD 08-MAY-2001		
	PF 08-DEC-1997 JP 1998526956		
	PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI		
	PC THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL		
	PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/525,C07K14/705,		
	PC C12N15/86,		
	PC A61K48/00,A61K38/17,A61K35/12		
	CC Strandedness: Single;		
	CC Topology: Linear;		
FEATURES	Key	Location/Qualifiers.	
source	1..786		
	/organism="synthetic construct"		
	/mol type="genomic DNA"		
	/db_xref="taxon:32630"		
ORIGIN			
Query Match	74.4%;	Score 642.8;	DB 6;
Best Local Similarity	99.7%;	Pred. No. 5.1e-157;	Length 786;
Matches	644;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	204	TCCAAAGAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAGAGATTGTTATTCAT	263
Db	138	TCATAGAAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAGATTGTTGTTATTCAT	197
Qy	264	GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA	323

Db	198	GAACACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAATGTGAGGA	257
Qy	324	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATTAATCTTAAACAAAGGAGAGCGAA	383
Db	258	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATTAATCTTAAACAAAGGAGAGCGAA	317
Qy	384	GAAAGAAAACAGCTTTTGAATGCAAAAAGTGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443
Db	318	GAAAGAAAACAGCTTTTGAATGCAAAAAGTGTGATCAGAAATCCTCAAAATTCGGGCACATGT	377
Qy	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTTACAGTGGGCTGAAAAGGATCTA	503
Db	378	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTTACAGTGGGCTGAAAAGGATCTA	437
Qy	504	CACCATGAGCAACAACTTGTTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGCA	563
Db	438	CACCATGAGCAACAACTTGTTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGCA	497
Qy	564	AGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGAGTCA	623
Db	498	AGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGAGTCA	557
Qy	624	AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	683
Db	558	AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT	617
Qy	684	CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAACAATCCATTCACCTTGGG	743
Db	618	CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAACAATCCATTCACCTTGGG	677
Qy	744	AGGAGTATTTGAATGCAACACAGTGTTCGGTGTGTTGTCATATGTGACTGATCCAAAGCCA	803
Db	678	AGGAGTATTTGAATGCAACACAGTGTTCGGTGTGTTGTCATATGTGACTGATCCAAAGCCA	737
Qy	804	AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC	849
Db	738	AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC	783
RESULT 3			
BD064003			
LOCUS			
DEFINITION	BD064003	786 bp DNA linear	PAT 27-AUG-2002
		Novel expression vectors containing accessory molecule ligand genes	
		and their use for immuno-modulation and treatment of malignancies	
		and autoimmune disease.	
ACCESSION	BD064003		
VERSION	BD064003.1	GI:22609606	
KEYWORDS	JP 2001505782-A/4.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 786)		
AUTHORS	Kipps,T.J., Sharma,S. and Cantwell,M.		
TITLE	Novel expression vectors containing accessory molecule ligand genes		
	and their use for immuno-modulation and treatment of malignancies		
	and autoimmune disease		
JOURNAL	Patent: JP 2001505782-A 4 08-MAY-2001;		
COMMENT	UNIVERSITY OF CALIFORNIA		
	PN JP 2001505782-A/4		
	PD 08-MAY-2001		
	PF 08-DEC-1997 JP 1998526956		
	PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI		
	PC THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL		
	PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/525,C07K14/705,		
	PC C12N15/86,		
	PC A61K48/00,A61K38/17,A61K35/12		
	CC Strandedness: Single;		
	CC Topology: Linear;		
FEATURES	Key	Location/Qualifiers.	
source	1..786		
	/organism="synthetic construct"		
ORIGIN			
Query Match	74.4%;	Score 642.8;	DB 6;
Best Local Similarity	99.7%;	Pred. No. 5.1e-157;	Length 786;
Matches	644;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	204	TCCAAAGAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAGAGATTGTTATTCAT	263
Db	138	TCATAGAAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAGATTGTTGTTATTCAT	197
Qy	264	GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA	323

```
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          74.4%; Score 642.8; DB 6; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCACAGAGGTTGGCAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 263
   |||||
Db 138 TCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT 197

QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTGAACTGTGAGA 323
   |||||
Db 198 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTGAACTGTGAGA 257

QY 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAAGAGAGACGAA 383
   |||||
Db 258 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAAGAGAGACGNA 317

QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCTCAAAATGCGGCACATGT 443
   |||||
Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCTCAAAATGCGGCACATGT 377

QY 444 CATAGTGGCCAGCAGTAAACACATCTGTGTACAGTGGGCTGAAAGGATCTTACT 503
   |||||
Db 378 CATAGTGGCCAGCAGTAAACACATCTGTGTACAGTGGGCTGAAAGGATCTTACT 437

QY 504 CACCATGAGCAACACTTGGTAACCTCGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
   |||||
Db 438 CACCATGAGCAACACTTGGTAACCTCGAAATGGGAAACAGCTGACCGTTTAAAGACA 497

QY 564 AGGACTATTATATCTATGCCCCAAGTCACTTCTGTGTTTGTCAATGCGGAGCTTCGAGTCA 623
   |||||
Db 498 AGGACTATTATATCTATGCCCCAAGTCACTTCTGTGTTTGTCAATGCGGAGCTTCGAGTCA 557

QY 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGATTCGAGAGATCTTACT 683
   |||||
Db 558 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGATTCGAGAGATCTTACT 617

QY 684 CAGAGCTGCAATATACCAAGTTCGCGCAACCTTGGCGGCAACAACTCCATTCACCTGGG 743
   |||||
Db 618 CAGAGCTGCAATATACCAAGTTCGCGCAACCTTGGCGGCAACAACTCCATTCACCTGGG 677

QY 744 AGGAGTATTTGAAATGCAACCAAGTGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803
   |||||
Db 678 AGGAGTATTTGAAATGCAACCAAGTGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 737

QY 804 AGTGAGCCATGGCAGCTTGCCTTACGCTTCTTGGCTTACTCAAACTC 849
   |||||
Db 738 AGTGAGCCATGGCAGCTTGCCTTACGCTTCTTGGCTTACTCAAACTC 783

RESULT 4
BD064005 786 bp DNA linear PAT 27-AUG-2002
LOCUS Novel expression vectors containing accessory molecule ligand genes
DEFINITION and their use for immuno-modulation and treatment of malignancies
and autoimmune disease.
ACCESSION BD064005
VERSION BD064005.1 GI:22609608
KEYWORDS JP 2001505782-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 786)
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.
TITLE Novel expression vectors containing accessory molecule ligand genes
and their use for immuno-modulation and treatment of malignancies
and autoimmune disease
JOURNAL Patent: JP 2001505782-A 6 08-MAY-2001;
UNIVERSITY OF CALIFORNIA
COMMENT PN JP 2001505782-A/6
```

```

VERSION      BD064006.1  GI:22609609
KEYWORDS     JP 2001505782-A/7.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 786)
AUTHORS      Kipps T.J., Sharma, S. and Cantwell, M.
TITLE        Novel expression vectors containing accessory molecule ligand genes
              and their use for immuno-modulation and treatment of malignancies
              and autoimmune disease
JOURNAL      Patent: JP 2001505782-A 7 08-MAY-2001;
              UNIVERSITY OF CALIFORNIA
COMMENT      PN JP 2001505782-A/7
              PD 08-MAY-2001
              PF 08-DEC-1997 JP 1998526956
              PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI
              THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL
              PC C12N15/12,C12N15/62,C07K14/48,C07K14/525,C07K14/705,
              C12N15/86,
              PC A61K48/00,A61K38/17,A61K35/12
              CC Strandedness: Single;
              CC Topology: linear;
              FH Key Location/Qualifiers.
FEATURES     source
              1..786
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
ORIGIN
Query Match 74.4%; Score 642.8; DB 6; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 TCCAGAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 138 TCATAGAAGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 197
QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 198 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 257
QY 324 GATTAAGCCAGCTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 383
DB 258 GATTAAGCCAGCTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 317
QY 384 GAAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 443
DB 318 GAAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 377
QY 444 CATAAAGTGAGGCCAGAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
DB 378 CATAAAGTGAGGCCAGAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437
QY 504 CACCATGAGCAACAACCTTGTAACCTTGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
DB 438 CACCATGAGCAACAACCTTGTAACCTTGAAATGGGAAACAGCTGACCGTTTAAAGACA 497
QY 564 AGGACTCTATTATATCTATGCCCACAGTCACTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 623
DB 498 AGGACTCTATTATATCTATGCCCACAGTCACTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 557
QY 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAACTCTTACT 683
DB 558 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAACTCTTACT 617
QY 684 CAGAGTCGAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 743
DB 618 CAGAGTCGAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 677
QY 744 AGGAGTATTGAAATGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCA 803
DB 678 AGGAGTATTGAAATGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCA 737

```

```

QY 804 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAATC 849
DB 738 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAATC 783
RESULT 6
LOCUS      AR044779 840 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION    AR044779.1 GI:5966244
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 840)
AUTHORS     Kehry, M. and Castle, B.
TITLE        Methods for proliferating and differentiating B cells with high
              density membrane CD40 ligand
JOURNAL     Patent: US 5817516-A 3 06-OCT-1998;
FEATURES     Location/Qualifiers
              1..840
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 TCCAGAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 159 TCATAGAAGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 218
QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 219 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278
QY 324 GATTAAGCCAGCTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 383
DB 279 GATTAAGCCAGCTTTGAAGGCTTTGTGAAGATATAATGTTTAAACAAGAGGAGACGAA 338
QY 384 GAAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 443
DB 339 GAAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAATTCGGGCACATGT 398
QY 444 CATAAAGTGAGGCCAGAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
DB 399 CATAAAGTGAGGCCAGAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 458
QY 504 CACCATGAGCAACAACCTTGTAACCTTGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
DB 459 CACCATGAGCAACAACCTTGTAACCTTGAAATGGGAAACAGCTGACCGTTTAAAGACA 518
QY 564 AGGACTCTATTATATCTATGCCCACAGTCACTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 623
DB 519 AGGACTCTATTATATCTATGCCCACAGTCACTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 578
QY 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAACTCTTACT 683
DB 579 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAACTCTTACT 638
QY 684 CAGAGTCGAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 743
DB 639 CAGAGTCGAAATACCCACAGTTCCGCCAAACCTTCGGGGCAACAATCCATTCACTTGGG 698
QY 744 AGGAGTATTGAAATGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCA 803
DB 699 AGGAGTATTGAAATGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCA 758
QY 804 AGTGAGCCATGGCACTGGCTTCAGTCTCCTTTGGCTTACTCAAATC 849

```


Db	759	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	804
RESULT 7			
AR076926			
LOCUS	AR076926	840 bp	DNA linear PAT 31-AUG-2000
DEFINITION	Sequence 11 from patent US 5961974.		
ACCESSION	AR076926		
VERSION	AR076926.1 GI:10003672		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 840)		
TITLE	Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.		
JOURNAL	Monoclonal antibodies to CD40 ligand, pharmaceutical composition		
FEATURES	comprising the same and hybridomas producing the same		
source	Patent: US 5961974-A 11 05-OCT-1999;		
	Location/Qualifiers		
	1..840		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
ORIGIN			
	Query Match	74.4%;	Score 642.8; DB 6; Length 840;
	Best Local Similarity	99.7%;	Pred. No. 5.1e-157;
	Matches 644;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	204	TCCAAGAGGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	263
Db	183	TCATAGAAGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTCAT	242
Qy	264	GAACAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323
Db	243	GAACAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA	302
Qy	324	GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	383
Db	303	GATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	362
Qy	384	GAAGAGAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	443
Db	363	GAAGAGAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT	422
Qy	444	CATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503
Db	423	CATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482
Qy	504	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563
Db	483	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	542
Qy	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA	623
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA	602
Qy	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT	683
Db	603	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT	662
Qy	684	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGTGTTCGATGCTGATCCAGGCA	743
Db	663	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGTGTTCGATGCTGATCCAGGCA	722
Qy	744	AGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCGATGCTGATCCAGGCA	803
Db	723	AGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCGATGCTGATCCAGGCA	782
Qy	804	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	849
Db	783	AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACCTC	828
RESULT 9			
AR085419			

RESULT 8	AR078316	840 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	Sequence 11 from patent US 5962406.				
DEFINITION	AR078316				
ACCESSION	AR078316.1	GI:10005062			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 840)				
AUTHORS	Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E. and McGrew, J.T.				
TITLE	Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same				
JOURNAL	Patent: US 5962406-A 11 05-OCT-1999;				
FEATURES	Location/Qualifiers				
source	1..840				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	74.4%;	Score 642.8;	DB 6;	Length 840;	
Best Local Similarity	99.7%;	Pred. No. 5.1e-157;			
Matches 644;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
Qy	204	TCCAAGAAGGTTGGCAAGATGAGAATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263		
Db	183	TCATAGAAGGTTGGCAAGATGAGAATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	242		
Qy	264	GAACAACGATACAGAGATGCAACACAGAGGAAAGATCCTTATCCTTACTGAACTGTGAGGA	323		
Db	243	GAACAACGATACAGAGATGCAACACAGAGGAAAGATCCTTATCCTTACTGAACTGTGAGGA	302		
Qy	324	GATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	383		
Db	303	GATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAGAGGAGACGAA	362		
Qy	384	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCACATGT	443		
Db	363	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCACATGT	422		
Qy	444	CATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	503		
Db	423	CATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTA	482		
Qy	504	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563		
Db	483	CACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	542		
Qy	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA	623		
Db	543	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA	602		
Qy	624	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTGAGATTTCGAGAGAAATCTTACT	683		
Db	603	AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTGAGATTTCGAGAGAAATCTTACT	662		
Qy	684	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGTGTTCGATGCTGATCCAGGCA	743		
Db	663	CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGGTGTTCGATGCTGATCCAGGCA	722		
Qy	744	AGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCGATGCTGATCCAGGCA	803		
Db	723	AGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCGATGCTGATCCAGGCA	782		
Qy	804	AGTGAGCCATGGCACTGGGCTTCACGTCCTTTGGCTTACTCAAACCTC	849		
Db	783	AGTGAGCCATGGCACTGGGCTTCACGTCCTTTGGCTTACTCAAACCTC	828		
RESULT 9	AR085419				

LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
FEATURES Location/Qualifiers
source
1..840
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 204 TCCAAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTTATCCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTTAAACAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTTAAACAAGAGGAGACGAA 362
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db 423 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 482
Qy 504 CACCATGAGCAACAACTTTGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTTGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 683
Db 603 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 662
Qy 684 CAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGGGCAACAACTCCATTCACTTGGG 743
Db 663 CAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGGGCAACAACTCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 803
Db 723 AGGAGTATTTGAAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTTCACGCTCCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTTCACGCTCCTTTGGCTTACTCAAACTC 828
RESULT 10
AR103375
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375

AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES Location/Qualifiers
source
1..840
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 204 TCCAAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTTATCCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTTAAACAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTTAAACAAGAGGAGACGAA 362
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db 423 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 482
Qy 504 CACCATGAGCAACAACTTTGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTTGTAACCTCGAAAAATGGGAAACAGCTGACCGTTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 683
Db 603 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 662
Qy 684 CAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGGGCAACAACTCCATTCACTTGGG 743
Db 663 CAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGGGCAACAACTCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 803
Db 723 AGGAGTATTTGAAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTTCACGCTCCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTTCACGCTCCTTTGGCTTACTCAAACTC 828
RESULT 11
AR106246
LOCUS AR106246 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6106832.
ACCESSION AR106246
VERSION AR106246.1 GI:12820776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.
TITLE Treatment of individuals exhibiting defective CD40L
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTGTTGATTTCAT 263
DB 183 TCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTGTTGATTTCAT 242
QY 264 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 243 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
DB 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
DB 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
QY 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
DB 423 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 482
QY 504 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
DB 483 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
QY 564 AGGACTCTATTATATCTATGCCCAGTCACTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA 623
DB 543 AGGACTCTATTATATCTATGCCCAGTCACTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA 602
QY 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT 683
DB 603 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT 662
QY 684 CAGAGCTCAATATACCAACAGTTCGGCCAAACCTTCGGGCAACCAATCCATTCACTTGGG 743
DB 663 CAGAGCTCAATATACCAACAGTTCGGCCAAACCTTCGGGCAACCAATCCATTCACTTGGG 722
QY 744 AGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 803
DB 723 AGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 782
QY 804 AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC 849
DB 783 AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC 828

RESULT 12
AR169232
LOCUS AR169232 840 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6290972.
ACCESSION AR169232
VERSION AR169232.1 GI:17907047
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibeon,M.G.

Method of augmenting a vaccine response by administering CD40 ligand
Patent: US 6290972-A 11 18-SEP-2001;
Location/Qualifiers
source 1..840
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTGTTGATTTCAT 263
DB 183 TCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTGTTGATTTCAT 242
QY 264 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 243 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
DB 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
DB 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
QY 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
DB 423 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 482
QY 504 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
DB 483 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
QY 564 AGGACTCTATTATATCTATGCCCAGTCACTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA 623
DB 543 AGGACTCTATTATATCTATGCCCAGTCACTCTGTGTTCCAAATCGGGAAGCTTCGAGTCA 602
QY 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT 683
DB 603 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAATCTTACT 662
QY 684 CAGAGCTCAATATACCAACAGTTCGGCCAAACCTTCGGGCAACCAATCCATTCACTTGGG 743
DB 663 CAGAGCTCAATATACCAACAGTTCGGCCAAACCTTCGGGCAACCAATCCATTCACTTGGG 722
QY 744 AGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 803
DB 723 AGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 782
QY 804 AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC 849
DB 783 AGTGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAACCTC 828

RESULT 13
AR171647
LOCUS AR171647 840 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6297052.
ACCESSION AR171647
VERSION AR171647.1 GI:17910597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Kehry,M. and Castle,B.
TITLE B cell culture system comprising high density membrane bound CD40 ligand
JOURNAL Patent: US 6297052-A 3 02-OCT-2001;

FEATURES		Location/Qualifiers	
source	1..840	/organism="unknown"	
		/mol_type="unassigned DNA"	
ORIGIN			
Query Match	74.4%;	Score 642.8;	DB 6; Length 840;
Best Local Similarity	99.7%;	Pred. No. 5.1e-157;	
Matches 644;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	204	TCCAAGAGGTTGGCAAGATAGAAGATGAAGGAATCTTCATCAAGATTTTGTATTTCAT	263
Db	159	TCATAGAAGGTTGGACAAGATAGAAGTGAAGGAATCTTCATGAAGATTTTGTATTTCAT	218
QY	264	GAACACGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGA	323
Db	219	GAACACGATACAGAGATGCAACACAGGAGAAAAGATCCTTATCCTTACTGAACTGTGAGGA	278
QY	324	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATTAATGTTAAACAAAGAGGAGACGAA	383
Db	279	GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATTAATGTTAAACAAAGAGGAGACGAA	338
QY	384	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCACATGT	443
Db	339	GAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCACATGT	398
QY	444	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTCGAAAAGGATACTA	503
Db	399	CATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGGCTCGAAAAGGATACTA	458
QY	504	CACCATGAGCAACAACTTGGTAACTCGGAAAATGGGAAAACAGCTGACCGTTAAAAAGACA	563
Db	459	CACCATGAGCAACAACTTGGTAACTCGGAAAATGGGAAAACAGCTGACCGTTAAAAAGACA	518
QY	564	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	623
Db	519	AGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA	578
QY	624	AGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTCGAGAGAACTCTTACT	683
Db	579	AGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTCGAGAGAACTCTTACT	638
QY	684	CAGAGCTGCAAAATACCCACAGTTTCGGCCAAACCTTTGGGGCAACAACTCCATTCCTTGGG	743
Db	639	CAGAGCTGCAAAATACCCACAGTTTCGGCCAAACCTTTGGGGCAACAACTCCATTCCTTGGG	698
QY	744	AGGAGTATTTGAAATGCAACCAAGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCCA	803
Db	699	AGGAGTATTTGAAATGCAACCAAGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCCA	758
QY	804	AGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC	849
Db	759	AGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC	804
RESULT 14			
BD190674	BD190674	840 bp	DNA linear PAT 17-JUL-2003
LOCUS	Method of activating dendritic cells.		
DEFINITION	BD190674		
ACCESSION	BD190674.1		
VERSION	BD190674.1 GI:33000413		
KEYWORDS	JP 2002514047-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 840)		
TITLE	Maraskovsky, E. and Mckenna, H.J.		
JOURNAL	Method of activating dendritic cells		
COMMENT	Patent: JP 2002514047-A 1 14-MAY-2002; IMMUNEX CORP		
	OS Homo sapiens (human)		
	PN JP 2002514047-A/1		

PD	14-MAY-2002																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
----	-------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 74.4%; Score 642.8; DB 6; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.1e-157;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAGGTTGGACAAGATGAGAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAT 263
Db |||||
Qy 159 TCATAGAAGTTGGACAAGATGAGAAGTGAAGGAATCTTCATGAAGATTTTGTATTCAT 218
Db |||||
Qy 264 GAAAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db |||||
Qy 219 GAAAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278
Db |||||
Qy 324 GATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTAAACAAAGAGGAGACGAA 383
Db |||||
Qy 279 GATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTAAACAAAGAGGAGACGAA 338
Db |||||
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db |||||
Qy 339 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 398
Db |||||
Qy 444 CATAGTGAGGCGACAGCTGAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
Db |||||
Qy 399 CATAGTGAGGCGACAGCTGAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 458
Db |||||
Qy 504 CACCATGAGCAACAACCTTGGTAAACCTGGAAAAACAGCTGACCGTTAAAGACA 563
Db |||||
Qy 459 CACCATGAGCAACAACCTTGGTAAACCTGGAAAAACAGCTGACCGTTAAAGACA 518
Db |||||
Qy 564 AGGACTCTATTATATCTATGCCAAGTCACCTTCCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db |||||
Qy 519 AGGACTCTATTATATCTATGCCAAGTCACCTTCCTGTTCCAAATCGGGAAGCTTCGAGTCA 578
Db |||||
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAATCTTACT 683
Db |||||
Qy 579 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAATCTTACT 638
Db |||||
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAAATCCATTCACCTGGG 743
Db |||||
Qy 639 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAAATCCATTCACCTGGG 698
Db |||||
Qy 744 AGGAGTATTGAAATGCAACAGAGTGTTCGGTGTTCCTCAATGTGATGATCCAAAGCA 803
Db |||||
Qy 699 AGGAGTATTGAAATGCAACAGAGTGTTCGGTGTTCCTCAATGTGATGATCCAAAGCA 758
Db |||||
Qy 804 AGTGAGCCATGGCACTGGCTTCACGCTCCTTTGGCTTACTCAAACTC 849
Db |||||
Qy 759 AGTGAGCCATGGCACTGGCTTCACGCTCCTTTGGCTTACTCAAACTC 804
Db |||||

Search completed: November 12, 2004, 07:54:38
Job time : 2487.19 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

Result No.	Query			ID	Description
	Score	Match	Length		
1	864	100.0	805	4	Aaf82933
2	810.4	93.8	866	4	Aaf82932
3	676.2	78.3	2209	4	Aaf82929
4	665	77.0	2252	4	Aaf82928
5	663.4	76.8	1470	6	ABK89857
6	663.4	76.8	1470	10	ADD25460
7	663.4	76.8	1470	10	ADD25588
8	663.4	76.8	1470	11	ADMA2735
9	642.8	74.4	786	2	Aa63959
10	642.8	74.4	786	2	AAV39002
11	642.8	74.4	786	2	AAV39000
12	642.8	74.4	786	2	AAV38997
13	642.8	74.4	786	2	AAV39003
14	642.8	74.4	786	2	AAV12852
15	642.8	74.4	840	2	AAQ41506
16	642.8	74.4	840	2	AAQ67123
17	642.8	74.4	840	2	AAT05763
18	642.8	74.4	840	2	AAT39782
19	642.8	74.4	840	2	AAV61063
20	642.8	74.4	840	2	AAZ27525
21	642.8	74.4	840	10	ADH50747

CC The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
CC CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 906 BP; 294 A; 179 C; 216 G; 217 T; 0 U; 0 Other;

Query Match 93.8%; Score 810.4; DB 4; Length 906;
Best Local Similarity 95.3%; Pred. No. 1.4e-219;
Matches 863; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

QY 1 AAGCTTGCGCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTCTGTTTGGATCTCG 60
DB |||||
1 AAGCTTGCGCCATGCTGTATACCTCTCAGCTGTAGGACTACTCTCTGTTTGGATCTCG 60
QY 61 GCTTCGAGATCTGTAGTAAATTAATTGTACAGACCAACAATACAGAAAGGTTA 120
DB |||||
61 GCTTCGAGATCTGTAGTAAATTAATTGTACAGACCAACAATACAGAAAGGTTA 120
QY 121 TCTATAGCACCGAGGAGCATTCTTATGCAAGAAACATATAGGAGATATAGACAA 180
DB |||||
121 TCTATAGCACCGAGGAGCATTCTTATGCAAGAAACATATAGGAGATATAGACAA 180
QY 181 GCACATTGTAACATTA-----GT 198
DB |||||
181 GCACATTGTAACATTAAGTGGCGGTGCTCAGGAGCGGTGGATCGCGGTGAGGT 240
QY 199 CCGGATCCAAGAGGTTGGCAAGATAGAGATGAAAGAAATCTTCAATGAAGATTTGTA 258
DB |||||
241 TCGGATCCAAGAGGTTGGCAAGATAGAGATGAAAGAAATCTTCAATGAAGATTTGTA 300
QY 259 TCCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCTTACTGAACTGT 318
DB |||||
301 TCCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCTTACTGAACTGT 360
QY 319 GAGGAGATTAAAGCCAGTTTCAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAG 378
DB |||||
361 GAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAG 420
QY 379 ACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGCA 438
DB |||||
421 ACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGCA 480
QY 439 CATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGA 498
DB |||||
481 CATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGA 540
QY 499 TACTACACCATGAGCAACAACTTGGTAACTGGGAAATGGGAAACAGCTGACCGTTAAA 558
DB |||||
541 TACTACACCATGAGCAACAACTTGGTAACTGGGAAATGGGAAACAGCTGACCGTTAAA 600
QY 559 AGACAAGGACTCTATTATATATATATCCCAAGTCACTTCTGTCCAAATCGGGAAGCTTCG 618
DB |||||
601 AGACAAGGACTCTATTATATATATATCCCAAGTCACTTCTGTCCAAATCGGGAAGCTTCG 660
QY 619 AGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGATC 678
DB |||||
661 AGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGATC 720
QY 679 TTACTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGGGAACAATCCATTCAC 738
DB |||||
721 TTACTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGGGAACAATCCATTCAC 780
QY 739 TTGGGAGGAGTATTTGAATTGCAACAGGTCGCTCGGTGTTTGTCAATGTGACTGATCCA 798
DB |||||
781 TTGGGAGGAGTATTTGAATTGCAACAGGTCGCTCGGTGTTTGTCAATGTGACTGATCCA 840
QY 799 AGCCAAGTGAGCCATGGGCACTGGCTTCAGCTCTTTGGCTTACTCAAACTCGAGTGATAA 858
DB |||||

Db 841 AGCCAAGTGACCATGGCAGCTTACGTCCTTTGGCTTACTCAAACTCGAGTGATAA 900

QY 859 TCTAGA 864
|||||

Db 901 TCTAGA 906
|||||

RESULT 3
AAF82929
ID AAF82929 standard; cDNA; 2209 BP.

XX AC AAF82929;
XX 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.

XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 13..2209
FT sig_peptide /*tag= a
FT /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /*tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1551
FT /*tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 1552..2209
FT /*tag= e
FT /note= "human CD154 long form extracellular domain coding sequence"

XX WO200126608-A2.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028414.

XX 14-OCT-1999; 99US-0159690P.

XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.

XX Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62334.

XX DNA vaccine for improving antigen-specific humoral and cellular immune
XX responses, comprising one or more antigens linked to a domain that binds
XX at least one receptor.

XX Example 1; Fig 3A; 55pp; English.

XX The invention provides a vaccine comprising one or more antigens linked
XX to a domain that binds at least one receptor to improve the antigen-
XX specific humoral and cellular immune response. The DNA vaccines induce
XX strong antigen-specific humoral and cellular immune responses. The
XX vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
XX present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
XX long form extracellular domain fusion protein linked by a ProAspPro
XX linker. (Updated on 11-SEP-2003 to standardise OS field)

```
SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;
Query Match 78.3%; Score 676.2; DB 4; Length 2209;
Best Local Similarity 94.2%; Pred. No. 2.6e-181;
Matches 702; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 120 ATCTATAGACACGAGGAGCATTTTATGCAAGAGAAACATATAAGGAGATATAAGACA 179
DB 1464 ATATAAGTAGTAAGAAATGAACCAATAGGAGTAGCACCACCCAGGGCAAGAGAGAAC 1523
QY 180 AGCAATTTGTAACATAGTCCGGATCCCAAGAGGTTGGACAAGATAGAAAGGAA 239
DB 1524 AGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
QY 240 TCTTCATGAGAGATTTGTTATCATGAAACGATACAGAGATGCAACAGAGAGAGATC 299
DB 1584 TCTTCATGAGAGATTTGTTATCATGAAACGATACAGAGATGCAACAGAGAGAGATC 1643
QY 300 CTTATCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATAT 359
DB 1644 CTTATCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATAT 1703
QY 360 AATGTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 419
DB 1704 AATGTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 1763
QY 420 GAATCCTCAAAATTCGGGCACATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTGT 479
DB 1764 GAATCCTCAAAATTCGGGCACATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTGT 1823
QY 480 ACAGTGGGCTGAAAAAGGATACACCATGAGCAACAACTTTGGTAAACCCCTGGAAAAATGG 539
DB 1824 ACAGTGGGCTGAAAAAGGATACACCATGAGCAACAACTTTGGTAAACCCCTGGAAAAATGG 1883
QY 540 GAAACAGCTGACCGTTAAAGACAAGGACTCTATATATATCTATGTCGCCAAGTCACTTCGT 599
DB 1884 GAAACAGCTGACCGTTAAAGACAAGGACTCTATATATATCTATGTCGCCAAGTCACTTCGT 1943
QY 600 TTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCC 659
DB 1944 TTCCAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCC 2003
QY 660 CGGTAGATTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGT 719
DB 2004 CGGTAGATTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGT 2063
QY 720 CGGGCAACAATCATTCACTTGGGAGGAGATTTGAAATGCAACAGAGTGTCTCGGTGT 779
DB 2064 CGGGCAACAATCATTCACTTGGGAGGAGATTTGAAATGCAACAGAGTGTCTCGGTGT 2123
QY 780 TGTCAATGTGACTGATCCAAGCCAGTGCAGCCATGCAGTGCCTTTCAGTCTTTCGGCTT 839
DB 2124 TGTCAATGTGACTGATCCAAGCCAGTGCAGCCATGCAGTGCCTTTCAGTCTTTCGGCTT 2183
QY 840 ACTCAAACTCGAGTGATATCTAGA 864
DB 2184 ACTCAAACTCGAGTGATATCTAGA 2208
```

```
RESULT 4
ID AAF82928
XX AAF82928 standard; cDNA; 2252 BP.
AC AAF82928;
XX
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX
DE HIV-1 gp120-human CD154 long form extracellular domain fusion cDNA.
XX
KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
```

```
XX Human immunodeficiency virus 1.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..2252
FT sig_peptide 13..72
FT /tag= a
FT /tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1593
FT /tag= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 1594..2252
FT /tag= e
FT /note= "human CD154 long form extracellular domain coding sequence"
XX
PN WO200126608-A2.
XX
XX 19-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028414.
XX
XX 14-OCT-1999; 99US-0159690P.
XX
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
XX
XX Ledbetter JA, Hayden-Ledbetter MS;
XX
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62333.
XX
XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.
XX
XX Example 1; Fig 3A; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3 linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 2252 BP; 808 A; 400 C; 495 G; 549 T; 0 U; 0 Other;
XX
Query Match 77.0%; Score 665; DB 4; Length 2252;
Best Local Similarity 100.0%; Pred. No. 3.9e-178;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 200 CGGATCCAAAGAGGTTGGACAAGATAGAAAGTAAGAAATCTTCATCAAGATTTTGTAT 259
DB 1586 CGGATCCAAAGAGGTTGGACAAGATAGAAAGTAAGAAATCTTCATCAAGATTTTGTAT 1645
QY 260 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCCTTATCTTACTGAACTGTG 319
DB 1646 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCCTTATCTTACTGAACTGTG 1705
QY 320 AGGAGATTAAAGCCAGTTTGAAGGCTTTGAAGGATATAATGTGTAAACAAAGAGGAGA 379
DB 1706 AGGAGATTAAAGCCAGTTTGAAGGCTTTGAAGGATATAATGTGTAAACAAAGAGGAGA 1765
QY 380 CGAAGAAAACAGAGCTTTGAATGCAAAAAGGATGATCAGAAATCCTCAATTCGGGCAC 439
DB 1766 CGAAGAAAACAGAGCTTTGAATGCAAAAAGGATGATCAGAAATCCTCAATTCGGGCAC 1825
```

Qy 440 ATGTCATTAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 499
Db 1826 ATGTCATTAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 1885
Qy 500 ACTACACCATGAGCAACAACTGGTAACCCCTGGAAAAATGGGAACAGCTGACCGTTAAAA 559
Db 1886 ACTACACCATGAGCAACAACTGGTAACCCCTGGAAAAATGGGAACAGCTGACCGTTAAAA 1945
Qy 560 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
Db 1946 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2005
Qy 620 GTCAAGCTCCATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 679
Db 2006 GTCAAGCTCCATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2065
Qy 680 TACTCAGAGCTGCAAAATACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
Db 2066 TACTCAGAGCTGCAAAATACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2125
Qy 740 TGGGAGGAGTATTGAAATGCAACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
Db 2126 TGGGAGGAGTATTGAAATGCAACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185
Qy 800 GCCAAGTGAGCCATGGCACTGGCTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
Db 2186 GCCAAGTGAGCCATGGCACTGGCTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2245
Qy 860 CTAGA 864
Db 2246 CTAGA 2250

RESULT 5
ABK89857
ID ABK89857 standard; DNA; 1470 BP.
AC ABK89857;
DT 05-NOV-2002 (first entry)
XX Synthetic mouse/human chimeric fusion gene #5.
DE
KW Immunosuppressive; antitumor; antithyroid; antidiabetic; mouse;
KW neuroprotective; gene therapy; single chain antibody; variable fragment;
KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
KW ulcerative colitis; inflammatory bowel disease; immunological effector;
KW cell mediated cytotoxicity; complement dependent cytotoxicity;
KW complement fixation; gene; ds; mouse; human.
OS
OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
FH Key Location/Qualifiers
FT misc_feature 1..808
FT /tag= b
FT /note= "Murine anti-human CD20 single chain antibody
FT variable fragment (scFv)"
FT 13..1461
FT /tag= a
FT /product= "Mouse/human chimeric fusion protein"
FT 814..1455
FT misc_feature
FT /tag= c
FT /note= "Human extracellular domain long form CD154"
PN WO200256910-A1.

XX 25-JUL-2002.
PD 17-JAN-2002; 2002WO-US001487.
XX 17-JAN-2001; 2001US-00765208.
PR (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter M;
PI WPI; 2002-599691/64.
DR P-PSDB; ABG31031.
XX New human binding domain-immunoglobulin fusion protein useful for
PT treating a subject having or suspected of having a B-cell disorder or
PT malignant condition e.g. rheumatoid arthritis.
XX Disclosure; Fig 7A-B; 136pp; English.
XX The invention describes a binding domain-immunoglobulin fusion protein
CC that is capable of at least one immunological activity, comprising a
CC binding domain polypeptide fused to an immunoglobulin hinge region
CC polypeptide capable of specifically binding to an antigen, or an
CC immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
CC to the hinge region polypeptide or to the CH2 constant region
CC polypeptide. The fusion protein is useful for treating a subject having
CC or suspected of having a B-cell disorder or malignant condition e.g.
CC rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
CC thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
CC erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,
CC psoriasis, scleroderma, cancer and inflammatory bowel disease such as
CC Chron's disease and ulcerative colitis. The fusion protein retains the
CC ability to participate in well known immunological effector activities
CC including antibody dependent cell mediated cytotoxicity and/or complement
CC fixation in complement dependent cell mediated cytotoxicity, despite having structures
CC that would not be expected to be capable of promoting the effector
CC activities. It can be produced in substantial quantities that are
CC typically greater than those routinely attained with single-chain
CC antibody constructs. This sequence encodes a chimeric fusion protein
CC created from the mouse anti-human CD20 single chain antibody variable
CC fragment (scFv) and the human extracellular domain long form CD154
XX SQ Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;
Query Match 76.8%; Score 663.4; DB 6; Length 1470;
Best Local Similarity 99.8%; Pred. No. 9.4e-178;
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 200 CGGATCCAAGAAGGTTGGACAGATAGAGAAGTGAAGGAATCTTTCATGAAGATTTTGTAT 259
Db 806 CTGATCCAAGAAGGTTGGACAGATAGAGAAGTGAAGGAATCTTTCATGAAGATTTTGTAT 865
Qy 260 TCATGAAAAACGATACAGATGCAACACAGAGAGAAAGATCTTATCTTACTGAACCTGTG 319
Db 866 TCATGAAAAACGATACAGATGCAACACAGAGAGAAAGATCTTATCTTACTGAACCTGTG 925
Qy 320 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 379
Db 926 AGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGA 985
Qy 380 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCTTCAAAATTCGGGCAC 439
Db 986 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCTTCAAAATTCGGGCAC 1045
Qy 440 ATGTCATTAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGGCTGAAAAAGGAT 499
Db 1046 ATGTCATTAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTGTACAGTGGCTGAAAAAGGAT 1105
Qy 500 ACTACACCATGAGCAACAACTGGTAACCCCTGGAAAAATGGGAACAGCTGACCGTTAAAA 559
Db 1106 ACTACACCATGAGCAACAACTGGTAACCCCTGGAAAAATGGGAACAGCTGACCGTTAAAA 1165

Qy	560	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCOAATCGGGAGCTTCGA	619
Db	1166	GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCOAATCGGGAGCTTCGA	1225
Qy	620	GTCAAGCTCCAAATTTATAGCCAGCCTCTGCCTAAAAGTCCCCCGGTAGATTCGAGAGAAATCT	679
Db	1226	GTCAAGCTCCAAATTTATAGCCAGCCTCTGCCTAAAAGTCCCCCGGTAGATTCGAGAGAAATCT	1285
Qy	680	TACTCAGAGCTGCAAAATACCAAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACCT	739
Db	1286	TACTCAGAGCTGCAAAATACCAAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACCT	1345
Qy	740	TGGGAGGAGTATTTTGAATTTGCAAACCAAGTGCTTCGGGTGTTTGTCAAATGTGACTGATCCAA	799
Db	1346	TGGGAGGAGTATTTTGAATTTGCAAACCAAGTGCTTCGGGTGTTTGTCAAATGTGACTGATCCAA	1405
Qy	800	GCCAAAGTGCCCATGGCACTGGCTTCAGTGCCCTTTGGCTTACTCAAACCTCGAGTGATAAT	859
Db	1406	GCCAAAGTGAGCCATGGGCACCTGGCTTTCAGTCCCTTTGGCTTACTCAAACCTCGAGTGATAAT	1465
Qy	860	CTAGA	864
Db	1466	CTAGA	1470

RESULT 6	
ADD25460	
ID	ADD25460 standard; DNA; 1470 BP.
XX	
XX	ADD25460;
XX	
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Binding domain-immunoglobulin fusion protein-associated DNA #11.
XX	
XX	ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW	antiarthritic; immunosuppressive; antidiabetic; antichyroid;
KW	neuroprotective; hinge region; immunoglobulin heavy chain;
KW	CH2 constant region; CH3 constant region; IgG1;
KW	antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW	rheumatoid condition; B-cell disorder; melanoma; sarcoma;
KW	myasthenia gravis; Grave's disease;
KW	type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX	
OS	Unidentified.
XX	
PN	US2003118592-A1.
XX	
PD	26-JUN-2003.
XX	
PF	25-JUL-2002; 2002US-00207655.
XX	
XX	17-JAN-2001; 2001US-0367358P.
PR	17-JAN-2002; 2002US-00053530.
PR	03-JUN-2002; 2002US-0385691P.
XX	
PA	(GENE-) GENE-CRAFT INC.
XX	
PI	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX	
DR	WPI; 2003-801317/75.
XX	
PT	New binding domain-immunoglobulin fusion protein, useful for treating a
FT	subject having or suspected of having a malignant condition or a B-cell
PT	disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX	
PS	Disclosure; SEQ ID NO 21; 157pp; English.
XX	
CC	Unidentified
XX	
SQ	Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;
	Query Match 76.8%; Score 663.4; DB 10; Length 1470;

[illegible]

PN	US2003118592-A1.	
XX		
PD	26-JUN-2003.	
XX		
PF	25-JUL-2002; 2002US-00207655.	
XX		
PR	17-JAN-2001; 2001US-0367358P.	
PR	17-JAN-2002; 2002US-00053530.	
PR	03-JUN-2002; 2002US-0385691P.	
XX		
PA	(GENE-) GENE-CRAFT INC.	
XX		
PI	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;	
XX		
DR	WPI; 2003-801317/75.	
XX		
PT	New binding domain-immunoglobulin fusion protein, useful for treating a	
PT	subject having or suspected of having a malignant condition or a B-cell	
PT	disorder, e.g. melanoma, Grave's disease or autoimmune disease.	
XX		
PS	Disclosure; SEQ ID NO 149; 157pp; English.	
XX		
PS	Unidentified	
CC		
XX		
SQ	Sequence 1470 BP; 409 A; 344 C; 367 G; 350 T; 0 U; 0 Other;	
Query Match 76.8%; Score 663.4; DB 10; Length 1470;		
Best Local Similarity 99.8%; Pred. No. 9.4e-178;		
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	200 CGGATCCAAAGGTTGGACAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTGTAT	259
Db	806 CTGATCCAAAGGTTGGACAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTGTAT	865
Qy	260 TCATGAAACCATACAGAGATGCACACAGAGAAAGATCCTTATCTTACTGAACCTGTG	319
Db	866 TCATGAAACCATACAGAGATGCACACAGAGAAAGATCCTTATCTTACTGAACCTGTG	925
Qy	320 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGA	379
Db	926 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGA	985
Qy	380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC	439
Db	986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC	1045
Qy	440 ATGTCATAAGTGAGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTCAAAAAGGAT	499
Db	1046 ATGTCATAAGTGAGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTCAAAAAGGAT	1105
Qy	500 ACTACACCATGAGCAACAACTTTGGTAAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA	559
Db	1106 ACTACACCATGAGCAACAACTTTGGTAAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA	1165
Qy	560 GACAAGGACTATATATCTATGATCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA	619
Db	1166 GACAAGGACTATATATCTATGATCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA	1225
Qy	620 GTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAGTCCCGGTAGATTCAGAGAGATCT	679
Db	1226 GTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAGTCCCGGTAGATTCAGAGAGATCT	1285
Qy	680 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAACAAATCCATTCACT	739
Db	1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAACAAATCCATTCACT	1345
Qy	740 TGGAGGAGTATTTGAATTCGAACAGAGTCTTCGGTGTGTTGTCAATGTGATGATCCAA	799
Db	1346 TGGAGGAGTATTTGAATTCGAACAGAGTCTTCGGTGTGTTGTCAATGTGATGATCCAA	1405
Qy	800 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCAGTGATAAT	859
Db	1406 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCAGTGATAAT	1465

Qy	860 CTAGA 864	
Db	1466 CTAGA 1470	
RESULT 8		
ADM42735		
ID	ADM42735 standard; cDNA; 1470 BP.	
XX		
AC	ADM42735;	
XX		
DT	03-JUN-2004 (first entry)	
XX		
DE	2H7-CD154 L2, a binding domain-Ig fusion protein for CD20/CD40, cDNA.	
XX		
KW	Mouse; ss; gene; antibody; single chain antibody; scFv;	
KW	binding domain-immunoglobulin fusion protein;	
KW	immunoglobulin hinge region; heavy chain CH2 constant region;	
KW	heavy chain CH3 constant region;	
KW	antibody dependent cell-mediated cytotoxicity; complement fixation; IgA;	
KW	IgG; CD19; CD20; CD37; CD40; L6; CD154; malignant condition; cancer;	
KW	B-cell disorder; autoantibody; rheumatoid arthritis; myasthenia gravis;	
KW	Grave's disease; type I diabetes mellitus; multiple sclerosis;	
KW	autoimmune disease; human.	
XX		
OS	Mus musculus.	
OS	Homo sapiens.	
OS	Synthetic.	
OS	Chimeric.	
XX		
FN	US2003133939-A1.	
XX		
PD	17-JUL-2003.	
XX		
PF	17-JAN-2002; 2002US-00053530.	
XX		
PR	17-JAN-2002; 2002US-00053530.	
XX		
PA	(GENE-) GENE-CRAFT INC.	
XX		
PI	Ledbetter JA, Hayden-Ledbetter MS;	
XX		
DR	WPI; 2003-843256/78.	
DR	P-PSDB; ADM42747.	
XX		
PT	New binding domain-immunoglobulin fusion protein for treating malignant	
PT	conditions (e.g. cancer) or B-cell disorders, comprises a binding domain	
PT	polypeptide and immunoglobulin heavy chain CH2 and CH3 constant region	
PT	polypeptides.	
XX		
XX	Example 4; SEQ ID NO 21; 80pp; English.	
XX		
CC	The invention relates to a binding domain-immunoglobulin fusion protein	
CC	comprising a binding domain polypeptide that is fused to an	
CC	immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain	
CC	CH2 constant region polypeptide that is fused to the hinge region	
CC	polypeptide, and an immunoglobulin heavy chain CH3 constant region	
CC	polypeptide that is fused to the CH2 constant region polypeptide. The	
CC	fusion protein is capable of at least one immunological activity such as	
CC	antibody dependent cell-mediated cytotoxicity and complement fixation,	
CC	and is capable of specifically binding to an antigen. The hinge region	
CC	polypeptide is selected from a mutated hinge region polypeptide that	
CC	contains no cysteine residues (and that is derived from a wild-type	
CC	immunoglobulin hinge region polypeptide having one or more cysteine	
CC	residues), a mutated hinge region polypeptide that contains one cysteine	
CC	residue (nd that is derived from a wild-type immunoglobulin hinge region	
CC	polypeptide having two or more cysteine residues), a wild-type human	
CC	immunoglobulin (IgA) hinge region polypeptide, a mutated human IgA hinge	
CC	region polypeptide that contains no cysteine residues (and that is	
CC	derived from a wild-type human IgA region polypeptide) and a mutated	
CC	human IgA hinge region polypeptide that contains one cysteine residue	
CC	(and that is derived from a wild-type human IgA region polypeptide). Also	

included are an isolated polynucleotide encoding the novel fusion protein, a recombinant expression construct comprising the polynucleotide, a host cell transformed or transfected with the expression construct, producing the novel fusion protein (comprising culturing the host cell under conditions that permit expression of the novel fusion protein and isolating the binding domain-immunoglobulin fusion protein from the host cell culture), a pharmaceutical composition comprising the novel fusion protein in combination with a carrier and treating a subject having or suspected of having a malignant condition or a B-cell disorder (comprising administering to the patient an amount of the novel fusion protein). The mutated hinge region polypeptide exhibits a reduced ability to dimerise, relative to a wild-type human immunoglobulin G hinge region polypeptide. The binding domain polypeptide comprises at least one immunoglobulin variable region polypeptide selected from an immunoglobulin light chain variable region polypeptide and an immunoglobulin heavy chain variable region polypeptide, and optionally at least one linker peptide that is fused to the immunoglobulin variable region polypeptide. The immunoglobulin variable and constant region polypeptides are derived from a human immunoglobulin. The immunoglobulin heavy chain constant region CH2 and CH3 polypeptides are of an isotype selected from human IgG and human IgA. The antigen is selected from CD19, CD20, CD37, CD40 and L6. The binding domain polypeptide comprises a CD154 extracellular domain, and optionally, at least one immunoglobulin variable region polypeptide (e.g. mouse V1 and Vh regions forming single chain antibodies which bind to one of the above antigens). The composition and methods are useful in treating malignant conditions (e.g. cancer) and B-cell disorders, including diseases characterised by autoantibody production, such as rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune diseases. The present sequence encodes a fusion protein of the invention comprising mouse antibody V1 and Vh regions fused to either human immunoglobulin sequence or CD154 extracellular domain.

Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;

Query Match	76.8%;	Score 663.4;	DB 11;	Length 1470;
Best Local Similarity	99.8%;	Pred. No. 9.4e-178;		
Matches 664;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 200 CGGATCCAAAGAGTTGGACAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTGTAT 259
DB 806 CTGATCCAAAGAGTTGGACAGATAGAAAGATGAAAGGAATCTTCATGAAGATTTGTAT 865

QY 260 TCATGAAACCATGACAGATGCAACACAGAGAGAGATCTTATCTTCTTACTGAACTGTG 319
DB 866 TCATGAAACCATGACAGATGCAACACAGAGAGAGATCTTATCTTCTTACTGAACTGTG 925

QY 320 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGAGA 379
DB 926 AGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGAGA 985

QY 380 CGAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAATCTCTCAAAATTCGGGCAC 439
DB 986 CGAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAATCTCTCAAAATTCGGGCAC 1045

QY 440 ATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTCTTACAGTGGCTGAAAAGAT 499
DB 1046 ATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTCTTACAGTGGCTGAAAAGAT 1105

QY 500 ACTACACCATGAGCAACCACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAA 559
DB 1106 ACTACACCATGAGCAACCACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAA 1165

QY 560 GACAGAGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCATCGGAAAGTTGGA 619
DB 1166 GACAGAGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCATCGGAAAGTTGGA 1225

QY 620 GTCAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAACT 679
DB 1226 GTCAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAACT 1285

QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAACAATCTTCACT 739

Db	1286	TACTCAGAGCTGCAAAATACCCACAGTTTCGGCCAAACCTTGGCGGCAACAATCTTCACT	1345
QY	740	TGGGAGAGATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCGAATGTGACTGATCCAA	799
Db	1346	TGGGAGAGATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCGAATGTGACTGATCCAA	1405
QY	800	GCCAAAGTGAGCCATGGCCTTACAGTCTTTCGCTTACTCAAACTCGAGTGATAAT	859
Db	1406	GCCAAAGTGAGCCATGGCCTTACAGTCTTTCGCTTACTCAAACTCGAGTGATAAT	1465
QY	860	CTAGA 864	
Db	1466	CTAGA 1470	

RESULT 9
AAQ63959
ID AAQ63959 standard; cDNA to mRNA; 786 BP.
AC AAQ63959;
XX 25-MAR-2003 (revised)
DT 11-JAN-1995 (first entry)
XX Human CD40-L type II transmembrane protein coding sequence.
XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS l..786
FT /product= "human CD40-L"
FT /note= "nucleotides 148-783 code for the extracellular
FT region (amino acids 50-261)"
XX WO9410308-A1.
PD 11-MAY-1994.
XX 20-OCT-1993; 93WO-US010034.
PP 23-OCT-1992; 92US-00969703.
PR 13-AUG-1993; 93US-00107353.
XX (IMMV) IMMUNEX CORP.
XX Spriggs MK, Srinivasan S;
XX WPI; 1994-167465/20.
DR P-PSDB; AAR53969.
XX Prepn. of soluble oligomeric mammalian proteins - using host cells to
FT express a fusion protein comprising a leucine zipper domain and a
FT heterologous mammalian protein.
XX Example 1; Page 22-23; 35pp; English.
XX A DNA fragment encoding the extracellular (soluble) region of human CD40-
CC L was ligated to a synthetic oligonucleotide sequence coding for a leader
CC peptide, a 33 amino acid leucine zipper sequence (AAR53968) and the Flag
CC (RTM) linker sequence. Cells expressing the fusion construct are grown to
CC accumulate oligomeric, soluble CD40-L in the supernatant. The leucine
CC zipper sequence spontaneously trimerises in solution and fusion proteins
CC comprising the sequence fused to a heterologous mammalian protein also
CC form oligomers. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 U; 0 Other;
SQ

```
Query Match      74.4%; Score 642.8; DB 2; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAGAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 138 TCATAGAGAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197

QY 264 GAAACAGATACAGAGATCAACACAGGAGAGATCTTATCTTCTTACTGAACTGTGAGGA 323
DB 198 GAAACAGATACAGAGATCAACACAGGAGAGATCTTATCTTCTTACTGAACTGTGAGGA 257

QY 324 GATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATATGTAAACAAGAGGAGACGAA 383
DB 258 GATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATATGTAAACAAGAGGAGACGAA 317

QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 443
DB 318 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 377

QY 444 CATAGAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
DB 378 CATAGAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 437

QY 504 CACCATGAGCAACACTTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563
DB 438 CACCATGAGCAACACTTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAGACA 497

QY 564 AGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
DB 498 AGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557

QY 624 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACT 683
DB 558 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACT 617

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAACACTTTGGCGGCAACAATCCATTCACTTGGG 743
DB 618 CAGAGCTGCAAAATACCCACAGTTCGCGCAACACTTTGGCGGCAACAATCCATTCACTTGGG 677

QY 744 AGGAGTATTTGAAATGCAACAGGCTTCGCTGTTTCTCAATGCTGACTGATCCAAAGCA 803
DB 678 AGGAGTATTTGAAATGCAACAGGCTTCGCTGTTTCTCAATGCTGACTGATCCAAAGCA 737

QY 804 AGTGAGCCATGGCAGTGGCTTCACTGCTTCTTGGCTTACTCAAACTC 849
DB 738 AGTGAGCCATGGCAGTGGCTTCACTGCTTCTTGGCTTACTCAAACTC 783

RESULT 10
AAV39002
ID AAV39002 standard; DNA; 786 BP.
XX AC AAV39002;
XX AC AAV39002;
XX AC AAV39002;
DT 17-OCT-2003 (revised)
DT 23-SEP-1998 (first entry)
XX DE Exemplary CD40 ligand gene used in the course of the invention.
XX DE Exemplary CD40 ligand gene used in the course of the invention.
KW CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX OS Chimeric.
XX FN WO9826061-A2.
XX FN WO9826061-A2.
PD 18-JUN-1998.
XX PF 08-DEC-1997; 97WO-US022740.
```

```
XX 09-DEC-1996; 96US-0032145P.
PR 01-DEC-1997; 97US-00982272.
XX (REGC ) UNIV CALIFORNIA.
XX Kipps TJ, Sharma S, Cantwell M;
XX WPI; 1998-348521/30.
DR Vectors containing accessory molecule ligand genes - used for altering
XX immunoreactivity of cells, particularly for treatment of neoplasia or
XX autoimmune disorders, e.g. rheumatoid arthritis.
XX Disclosure; Page 106; 167pp; English.
XX The present sequence represents an exemplary CD40 ligand gene, comprising
CC nucleotides encoding the extracellular domains (Domains III and IV) and
CC transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998)
CC operatively linked to nucleotides encoding the cytoplasmic domain (Domain
CC I) of the murine CD40 ligand gene (AAV38997). The sequence is used to
CC exemplify the method of the invention. The specification describes a
CC method for altering the immunoreactivity of human cells which comprises
CC introducing a gene encoding an accessory molecule ligand (AML) into the
CC cells so that the AML is expressed on the surface of the cells. Vectors
CC containing the AML gene can be used in gene therapy for treating
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can
CC also be used for vaccination to produce immunity against a virus cell,
CC bacteria, protein, fungus or neoplasia. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX Sequence 786 BP; 250 A; 166 C; 171 G; 199 T; 0 U; 0 Other;
```

```
Query Match      74.4%; Score 642.8; DB 2; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAGAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 138 TCATAGAGAGTTGGACAAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 197

QY 264 GAAACAGATACAGAGATCAACACAGGAGAGATCTTATCTTCTTACTGAACTGTGAGGA 323
DB 198 GAAACAGATACAGAGATCAACACAGGAGAGATCTTATCTTCTTACTGAACTGTGAGGA 257

QY 324 GATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATATGTAAACAAGAGGAGACGAA 383
DB 258 GATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATATGTAAACAAGAGGAGACGAA 317

QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 443
DB 318 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGACATGT 377

QY 444 CATAGAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 503
DB 378 CATAGAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAAGGATACTA 437

QY 504 CACCATGAGCAACACTTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAGACA 563
DB 438 CACCATGAGCAACACTTTGGTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAGACA 497

QY 564 AGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
DB 498 AGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557

QY 624 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACT 683
DB 558 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAAATCTTACT 617

QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAACACTTTGGCGGCAACAATCCATTCACTTGGG 743
DB 618 CAGAGCTGCAAAATACCCACAGTTCGCGCAACACTTTGGCGGCAACAATCCATTCACTTGGG 677
```


Vectors containing accessory molecule ligand genes - used for altering
 immunoreactivity of cells, particularly for treatment of neoplasia or
 autoimmune disorders, e.g. rheumatoid arthritis.
 Disclosure; Page 104; 167pp; English.
 The present sequence represents the CD40 ligand gene. The sequence is
 used to exemplify the method of the invention. The specification
 describes a method for altering the immunoreactivity of human cells which
 comprises introducing a gene encoding an accessory molecule ligand (AML)
 into the cells so that the AML is expressed on the surface of the cells.
 Vectors containing the AML genes can be used in gene therapy for treating
 neoplasia or autoimmune disorders such as rheumatoid arthritis. They can
 also be used for vaccination to produce immunity against a virus cell,
 bacteria, protein, fungus or neoplasia
 Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 U; 0 Other;

Query Match	74.4%	Score 642.8;	DB 2;	Length 786;
Best Local Similarity	99.7%	Pred. No. 5.2e-172;		
Matches 644;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0				

204	Qy	TCC	AAGAGGTTGG	ACAAGATAGAAGGAACTCTCATGAAGATTTTGTATTCA	263
138	Db	TCAT	AAGAGGTTGG	ACAAGATAGAAGGAACTCTCATGAAGATTTTGTATTCA	197
264	Qy	GAAA	CCGATACAGAGATG	CAACACAGGAGAAAGATCCCTTACTCTGAACTGTGAGGA	323
198	Db	GAAA	CCGATACAGAGATG	CAACACAGGAGAAAGATCCCTTACTCTGAACTGTGAGGA	257
324	Qy	GATT	TAAGCCAGTTTGAAG	CTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	383
258	Db	GATT	TAAGCCAGTTTGAAG	CTTTGTGAAGGATATAATGTTTAAACAAAGAGGAGACGAA	317
384	Qy	GAAG	AAACACAGCTTTGAA	TGCAAAAGGTGATCAGAACTCTCAAAATGCGGCACATGT	443
318	Db	GAAG	AAACACAGCTTTGAA	TGCAAAAGGTGATCAGAACTCTCAAAATGCGGCACATGT	377
444	Qy	CATA	AGTGAGGCCACGAC	TAGAAAAACAATCTGTGTTACAGTGGCTGAAAAAGGATACTA	503
378	Db	CATA	AGTGAGGCCACGAC	TAGAAAAACAATCTGTGTTACAGTGGCTGAAAAAGGATACTA	437
504	Qy	CAC	CATGAGCAACAACTTGG	TAAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTTAAAGACA	563
438	Db	CAC	CATGAGCAACAACTTGG	TAAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTTAAAGACA	497
564	Qy	AGG	ACTCTATTATATCTAT	GCACCAAGTCACTCTGTTCCAAATCGGGAAGCTTCAGAGCA	623
498	Db	AGG	ACTCTATTATATCTAT	GCACCAAGTCACTCTGTTCCAAATCGGGAAGCTTCAGAGCA	557
624	Qy	AGCT	CCCATTTATAGCCAG	CCCTCTGCTAAAGTCCCCCGGTAGATTCGAGAGAACTCTTACT	683
558	Db	AGCT	CCCATTTATAGCCAG	CCCTCTGCTAAAGTCCCCCGGTAGATTCGAGAGAACTCTTACT	617
684	Qy	CAG	AGCTGCAAAATACCA	CAGTTTCGGCCAAACCTTTCGGGGCAACAAATCCATTCACCTTGGG	743
618	Db	CAG	AGCTGCAAAATACCA	CAGTTTCGGCCAAACCTTTCGGGGCAACAAATCCATTCACCTTGGG	677
744	Qy	AGG	AGTATTTCGAAATG	CAACACAGGTGCTTCGGTGTTCCTCAATGTACTGATCCAAAGCA	803
678	Db	AGG	AGTATTTCGAAATG	CAACACAGGTGCTTCGGTGTTCCTCAATGTACTGATCCAAAGCA	737
804	Qy	AGT	GAGCCATGGCACTGG	CTTCAAGTCTCTTTGGCTTACTCAAACTC	849
738	Db	AGT	GAGCCATGGCACTGG	CTTCAAGTCTCTTTGGCTTACTCAAACTC	783

RESULT 13
AAV39003
ID AAV39003 standard; DNA; 786 BP.
XX
AC AAV39003;

XX	17-OCT-2003 (revised)	
DT	23-SEP-1998 (first entry)	
XX		
DE	Exemplary CD40 ligand gene used in the course of the invention.	
XX		
KW	CD40 ligand; alteration; immunoreactivity; human cell;	
KW	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;	
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.	
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
FN	WO9826061-A2.	
XX		
PD	18-JUN-1998.	
XX		
PF	08-DEC-1997; 97WO-US022740.	
XX		
PR	09-DEC-1996; 96US-0032145P.	
PR	01-DEC-1997; 97US-00982272.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Kipps TJ, Sharma S, Cantwell M;	
XX	WPI, 1998-348521/30.	
DR		
XX	Vectors containing accessory molecule ligand genes - used for altering	
PT	immunoreactivity of cells, particularly for treatment of neoplasia or	
PT	autoimmune disorders, e.g. rheumatoid arthritis.	
XX		
PS	Disclosure; Page 107; 167pp; English.	
XX		
CC	The present sequence represents an exemplary CD40 ligand gene, comprising	
CC	nucleotides encoding the extracellular domains (Domains III and IV) of	
CC	the human CD40 ligand gene (AAV38998) operatively linked to nucleotides	
CC	encoding the cytoplasmic domain (Domain I) and transmembrane domain	
CC	(Domain II) of the murine CD40 ligand gene (AAV38997). The sequence is	
CC	used to exemplify the method of the invention. The specification	
CC	describes a method for altering the immunoreactivity of human cells which	
CC	comprises introducing a gene encoding an accessory molecule ligand (AML)	
CC	into the cells so that the AML is expressed on the surface of the cells.	
CC	Vectors containing the AML genes can be used in gene therapy for treating	
CC	neoplasia or autoimmune disorders such as rheumatoid arthritis. They can	
CC	also be used for vaccination to produce immunity against a virus cell,	
CC	bacteria, protein, fungus or neoplasia. (Updated on 17-OCT-2003 to	
CC	standardise OS field)	
XX		
QQ	Sequence 786 BP; 250 A; 166 C; 170 G; 200 T; 0 U; 0 Other;	

Query Match 74.4%; Score 642.8; DB 2; Length 786;
Best Local Similarity 99.7%; Pred. No. 5.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy	204	TCCAAGAGGTTGGACAAGATAGAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTTCAT	263
Db	138	TCATAGAAGGTTGGACAAGATAGAAGATAGAAGGNAATCTTCATGAAGATTTTGTATTTCAT	197
Qy	264	GAAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCCTTACTGAACTGTGAGGA	323
Db	198	GAAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCCTTACTGAACTGTGAGGA	257
Qy	324	GATTTAAAGCCAGTTTCGAAGGCTTTGTGAAGGATATTAATGTTTAAACAAAGAGGAGAGCGAA	383
Db	258	GAATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATTAATGTTTAAACAAAGAGGAGAGCGAA	317
Qy	384	GAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAACTCCATAATTCGGGCACATGTT	443
Db	318	GAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAACTCCATAATTCGGGCACATGTT	377
Qy	444	CATAAGTGAAGCCACGACAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACATA	503

```
|||||
378 CATAGTGGCCAGCAGTAAACACACATCTGTGTACAGTGGCTGAAAAGGATCTA 437
|||||
504 CACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563
|||||
438 CACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 497
|||||
564 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
|||||
498 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
|||||
624 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 683
|||||
558 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 617
|||||
684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACCTGGG 743
|||||
618 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACCTGGG 677
|||||
744 AGGAGTATTTCAATTGCAACCAAGTGTTCGGTGTGTGTCATGTGACTGATCCAAAGCCA 803
|||||
678 AGGAGTATTTGAAATTGCAACCAAGTGTTCGGTGTGTGTCATGTGACTGATCCAAAGCCA 737
|||||
804 AGTGAGCCATGGCACTGGCTTTCAGCTCCTTTGGCTTACTCAAACCTC 849
|||||
738 AGTGAGCCATGGCACTGGCTTTCAGCTCCTTTGGCTTACTCAAACCTC 783
```

RESULT 14
AAV12852

ID AAV12852 standard; cDNA to mRNA; 786 BP.

XX AAV12852;

DT 13-MAY-1998 (first entry)

DE CD40 ligand coding sequence.

XX Leucine zipper; fusion protein production; soluble oligomeric protein;
KW heterologous mammalian type II transmembrane protein; activated T cell;
KW heterologous mammalian type I transmembrane protein; antibody production;
KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.

XX Homo sapiens.

Key	Location/Qualifiers
FT	1..786
FT	/*tag= a

XX US5716805-A.

XX 10-FEB-1998.

XX 18-MAY-1995; 95US-00446922.

XX 25-OCT-1991; 91US-00783707.

XX 05-DEC-1991; 91US-00805723.

XX 23-OCT-1992; 92US-00969703.

XX 13-AUG-1993; 93US-00107353.

XX (IMMV) IMMUNEX CORP.

XX Spriggs MK, Srinivasean S;

XX WPI; 1998-144799/13.

XX P-PSDB; AAW41178.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused to

XX extracellular region of transmembrane protein.

XX Example 1; Col 19-20; 21pp; English.

XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).

CC The encoded protein can be used in a fusion protein produced using the
CC method of the invention. The method is for preparing soluble oligomeric
CC protein by culturing a host cell transfected with a vector for the fusion
CC protein. The soluble oligomeric protein comprises a leucine zipper fused
CC to the N terminus of the extracellular region of a heterologous mammalian
CC type II transmembrane protein or to the C terminus of the extracellular
CC region of a heterologous mammalian type I transmembrane protein, where
CC the leucine zipper is a peptide comprising at least part of AAW41171 or
CC AAW41172, optionally with conservative amino acid substitutions, provided
CC that the peptide trimerises in solution. A soluble fusion protein
CC comprising the leucine zipper of AAW41171 linked to the extracellular
CC region of CD40-L (a type II transmembrane protein that is found on
CC activated T cells and acts as a ligand for the B-cell antigen CD40)
CC stimulates B-cell proliferation and antibody production in a similar
CC manner to membrane-bound CD40-L. A soluble fusion protein comprising the
CC leucine zipper of AAW41172 linked to the extracellular region of CD27-L
CC (a type II transmembrane protein that binds to the lymphocyte antigen
CC CD27) inhibits binding of CD27c (a fusion protein comprising the
CC extracellular region of CD27 and a human IgG1 Fc region) to EBV-
CC transformed B cells expressing CD27-L

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 U; 0 Other;

Query Match 74.4%; Score 642.8; DB 2; Length 786;

Best Local Similarity 99.7%; Pred. No. 5.2e-172;

Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAAGAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAGATTTTGTATTCAT 263

DB 138 TCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAGATTTTGTATTCAT 197

QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGA 323

DB 198 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGA 257

QY 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTAAACAAGAGGAGACGAA 383

DB 258 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTAAACAAGAGGAGACGAA 317

QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATGGGCAATGT 443

DB 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATGGGCAATGT 377

QY 444 CATAGTGAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAAGGATACTA 503

DB 378 CATAGTGAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAAGGATACTA 437

QY 504 CACCATGAGCAACAACTTGGTAAACCTTGAAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563

DB 438 CACCATGAGCAACAACTTGGTAAACCTTGAAAAATGGGAAAACAGCTGACCGTTAAAAGACA 497

QY 564 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623

DB 498 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557

QY 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 683

DB 558 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACTTCTACT 617

QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGCAACAATCCATTCACCTGGG 743

DB 618 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGGCGGCAACAATCCATTCACCTGGG 677

QY 744 AGGAGTATTTGAAATTGCAACCAAGTGTTCGGTGTGTTCATGTGACTGATCCAAAGCCA 803

DB 678 AGGAGTATTTGAAATTGCAACCAAGTGTTCGGTGTGTTCATGTGACTGATCCAAAGCCA 737

QY 804 AGTGAGCCATGGCACTGGCTTTCAGCTCCTTTGGCTTACTCAAACCTC 849

DB 738 AGTGAGCCATGGCACTGGCTTTCAGCTCCTTTGGCTTACTCAAACCTC 783

RESULT 15

AAQ41506
ID AAQ41506 standard; DNA; 840 BP.
XX
AC AAQ41506;
XX
DT 25-MAR-2003 (revised)
DT 12-AUG-1993 (first entry)
XX
DE CD40-L DNA.
XX
XX Human; CD40-L; CD40: type II; membrane; polypeptide; extracellular;
KW transmembrane; region; intracellular; soluble; activity; B cell;
KW proliferation; induction; antibody; secretion; IGE; agonist; antagonist;
KW binding assay; ss.
XX
XX Homo sapiens.
XX
XX OS
XX FH Key Location/Qualifiers
FT CDS 46..831
FT /*tag= a
XX
XX PN W09308207-A1.
XX
XX PD 29-APR-1993.
XX
XX PF 23-OCT-1992; 92WO-US008990.
XX
XX PR 25-OCT-1991; 91US-00783707.
XX
XX PR 05-DEC-1991; 91US-00805723.
XX
XX PA (IMMV) IMMUNEX CORP.
XX
XX PI Armitage RJ, Fanslow WC, Spriggs MK;
XX
XX DR WPI; 1993-152417/18.
XX
XX DR P-PSDB; AAR36701.
XX
XX PT New cytokine CD40-L as CD40 agonist and antagonist - is used for treating
XX PT allergies, lupus, rheumatoid arthritis, graft-versus-host disease and
XX PT insulin-dependent diabetes mellitus.
XX
XX PS Claim 1; Fig 2; 80pp; English.
XX
XX CC This sequence encodes a human CD40-L polypeptide which binds to CD40.
XX CC CD40-L is a type II membrane polypeptide which has an extracellular
XX CC region at its C-terminus, a transmembrane region and an intracellular
XX CC region at its N-terminus. A soluble form of CD40-L lacks the
XX CC transmembrane domain. CD40-L activity is mediated by binding with CD40 an
XX CC transmembrane domain. CD40-L induces B cell proliferation and induction of antibody secretion,
XX CC including IGE. Membrane bound CD40-L acts as a CD40 agonist and soluble
XX CC CD40-L acts as a CD40 antagonist. CD40-L can be used in a binding assay
XX CC to detect cells expressing CD40. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX
XX SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 U; 0 Other;

Query Match 74.4%; Score 642.8; DB 2; Length 840;
Best Local Similarity 99.7%; Pred. No. 5.3e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 TCCAGAGAGGTTGGACAGATAGAGATCAAGAGGATCTTCATGAAGATTTTGTATTTCAT 263
DB 193 TCATAGAGGTTGGACAGATAGAGATGAAGGATCTTCATGAAGATTTTGTATTTCAT 242
QY 264 GAAACAGATACAGAGATCAACACAGGAGAGAGATCCCTTATCCTTATCTGAATCTGTGAGGA 323
DB 243 GAAACAGATACAGAGATCAACACAGGAGAGAGATCCCTTATCCTTATCTGAATCTGTGAGGA 302
QY 324 GATTAAAGCCAGTTTGAAGGCTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
DB 303 GATTAAAGCCAGTTTGAAGGCTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
QY 384 GAAAGAAAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAATCCTCAAAATTGGCGCACATGT 443

Search completed: November 12, 2004, 01:29:48
Job time : 287.413 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 50.4251 Seconds
(without alignments)
12178.890 Million cell updates/sec

Title: US-09-687-864A-17
Perfect score: 864
Sequence: 1 aagcttgccgcacgtcgtgta.....aactcgagtgataatctaga 864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	642.8	74.4	786	1	US-08-446-922-3
2	642.8	74.4	786	5	PCT-US93-10034-3
3	642.8	74.4	840	1	US-07-940-605A-1
4	642.8	74.4	840	1	US-08-184-422-7
5	642.8	74.4	840	1	US-08-360-923A-1
6	642.8	74.4	840	1	US-08-431-055-3
7	642.8	74.4	840	2	US-08-690-096-1
8	642.8	74.4	840	2	US-08-249-189-11
9	642.8	74.4	840	2	US-08-484-624A-11
10	642.8	74.4	840	2	US-08-477-733B-11
11	642.8	74.4	840	3	US-08-763-995-1
12	642.8	74.4	840	3	US-09-088-913A-11
13	642.8	74.4	840	3	US-08-589-771B-7
14	642.8	74.4	840	3	US-08-769-819-11
15	642.8	74.4	840	3	US-08-770-974-11
16	642.8	74.4	840	3	US-08-858-197-3
17	642.8	74.4	840	3	US-08-770-981-11
18	642.8	74.4	840	4	US-09-399-106-11
19	642.8	74.4	840	4	US-09-430-448-1
20	642.8	74.4	879	4	US-03-645-926A-1
21	642.8	74.4	1803	4	US-09-909-595-3
22	642.8	74.4	1816	4	US-09-645-926A-5
23	636	73.6	929	1	US-08-446-922-10
24	636	73.6	929	2	US-08-249-189-20
25	636	73.6	929	2	US-08-484-624A-20
26	636	73.6	929	2	US-08-477-733B-20
27	636	73.6	929	3	US-09-088-913A-20

28	636	73.6	929	3	US-08-769-819-20	Sequence 20, Appl
29	636	73.6	929	3	US-08-770-974-20	Sequence 20, Appl
30	636	73.6	929	3	US-08-770-981-20	Sequence 20, Appl
31	636	73.6	929	4	US-09-399-106-20	Sequence 20, Appl
32	635.2	73.5	1425	2	US-08-249-189-15	Sequence 15, Appl
33	635.2	73.5	1425	2	US-08-484-624A-15	Sequence 15, Appl
34	635.2	73.5	1425	2	US-08-477-733B-15	Sequence 15, Appl
35	635.2	73.5	1425	3	US-09-088-913A-15	Sequence 15, Appl
36	635.2	73.5	1425	3	US-08-769-819-15	Sequence 15, Appl
37	635.2	73.5	1425	3	US-08-770-974-15	Sequence 15, Appl
38	635.2	73.5	1425	3	US-08-770-981-15	Sequence 15, Appl
39	635.2	73.5	1425	4	US-09-399-106-15	Sequence 15, Appl
40	627.6	72.6	839	4	US-03-023-655-919	Sequence 919, App
41	497.2	57.5	780	4	US-09-322-409-75	Sequence 75, Appl
c 42	497.2	57.5	780	4	US-09-322-409-76	Sequence 76, Appl
c 43	497.2	57.5	780	4	US-09-451-527-75	Sequence 75, Appl
c 44	497.2	57.5	780	4	US-09-451-527-76	Sequence 76, Appl
45	497.2	57.5	885	4	US-09-322-409-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-446-922-3
; Sequence 3, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: 1..783
; US-08-446-922-3

Query Match      74.4%; Score 642.8; DB 1; Length 786;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAGGTTGACCAAGATAGAGATGAAAGAAATCTTCATGAAGATTTTGTATTTCAT 263
Db 138 TCATAGAAGGTTGACCAAGATAGAGATGAAAGAAATCTTCATGAAGATTTTGTATTTCAT 197
Qy 264 GAAACCATGACAGAGATGACACAGGAGAGAGATCTTATCTTACTGAACTGTGAGGA 323
Db 198 GAAACCATGACAGAGATGACACAGGAGAGAGATCTTATCTTACTGAACTGTGAGGA 257
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 317
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 443
Db 318 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 377
Qy 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db 378 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437
Qy 504 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497
Qy 564 AGGACTCTATTATATCTATGTCAGCAAGTCACTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGTCAGCAAGTCACTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 557
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT 683
Db 558 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT 617
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 677
Qy 744 AGGAGTATTGAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 803
Db 678 AGGAGTATTGAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 737
Qy 804 AGTGAGCCATGCGACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 849
Db 738 AGTGAGCCATGCGACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 783
```

```
RESULT 2
PCT-US93-10034-3
; Sequence 3, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
; PCT-US93-10034-3
```

```
Query Match      74.4%; Score 642.8; DB 5; Length 786;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAGGTTGACCAAGATAGAGATGAAAGAAATCTTCATGAAGATTTTGTATTTCAT 263
Db 138 TCATAGAAGGTTGACCAAGATAGAGATGAAAGAAATCTTCATGAAGATTTTGTATTTCAT 197
Qy 264 GAAACCATGACAGAGATGACACAGGAGAGAGATCTTATCTTACTGAACTGTGAGGA 323
Db 198 GAAACCATGACAGAGATGACACAGGAGAGAGATCTTATCTTACTGAACTGTGAGGA 257
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 317
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 443
Db 318 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 377
Qy 444 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db 378 CATAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 437
Qy 504 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 497
Qy 564 AGGACTCTATTATATCTATGTCAGCAAGTCACTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGTCAGCAAGTCACTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 557
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT 683
Db 558 AGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAACTTTACT 617
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGG 677
Qy 744 AGGAGTATTGAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 803
Db 678 AGGAGTATTGAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAAAGCCA 737
```

QY 804 AGTGGCCATGGCAGCTTTCAGCTCCTTTGGCTTACTCAAACTC 849
|||||
Db 738 AGTGGCCATGGCAGCTTTCAGCTCCTTTGGCTTACTCAAACTC 783
|||||

RESULT 3

US-07-940-605A-1
; Sequence 1, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
US-07-940-605A-1

Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 TCCAGAGGTTGGCAAGATGAGATGCAAGGAACTTTCATGAAGATTTTGTATTCAT 263
Db 159 TCATAGAGTTGGCAAGATGAGATGCAAGGAACTTTCATGAAGATTTTGTATTCAT 218
QY 264 GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTCTGAACTGTGAGGA 323
Db 219 GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTCTGAACTGTGAGGA 278
QY 324 GATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAGAGGAGACGAA 383
Db 279 GATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAGAGGAGACGAA 338
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGATGATCAGAACTCCTCAAAATTTGGGCACATGT 443
Db 339 GAAAGAAACAGCTTTGAAATGCAAAAAGGATGATCAGAACTCCTCAAAATTTGGGCACATGT 398
QY 444 CATAGTGAGGCCACGCTGAGTAAACAACATCTGTGTTCAGTGGGCTGAAAAGGATCTA 503
|||||

Db 399 CATAGTGAGGCCACGCTGAGTAAACAACATCTGTGTTCAGTGGGCTGAAAAGGATCTA 458
QY 504 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563
Db 459 CACCATGAGCAACAACTTTGGTAAACCTCGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 518
QY 564 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 519 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 578
QY 624 AGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGGTAAGTTCCTCAATCGGGAAGCTTCGAGTCA 683
Db 579 AGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGGTAAGTTCCTCAATCGGGAAGCTTCGAGTCA 638
QY 684 CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTTGCGGGCAACAAATCCATTCACTTGGG 743
Db 639 CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTTGCGGGCAACAAATCCATTCACTTGGG 698
QY 744 AGGAGTATTTGAATTTGCAACCCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAGGCA 803
Db 699 AGGAGTATTTGAATTTGCAACCCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAGGCA 758
QY 804 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 849
Db 759 AGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 804

RESULT 4

US-08-184-422-7
; Sequence 7, Application US/08184422
; Patent No. 5565321
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: DAVISON, BARRY
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: RENSHAW, BLAIR
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: WIDMER, MICHAEL
; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
; TITLE OF INVENTION: IN A CD40 LIGAND GENE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: MS Word for Apple 5.1, Version a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,422
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/009,258
; FILING DATE: 01/22/93
; ATTORNEY/AGENT INFORMATION:
; NAME: PERKINS, PATRICIA ANNE
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2810-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-184-422-7

Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAGAGAGGTTGGACAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

Qy 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 302

Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 362

Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422

Qy 444 CATAGTGAGGCCAGCAGTAAACAAACATCTGTGTGTTACAGTGGGCTGAAAAGGATCTA 503
Db 423 CATAGTGAGGCCAGCAGTAAACAAACATCTGTGTGTTACAGTGGGCTGAAAAGGATCTA 482

Qy 504 CACCATGAGCAACACTTTGGTAACCTCGAATAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACACTTTGGTAACCTCGAATAATGGGAAACAGCTGACCGTTAAAGACA 542

Qy 564 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 602

Qy 624 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGCTAGATTCGAGAGAACTTCTACT 683
Db 603 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGCTAGATTCGAGAGAACTTCTACT 662

Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCAACCTTTCGCGGCAACAAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCAACCTTTCGCGGCAACAAATCCATTCACTTGGG 722

Qy 744 AGGAGTATTGAAATGCAACAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTGAAATGCAACAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAAAGCCA 782

Qy 804 AGTGAGCAATGGCACTGGCTTCACGCTCCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCAATGGCACTGGCTTCACGCTCCTTTGGCTTACTCAAACTC 828
```

```

RESULT 5
US-08-360-923A-1
; Sequence 1, Application US/08360923A
; Patent No. 5674492
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANLOW, WILLIAM
; APPLICANT: LONGO, DAN L.
; APPLICANT: MURPHY, WILLIAM
; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
; TITLE OF INVENTION: EXPRESSING CD40
```

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,923A
; FILING DATE: December 21, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/172,664
; FILING DATE: December 23, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2818-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-360-923A-1

Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAGAGGTTGGACAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

Qy 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 302

Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 362

Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422

Qy 444 CATAGTGAGGCCAGCAGTAAACAAACATCTGTGTGTTACAGTGGGCTGAAAAGGATCTA 503
Db 423 CATAGTGAGGCCAGCAGTAAACAAACATCTGTGTGTTACAGTGGGCTGAAAAGGATCTA 482

Qy 504 CACCATGAGCAACACTTTGGTAACCTCGAATAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACACTTTGGTAACCTCGAATAATGGGAAACAGCTGACCGTTAAAGACA 542
```


QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db |||||
543 AGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 602
QY 624 AGCTCATTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 683
Db |||||
603 AGCTCATTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 662
QY 684 CAGAGCTGCAATACCCACAGTTCGCGCAAACTTCGCGGCAACAATCCATTCACTTGGG 743
Db |||||
663 CAGAGCTGCAATACCCACAGTTCGCGCAAACTTCGCGGCAACAATCCATTCACTTGGG 722
QY 744 AGGAGTATTGAATTCGAACCAAGTGCTTCGCTGTTGTCATGTGACTGATTCGAAGCCA 803
Db |||||
723 AGGAGTATTGAATTCGAACCAAGTGCTTCGCTGTTGTCATGTGACTGATTCGAAGCCA 782
QY 804 AGTGAGCCATGGCACTGGCTTCACGCTCTTGGCTTACTCAAACTC 849
Db |||||
783 AGTGAGCCATGGCACTGGCTTCACGCTCTTGGCTTACTCAAACTC 828

RESULT 6

US-08-431-055-3
; Sequence 3, Application US/08431055
; Patent No. 5817516
; GENERAL INFORMATION:
; APPLICANT: KEHRY, MERILYN R
; APPLICANT: CASTLE, BRIAN E
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 100 NEW YORK AVE. N.W. SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,055
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,580
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
US-08-431-055-3

Query Match 74.4%; Score 642.8; DB 1; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAAGAGGTGGTGAAGAAGATGAAGAATCTTTCATGAAGATTTTGTATTCAT 263
Db |||||
159 TCATGAAGGTGGTGAAGAAGATGAAGAATCTTTCATGAAGATTTTGTATTCAT 218
QY 264 GAAACCATGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 323
Db |||||
219 GAAACCATGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACCTGTGAGGA 278
QY 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTTAAACAAAGAGGAGACGAA 383
Db |||||
279 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTTAAACAAAGAGGAGACGAA 338
QY 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 443
Db |||||
339 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 398
QY 444 CATAGTGAGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACATA 503
Db |||||
399 CATAGTGAGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACATA 458
QY 504 CACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 563
Db |||||
459 CACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAAGACA 518
QY 564 AGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db |||||
519 AGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 578
QY 624 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 683
Db |||||
579 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 638
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 743
Db |||||
639 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 698
QY 744 AGGAGTATTGAATTCGAATGCAACAGAGTCTCGGTGTTGTCATGTGACTGATCCAGCCA 803
Db |||||
699 AGGAGTATTGAATTCGAATGCAACAGAGTCTCGGTGTTGTCATGTGACTGATCCAGCCA 758
QY 804 AGTGAGCCATGGCACTGGCTTCACGCTCTTGGCTTACTCAAACTC 849
Db |||||
759 AGTGAGCCATGGCACTGGCTTCACGCTCTTGGCTTACTCAAACTC 804

RESULT 7

US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605

```
/ FILING DATE: 04-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistock, S. Lealie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 5624-184
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 840 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 22..807
US-08-690-096-1

Query Match 74.4%; Score 642.8; DB 2; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 159 TCATAGAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 218

QY 264 GAAACGATACAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 219 GAAACGATACAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278

QY 324 GATTAAGCCAGTTTGAAGGCTTGTGAAGGATATATGTTAAACAAGAGGAGACGAA 383
DB 279 GATTAAGCCAGTTTGAAGGCTTGTGAAGGATATATGTTAAACAAGAGGAGACGAA 338

QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGGCGCACATGT 443
DB 339 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGGCGCACATGT 398

QY 444 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTCACAGTGGGCTGAAAAGGATCTA 503
DB 399 CATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTCACAGTGGGCTGAAAAGGATCTA 458

QY 504 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
DB 459 CACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 518

QY 564 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 623
DB 519 AGGACTCTATTATATCTATGCCCAGTCAACCTTCTGTTTCCAATCGGGAAGCTTCGAGTCA 578

QY 624 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT 683
DB 579 AGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCCCGGTAGATTCGAGAGAAATCTTACT 638

QY 684 CAGAGCTGCAATATACCAAGTTCGCGCAACCTTGGCGGCAACAAATCCATTCACCTGGG 743
DB 639 CAGAGCTGCAATATACCAAGTTCGCGCAACCTTGGCGGCAACAAATCCATTCACCTGGG 698

QY 744 AGGAGTATTGTAATTCGAACAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCCAAGCA 803
DB 699 AGGAGTATTGTAATTCGAACAGGTGCTTCGGTGTTTGTCAATGTGACTGATCCCAAGCA 758

QY 804 AGTGAGCCATGCACTGGCTTCACGTCCTTTGGCTTACTTCAAACTC 849
DB 759 AGTGAGCCATGCACTGGCTTCACGTCCTTTGGCTTACTTCAAACTC 804
```

RESULT 8

US-08-249-189-11

; Sequence 11, Application US/08249189

```
/ Patent No. 5961974
/ GENERAL INFORMATION:
/ APPLICANT: ARMITAGE, RICHARD
/ APPLICANT: FANSLAW, WILLIAM
/ APPLICANT: SPRIGGS, MELANIE
/ APPLICANT: SRINIVASAN, SUBHASHINI
/ APPLICANT: GIBSON, MARYLOU
/ TITLE OF INVENTION: NOVEL CYTOKINE
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: IMMUNEX CORPORATION
/ STREET: 51 UNIVERSITY STREET
/ CITY: SEATTLE
/ STATE: WASHINGTON
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.1
/ SOFTWARE: Microsoft Word for Apple, version 5.1a
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/249,189
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/969,703
/ FILING DATE: October 23, 1992
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/805,723
/ FILING DATE: December 5, 1991
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/783,707
/ FILING DATE: October 25, 1991
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia A.
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2802-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 2065870430
/ TELEFAX: 2065870606
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 840 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ IMMEDIATE SOURCE:
/ CLONE: CD40-L
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 46..831
US-08-249-189-11
```

```
Query Match 74.4%; Score 642.8; DB 2; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
DB 183 TCATAGAAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

QY 264 GAAACGATACAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
DB 243 GAAACGATACAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
```

QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383
Db |||||
QY 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362
Db |||||
QY 384 GAAAGAAACAGCTTTGAAGTGCRAAAAGGTGATCAGATCTCTCAATGGCGCACATGT 443
Db |||||
QY 363 GAAAGAAACAGCTTTGAAGTGCRAAAAGGTGATCAGATCTCTCAATGGCGCACATGT 422
Db |||||
QY 444 CATAGTGAGGCGCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 503
Db |||||
QY 423 CATAGTGAGGCGCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 482
Db |||||
QY 504 CACCATGAGCAACAACTTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
Db |||||
QY 483 CACCATGAGCAACAACTTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 542
Db |||||
QY 564 AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTTTCCATCGGGAAGCTTCGAGTCA 623
Db |||||
QY 543 AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTTTCCATCGGGAAGCTTCGAGTCA 602
Db |||||
QY 624 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 683
Db |||||
QY 603 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 662
Db |||||
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTTGCGGCAACCAATCCATTCCTTGGG 743
Db |||||
QY 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTTGCGGCAACCAATCCATTCCTTGGG 722
Db |||||
QY 744 AGGAGTATTGAAATGCAACACAGTTCCTCGGTGTTGTTCAATGACTGATCCAGGCA 803
Db |||||
QY 723 AGGAGTATTGAAATGCAACACAGTTCCTCGGTGTTGTTCAATGACTGATCCAGGCA 782
Db |||||
QY 804 AGTGAGCCATGCGACTGCTTCACTGCTTCTGCTTCTGCTTCTTCTGCTTCTTCTGCTTCT 849
Db |||||
QY 783 AGTGAGCCATGCGACTGCTTCACTGCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCT 828
Db |||||

RESULT 9

US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,624A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-484-624A-11

Query Match 74.4%; Score 642.8; DB 2; Length 840;

Best Local Similarity 99.7%; Pred. No. 1.2e-172;

Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAAGAGGTTGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db |||||
QY 183 TCATAGAAGGTTGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Db |||||
QY 264 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCTTACTTGAACCTGTGAGGA 323
Db |||||
QY 243 GAAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCTTACTGAACTGTGAGGA 302
Db |||||
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 383
Db |||||
QY 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGAA 362
Db |||||
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCTCAATTTGCGGCGCACATGT 443
Db |||||
QY 363 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCTCAATTTGCGGCGCACATGT 422
Db |||||
QY 444 CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 503
Db |||||
QY 423 CATAAGTGAGGCCAGCAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 482
Db |||||
QY 504 CACCATGAGCAACAACTTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
Db |||||
QY 483 CACCATGAGCAACAACTTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTTAAAGACA 542
Db |||||
QY 564 AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTTTCCATCGGGAAGCTTCGAGTCA 623
Db |||||
QY 543 AGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTTTCCATCGGGAAGCTTCGAGTCA 602
Db |||||
QY 624 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 683
Db |||||
QY 603 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACTTACT 662
Db |||||
QY 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTTGCGGCAACCAATCCATTCCTTGGG 743
Db |||||


```

;
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Macintosh 7200/90
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,995
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/677,762
; FILING DATE: 10 JUL 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2845-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
; US-08-763-995-1

Query Match 74.4%; Score 642.8; DB 3; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCATGAAGATTGTGATTTCAT 263
Db 183 TCATAGAAGTTGGCAAGATAGAGATGAAGGAATCTTCATGAAGATTGTGATTTCAT 242
Qy 264 GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAGAGGTTGGAAGGCTTTGGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAGAGGTTGGAAGGCTTTGGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 503
Db 423 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAAGGATCTA 482
Qy 504 CACCATGAGCAACACTTGGTAACCTCGAAAAAGGAGAAAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACACTTGGTAACCTCGAAAAAGGAGAAAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAGTACACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAGTACACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGTCCATTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 683

```

```

Db 603 AGCTCCATTATAGCCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 662
Qy 684 CAGAGCTGCAATATACCAACAGTTCGCCAAACCTTGGGGCAACAATCCATTCTGGG 743
Db 663 CAGAGCTGCAATATACCAACAGTTCGCCAAACCTTGGGGCAACAATCCATTCTGGG 722
Qy 744 AGGAGTATTTGAATTCGAAACAGGCTGCTTCGGTGTTCATGTGATGATCCAGGCA 803
Db 723 AGGAGTATTTGAATTCGAAACAGGCTGCTTCGGTGTTCATGTGATGATCCAGGCA 782
Qy 804 AGTGAGCCATGGCCTGCTTACGCTTTCAGTCTTCTTTGGGCTTACTCAAACCTC 849
Db 783 AGTGAGCCATGGCCTGCTTACGCTTTCAGTCTTCTTTGGGCTTACTCAAACCTC 828

RESULT 12
US-09-088-913A-11
; Sequence 11, Application US/09088913A
; Patent No. 6087329
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, JEFFERY
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA: US/09/088,913A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```

```
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
US-09-088-913A-11

Query Match 74.4%; Score 642.8; DB 3; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAGAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 422
Qy 444 CATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db 423 CATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 482
Qy 504 CACATGAGCAACAACTTGTGAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACATGAGCAACAACTTGTGAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAGTCACTCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAGTCACTCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 683
Db 603 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCG 722
Qy 744 AGGAGATTTGAAATGCAACAGAGTGTCTCGGTGTTTCTCAATGATGATGATGATGATGATGATGATGAT 803
Db 723 AGGAGATTTGAAATGCAACAGAGTGTCTCGGTGTTTCTCAATGATGATGATGATGATGATGATGATGAT 782
Qy 804 AGTGAGCATGGCACTGCTTCAGTCTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCATGGCACTGCTTCAGTCTCTTGGCTTACTCAAACTC 828

RESULT 13
US-08-589-771B-7
; Sequence 7, Application US/08589771B
; Patent No. 6106832
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: DAVISON, BARRY
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: RENSLOW, BLAIR
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: WIDMER, MICHAEL
; TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
; TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
```

```
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,771B
; FILING DATE: January 22, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/009,258
; FILING DATE: 01/22/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY, JANIS C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2810-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
US-08-589-771B-7

Query Match 74.4%; Score 642.8; DB 3; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAGATAGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACAGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 422
Qy 444 CATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 503
Db 423 CATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATACTA 482
Qy 504 CACATGAGCAACAACTTGTGAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACATGAGCAACAACTTGTGAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAGTCACTCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAGTCACTCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 683
Db 603 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCGCAAAACCTTTCGCG 722
Qy 744 AGGAGATTTGAAATGCAACAGAGTGTCTCGGTGTTTCTCAATGATGATGATGATGATGATGATGATGAT 803
Db 723 AGGAGATTTGAAATGCAACAGAGTGTCTCGGTGTTTCTCAATGATGATGATGATGATGATGATGATGAT 782
Qy 804 AGTGAGCATGGCACTGCTTCAGTCTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCATGGCACTGCTTCAGTCTCTTGGCTTACTCAAACTC 828
```

Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGCGTAGATTCCGAGAGAATCTTACT 683
Db 603 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCCGCGTAGATTCCGAGAGAATCTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAATTGCAACAGGTGCTTCGCTGTTTGTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTGCAACAGGTGCTTCGCTGTTTGTCAATGTGACTGATCCAAAGCCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACTC 828

RESULT 14

US-08-769-819-11
; Sequence 11, Application US/08769819
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
US-08-769-819-11

Query Match 74.4%; Score 642.8; DB 3; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAAAGTTGGACCAAGATAGAAGATGAAGAAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACCAAGATAGAAGATGAAGAAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTATAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTATAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAAACAGCTTTGAAATGCAAAAGAGGTGATCAGAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAGAGGTGATCAGAATCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAGAGTACTA 503
Db 423 CATAGTGAAGCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAGAGTACTA 482
Qy 504 CACCATGAGCAACAACTTGTAAACCTGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTGTAAACCTGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGTAGATTCGAGAGAATCTTACT 683
Db 603 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGTAGATTCGAGAGAATCTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTCGCGGCAACAATCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAATTGCAACAGGTGCTTCGCTGTTTGTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTGCAACAGGTGCTTCGCTGTTTGTCAATGTGACTGATCCAAAGCCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCACGTCTCTTGGCTTACTCAAACTC 828

RESULT 15
US-08-770-974-11
; Sequence 11, Application US/08770974
; Patent No. 6290972
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-770-974-11

Query Match 74.4%; Score 642.8; DB 3; Length 840;
Best Local Similarity 99.7%; Pred. No. 1.2e-172;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 204 TCCAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAACGATACAGATGTCACACAGGAGGAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGATGTCACACAGGAGGAAGATCCTTATCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383

Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAAAACAGCTTTTGAAATGCAAAAAAGGTGATCAGAACTCCTCAAAATTTGGGGCACATGT 443
Db 363 GAAAGAAAAACAGCTTTTGAAATGCAAAAAAGGTGATCAGAACTCCTCAAAATTTGGGGCACATGT 422
Qy 444 CATAAGTGAGGCCAGCAGTAGTAAAAACAACATCTGTGTGTTACAGTGGGCTGAAAAAGGATACTA 503
Db 423 CATAAGTGAGGCCAGCAGTAGTAAAAACAACATCTGTGTGTTACAGTGGGCTGAAAAAGGATACTA 482
Qy 504 CACCATGAGCAACAACTTTGTAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTAAAAAGACA 563
Db 483 CACCATGAGCAACAACTTTGTAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTAAAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTTCCAAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTTATAGCCAGCCTCTGCGCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT 683
Db 603 AGCTCCATTTTATAGCCAGCCTCTGCGCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGGGGGCAACAATCCATTCATCTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGGGGGCAACAATCCATTCATCTTGGG 722
Qy 744 AGGAGTATTTGAAATTCGAATTCGAACAGTGCTTCGGTGTGTTGTCAATGCTGATGATCCAAAGCA 803
Db 723 AGGAGTATTTGAAATTCGAATTCGAACAGTGCTTCGGTGTGTTGTCAATGCTGATGATCCAAAGCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCAAGTCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCAAGTCTTTGGCTTACTCAAACTC 828

Search completed: November 12, 2004, 12:57:45
Job time : 52.6251 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	663.4	76.8	1470	15	US-10-207-655-21	Sequence 21, Appl
2	663.4	76.8	1470	15	US-10-207-655-149	Sequence 149, Appl
3	663.4	76.8	1470	15	US-10-053-530-21	Sequence 21, Appl
4	642.8	74.4	840	10	US-09-365-940-11	Sequence 11, Appl
5	642.8	74.4	840	14	US-10-294-176-1	Sequence 1, Appl
6	642.8	74.4	840	15	US-10-200-242-11	Sequence 11, Appl
7	642.8	74.4	840	16	US-10-200-242-11	Sequence 11, Appl
8	642.8	74.4	879	14	US-10-242-212-1	Sequence 1, Appl
9	642.8	74.4	1800	15	US-10-131-997-125	Sequence 125, Appl
10	642.8	74.4	1803	10	US-09-909-595-3	Sequence 3, Appl
11	642.8	74.4	1803	15	US-10-272-411-3	Sequence 3, Appl
12	642.8	74.4	1803	15	US-10-218-547-9	Sequence 9, Appl

Db 806 CTGATCCAAAGAGGTTGGACAAGATAGAAAGGAATCTTTCATGAAGATTTGTAT 865
QY 260 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGAACTGTG 319
Db 866 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGAACTGTG 925
QY 320 AGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTTAAACAAAGAGGAGA 379
Db 926 AGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTTAAACAAAGAGGAGA 985
QY 380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATGCGGCAC 439
Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATGCGGCAC 1045
QY 440 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 499
Db 1046 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 1105
QY 500 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 559
Db 1106 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 1165
QY 560 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGAAAGCTTGA 619
Db 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGAAAGCTTGA 1225
QY 620 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCT 679
Db 1226 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCT 1285
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCATTCACT 739
Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCATTCACT 1345
QY 740 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAAATGAGTCTGATCAA 799
Db 1346 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAAATGAGTCTGATCAA 1405
QY 800 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTCAGTGATAT 859
Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTCAGTGATAT 1465
QY 860 CTAGA 864
Db 1466 CTAGA 1470

RESULT 2

US-10-207-655-149
; Sequence 149, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse-Human hybrid fusion protein
US-10-207-655-149

Query Match 76.8%; Score 663.4; DB 15; Length 1470;
Best Local Similarity 99.8%; Pred. No. 2e-175;
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 200 CGGATCCAAAGAGGTTGGACAAGATAGAAAGGAATCTTTCATGAAGATTTGTAT 259

Db 806 CTGATCCAAAGAGGTTGGACAAGATAGAAAGGAATCTTTCATGAAGATTTGTAT 865
QY 260 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGAACTGTG 319
Db 866 TCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGAACTGTG 925
QY 320 AGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTTAAACAAAGAGGAGA 379
Db 926 AGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTGTTAAACAAAGAGGAGA 985
QY 380 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATGCGGCAC 439
Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATGCGGCAC 1045
QY 440 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 499
Db 1046 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 1105
QY 500 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 559
Db 1106 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 1165
QY 560 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGAAAGCTTGA 619
Db 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGAAAGCTTGA 1225
QY 620 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCT 679
Db 1226 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCT 1285
QY 680 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCATTCACT 739
Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCATTCACT 1345
QY 740 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAAATGAGTCTGATCAA 799
Db 1346 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAAATGAGTCTGATCAA 1405
QY 800 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTCAGTGATAT 859
Db 1406 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTCAGTGATAT 1465
QY 860 CTAGA 864
Db 1466 CTAGA 1470

RESULT 3

US-10-053-530-21
; Sequence 21, Application US/10053530
; Publication No. US2003013393A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069, 401
; CURRENT APPLICATION NUMBER: US/10/053,530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MOUSE-HUMAN HYBRID
; NAME/KEY: misc_feature
; LOCATION: (1)..(808)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV
; NAME/KEY: misc_feature

LOCATION: (814)..(1455)
OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154
US-10-053-530-21

Query Match 76.8%; Score 663.4; DB 15; Length 1470;
Best Local Similarity 99.8%; Pred. No. 2e-175;
Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

200 CGGATCCAAAGAGTTGGACAGATAGAAAGATGAAGAAATCTTCATGAAGATTTGTAT 259
260 TCATGAAACCATACAGAGATGCAACACAGAGAGAAAGATCTTATCTCTTACTGAACATGTG 319
866 TCATGAAACCATACAGAGATGCAACACAGAGAGAAAGATCTTATCTCTTACTGAACATGTG 925
320 AGGAGATTAAAGCCAGTTTGAAGCTTTGGAAGGATATATGTTAAACAAAGAGAGA 379
926 AGGAGATTAAAGCCAGTTTGAAGCTTTGGAAGGATATATGTTAAACAAAGAGAGA 985
380 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCTCAAAATTCGGCAC 439
986 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCTCAAAATTCGGCAC 1045
440 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAGGAT 499
1046 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAGGAT 1105
500 ACTACACCATGACCAACTTGGTAAACCTGGAAGATGGAAGAGAGAGAGAGAGAGAGAG 559
1106 ACTACACCATGACCAACTTGGTAAACCTGGAAGATGGAAGAGAGAGAGAGAGAGAGAG 1165
560 GACAGAGACTCTATTATCTATGATCCCAAGTCACCTCTGTTCCAAATCGGAAAGCTTGA 619
1166 GACAGAGACTCTATTATCTATGATCCCAAGTCACCTCTGTTCCAAATCGGAAAGCTTGA 1225
620 GTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGGAGTAGATTCAGAGAGATCT 679
1226 GTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGGAGTAGATTCAGAGAGATCT 1285
680 TACTCAGAGCTGCAATATCCACAGTTCGGCCAAACCTTGGGGGCAACATCCATTCACT 739
1286 TACTCAGAGCTGCAATATCCACAGTTCGGCCAAACCTTGGGGGCAACATCCATTCACT 1345
740 TGGGAGGAGTATTGAAATGCAACAGAGTCTTGGGTGTTGTCAATGACTGATCCAA 799
1346 TGGGAGGAGTATTGAAATGCAACAGAGTCTTGGGTGTTGTCAATGACTGATCCAA 1405
800 GCCAAGTCAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTCGAGTGATAAT 859
1406 GCCAAGTCAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTCGAGTGATAAT 1465

860 CTAGA 864
1466 CTAGA 1470

RESULT 4
US-09-365-940-11
Sequence 11, Application US/09365940
Publication No. US20030091564A1
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/365,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870806
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-09-365-940-11

Query Match 74.4%; Score 642.8; DB 10; Length 840;
Best Local Similarity 99.7%; Pred. No. 9.2e-170;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAGAAAGGTTGGACAGATAGAAAGATCTTCATGAAGATTTGTATTTCAT 263
DB 183 TCATAGAGGTTGGACAGATAGAAAGATCTTCATGAAGATTTGTATTTCAT 242
QY 264 GAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCCTTACTGAACTGTGAGGA 323
DB 243 GAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCCTTACTGAACTGTGAGGA 302
QY 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
DB 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGGGCATGT 443

Db 363 GAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 503
Db 423 CATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 482
Qy 504 CACCATGAGCAACACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTGCGAGAAATCTTACT 683
Db 603 AGCTCCATTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTGCGAGAAATCTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAACTCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAACTCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTGTCATGTGATGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTGTCATGTGATGATCCAAAGCCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTC 828

RESULT 5

US-10-294-176-1
; Sequence 1, Application US/10294176
; Publication No. US20030077263A1
; GENERAL INFORMATION:
; APPLICANT: MARASKOVSKY, EUGENE
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Macintosh 7200/90
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/294,176
; FILING DATE: 14-NO. US20030077263A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/430,448
; FILING DATE: 29-Oct-1999
; APPLICATION NUMBER: 08/763,995
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2845-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-294-176-1

Query Match 74.4%; Score 642.8; DB 14; Length 840;
Best Local Similarity 99.7%; Pred. No. 9.2e-170; Indels 0; Gaps 0;
Matches 644; Conservative 0; Mismatches 2;
Qy 204 TCCAAGAAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
Qy 264 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 243 GAAAAAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAAAGATACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAAAGATACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
Qy 444 CATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 503
Db 423 CATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGATCTA 482
Qy 504 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAGCTGACCGTTAAAGACA 542
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTGCGAGAAATCTTACT 683
Db 603 AGCTCCATTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTGCGAGAAATCTTACT 662
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAACTCCATTCACTTGGG 743
Db 663 CAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAACTCCATTCACTTGGG 722
Qy 744 AGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTGTCATGTGATGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTGTCATGTGATGATCCAAAGCCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTC 828

RESULT 6

US-10-200-242-11
; Sequence 11, Application US/10200242
; Publication No. US20030144182A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242

```
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11

Query Match      74.4%; Score 642.8; DB 15; Length 840;
Best Local Similarity 99.7%; Pred. No. 9.2e-170;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAAAGGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

Qy 264 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAGGAGGA 323
Db 243 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAGGAGGA 302

Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362

Qy 384 GAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422

Qy 444 CATAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 503
Db 423 CATAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 482

Qy 504 CACCATGAGCAACCACTTGGTAAACCTCGAAATGGGAAACAGCTGACCGTTAAAGAGCA 563
Db 483 CACCATGAGCAACCACTTGGTAAACCTCGAAATGGGAAACAGCTGACCGTTAAAGAGCA 542

Qy 564 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTGTTTCCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTGTTTCCAATCGGGAAGCTTCGAGTCA 602

Qy 624 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 683
Db 603 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 662

Qy 684 CAGAGCTGCAATACCCACAGTTCCGCAAACTTTGGCGGCAACCAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAATACCCACAGTTCCGCAAACTTTGGCGGCAACCAATCCATTCACTTGGG 722

Qy 744 AGGAGTATTTGAATTCGAACCAAGGTGCTTCGGTGTGTTTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTCGAACCAAGGTGCTTCGGTGTGTTTCAATGTGACTGATCCAAAGCCA 782

Qy 804 AGTGAGCAATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTC 849
Db 783 AGTGAGCAATGGCACTGGCTTCAGTCTTTGGCTTACTCAAACTC 828
```

RESULT 7

US-10-200-242-11

; Sequence 11, Application US/1020242

```
; Publication No. US2004000606A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11
```

```
Query Match      74.4%; Score 642.8; DB 16; Length 840;
Best Local Similarity 99.7%; Pred. No. 9.2e-170;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 TCCAAGAAAGGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGGTTGGCAAGATGAGATGAAAGGAATCTTCATGAAGATTTTGTATTTCAT 242

Qy 264 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAGGAGGA 323
Db 243 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTGAGGAGGA 302

Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362

Qy 384 GAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422

Qy 444 CATAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 503
Db 423 CATAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 482

Qy 504 CACCATGAGCAACCACTTGGTAAACCTCGAAATGGGAAACAGCTGACCGTTAAAGAGCA 563
Db 483 CACCATGAGCAACCACTTGGTAAACCTCGAAATGGGAAACAGCTGACCGTTAAAGAGCA 542

Qy 564 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTGTTTCCAATCGGGAAGCTTCGAGTCA 623
Db 543 AGGACTCTATTATATCTATATGCCCAGTCACTTCTGTGTTTCCAATCGGGAAGCTTCGAGTCA 602

Qy 624 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 683
Db 603 AGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTTACT 662

Qy 684 CAGAGCTGCAATACCCACAGTTCCGCAAACTTTGGCGGCAACCAATCCATTCACTTGGG 743
Db 663 CAGAGCTGCAATACCCACAGTTCCGCAAACTTTGGCGGCAACCAATCCATTCACTTGGG 722

Qy 744 AGGAGTATTTGAATTCGAACCAAGGTGCTTCGGTGTGTTTCAATGTGACTGATCCAAAGCCA 803
Db 723 AGGAGTATTTGAATTCGAACCAAGGTGCTTCGGTGTGTTTCAATGTGACTGATCCAAAGCCA 782
```

Qy 804 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGGCTTACTCAAACTC 849
|||||
Db 783 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGGCTTACTCAAACTC 828
|||||

RESULT 6
US-10-242-212-1
; Sequence 1, Application US/10242212
; Publication No. US20030099644A1
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEEMA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242,212
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/09/645,926
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-212-1

Query Match 74.4%; Score 642.8; DB 14; Length 879;
Best Local Similarity 99.7%; Pred. No. 9.4e-170;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 204 TCCAAGAGGTTGGCAAGATAGAGATGAAGGATCTTCATGAAGATTTTGTATTCAT 263
Db 159 TCATAGAAGGTTGGCAAGATAGAGATGAAGGATCTTCATGAAGATTTTGTATTCAT 218
|||
Qy 264 GAAAACGATACAGAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 219 GAAAACGATACAGAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 278
|||
Qy 324 GATTAAGGCGAGTTTGAAGGCTTTGTGAAGATATAATGTGTAAACAAAGAGGAGACGAA 383
Db 279 GATTAAGGCGAGTTTGAAGGCTTTGTGAAGATATAATGTGTAAACAAAGAGGAGACGAA 338
|||
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 443
Db 339 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 398
|||
Qy 444 CATAGTGAGGCGAGCTGAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db 399 CATAGTGAGGCGAGCTGAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 458
|||
Qy 504 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 459 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAGACA 518
|||
Qy 564 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 519 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 578
|||
Qy 624 AGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 683
Db 579 AGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 638
|||
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAACAAATCCATTCACCTGGG 743
Db 639 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAACAAATCCATTCACCTGGG 698
|||
Qy 744 AGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAGGCA 803
Db 699 AGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAGGCA 758
|||
Qy 804 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGGCTTACTCAAACTC 849
|||||

Db 759 AGTGAGCCATGGCACTGGCTTACGTCCTTTGGGCTTACTCAAACTC 804

RESULT 9
US-10-191-997-125
; Sequence 125, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: XM_042961
US-10-191-997-125

Query Match 74.4%; Score 642.8; DB 15; Length 1800;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 204 TCCAAGAGGTTGGCAAGATAGAGATGAAGGATCTTCATGAAGATTTTGTATTCAT 263
Db 177 TCATAGAAGGTTGGCAAGATAGAGATGAAGGATCTTCATGAAGATTTTGTATTCAT 236
|||
Qy 264 GAAAACGATACAGAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db 237 GAAAACGATACAGAGATCAACACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 296
|||
Qy 324 GATTAAGGCGAGTTTGAAGGCTTTGTGAAGATATAATGTGTAAACAAAGAGGAGACGAA 383
Db 297 GATTAAGGCGAGTTTGAAGGCTTTGTGAAGATATAATGTGTAAACAAAGAGGAGACGAA 356
|||
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 443
Db 357 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCACATGT 416
|||
Qy 444 CATAGTGAGGCGAGCTGAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db 417 CATAGTGAGGCGAGCTGAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 476
|||
Qy 504 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAGACA 563
Db 477 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAGACA 536
|||
Qy 564 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 537 AGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 596
|||
Qy 624 AGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 683
Db 597 AGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCTTACT 656
|||
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAACAAATCCATTCACCTGGG 743
Db 657 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAACAAATCCATTCACCTGGG 716
|||
Qy 744 AGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAGGCA 803
Db 717 AGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAGGCA 776
|||||

QY 804 AGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTC 849
Db 777 AGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTC 822

RESULT 10

US-09-909-595-3

; Sequence 3, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 3
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (46)...(831)
US-09-909-595-3

Query Match 74.4%; Score 642.8; DB 10; Length 1803;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAAAGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
QY 264 GAAACGATACAGATGCAACACAGGAGAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGATGCAACACAGGAGAAGATCCTTATCTTACTGAACTGTGAGGA 302
QY 324 GATTAAGAGCCAGTTTGAAGGCTTTGCAAGATATAATGTTAAACAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGCAAGATATAATGTTAAACAAGAGGAGACGAA 362
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
QY 444 CATAAAGTGAGGCGCAGCTGAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 503
Db 423 CATAAAGTGAGGCGCAGCTGAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 482
QY 504 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGSGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGSGAAACAGCTGACCGTTAAAGACA 542
QY 564 AGGACTCTATTATATCTATGCCCAGTCACTCTTGTTCCTCAATCGGGAAGCTTCAGTCA 623
Db 543 AGGACTCTATTATATCTATGCCCAGTCACTCTTGTTCCTCAATCGGGAAGCTTCAGTCA 602
QY 624 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 683
Db 603 AGCTCCATTTATAGCAGCCTCTGCTAAAGTCCCGGTAGATTCGAGAGAACTTACT 662
QY 684 CAGAGCTCAAAATACCCAGCTTCGCGCAACCTTGGCGGCAACAACTCACTTCCTGGG 743
Db 663 CAGAGCTCAAAATACCCAGCTTCGCGCAACCTTGGCGGCAACAACTCACTTCCTGGG 722
QY 744 AGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 803
Db 723 AGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCCTCAATGTGACTGATCCAAAGCA 782
QY 804 AGTGAGCCATGGCACTGGCTTCAAGTCTCTTGGCTTACTCAAACTC 849

Db 783 AGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTC 828

RESULT 11

US-10-272-411-3

; Sequence 3, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/X67878.1
; DATABASE ENTRY DATE: 1997-06-06
; RELEVANT RESIDUES: (1)..(1803)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/X68550.1
; DATABASE ENTRY DATE: 1993-06-30
; RELEVANT RESIDUES: (1)..(1803)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/NM_000074.1
; DATABASE ENTRY DATE: 2002-04-10
; RELEVANT RESIDUES: (1)..(1803)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/L07414.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1803)
US-10-272-411-3

Query Match 74.4%; Score 642.8; DB 15; Length 1803;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 TCCAAGAGGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTTCAT 263
Db 183 TCATAGAAGTTGGACAAGATAGAAAGTGAAGGAATCTTCATGAAGATTTTGTATTTCAT 242
QY 264 GAAACGATACAGATGCAACACAGGAGAAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 243 GAAACGATACAGATGCAACACAGGAGAAGATCCTTATCTTACTGAACTGTGAGGA 302
QY 324 GATTAAGAGCCAGTTTGAAGGCTTTGTAAGATATAATGTTAAACAAGAGGAGACGAA 383
Db 303 GATTAAGAGCCAGTTTGAAGGCTTTGTAAGATATAATGTTAAACAAGAGGAGACGAA 362
QY 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 363 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 422
QY 444 CATAAAGTGAGGCGCAGCTGAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 503
Db 423 CATAAAGTGAGGCGCAGCTGAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGATACCTA 482
QY 504 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGSGAAACAGCTGACCGTTAAAGACA 563
Db 483 CACCATGAGCAACAACTTGGTAAACCTCGAAAATGSGAAACAGCTGACCGTTAAAGACA 542
QY 564 AGGACTCTATTATATCTATGCCCAGTCACTCTTGTTCCTCAATCGGGAAGCTTCAGTCA 623

444	Qy	CATAAGTGAGGCCAGGCAATGTAACCAACATCTGTGTGTACAGTGGGCTGAAAAGCGATACTA	503
423	Db	CATAAGTGAGGCCAGGCAATGTAACCAACATCTGTGTGTACAGTGGGCTGAAAAGCGATACTA	482
504	Qy	CACCATTGAGCAACAACCTTGTTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	563
483	Db	CACCATTGAGCAACAACCTTGTTAAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA	542
564	Qy	AGSACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTTCGAGTCA	623
543	Db	AGSACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTTCGAGTCA	602
624	Qy	AGTCCATTATTAGCCAGGCTCTGCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	683
603	Db	AGTCCATTATTAGCCAGGCTCTGCTTAAAGTCCCCCGGTAGATTTCGAGAGAAATCTTACT	662
684	Qy	CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTGGGGCGCAACAATCCATTCACATTGGG	743
663	Db	CAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTGGGGCGCAACAATCCATTCACATTGGG	722
744	Qy	AGGAGTATTTTGAATTGCAACCAAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAAGCCA	803
723	Db	AGGAGTATTTTGAATTGCAACCAAGGTGCTTCGGTGTTTGTCAAATGTGACTGATCCAAAGCCA	782
804	Qy	AGTGAGCCATGSCACTGGGCTTCAAGTCTTTGGGCTTACTCAAATCTC	849
783	Db	AGTGAGCCATGSCACTGGGCTTCAAGTCTTTGGGCTTACTCAAATCTC	822

RESULT 14

```

US-10-310-793-15
; Sequence 15, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Disease
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310. 793

```

Query Match	74.4%	Score 642.8	DB 15	Length 1803
Best Local Similarity	99.7%	Pred. No. 1.3e-169		
Matches 644	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	204	TCCAAGAAGGTTTGGCAAGAATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	263	
DB	183	TCATAGAAGGTTTGGCAAGAATAGAAAGATGAAAGGAATCTTTCATGAAGATTTTGTATTTCAT	242	
QY	264	GAAGAAGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGNACTTGTGAGGA	323	
DB	243	GAAGAAGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCCTTACTGNACTTGTGAGGA	302	
QY	324	GATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGACGAA	383	
DB	303	GATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGACGAA	362	
QY	384	GAAGAAGAAACAGCTTTGAAATGCAAAAGGTGATACGAATCCTCAAAATTCGCGGCACATGT	443	
DB	363	GAAGAAGAAACAGCTTTGAAATGCAAAAGGTGATACGAATCCTCAAAATTCGCGGCACATGT	422	
QY	444	CATAAGTGAAGCCAGCAGTAAACACACATCTGTGTTACAGTGGGCTGAAAGAGTACTA	503	
DB	423	CATAAGTGAAGCCAGCAGTAAACACACATCTGTGTTACAGTGGGCTGAAAGAGTACTA	482	
QY	504	CACCATGAGCAACAACCTTGTTAAACCTTGGAATAATGGAAACACAGCTGACCGTTTAAAGACA	563	
DB	483	CACCATGAGCAACAACCTTGTTAAACCTTGGAATAATGGAAACACAGCTGACCGTTTAAAGACA	542	
QY	564	AGCACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGAGACCTTCGAGTCA	623	
DB	543	AGCACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGAGACCTTCGAGTCA	602	
QY	624	AGCTCCATTATTAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTGAGAGAAATCTTTACT	683	
DB	603	AGCTCCATTATTAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTGAGAGAAATCTTTACT	662	
QY	684	CAGAGCTGCAATACCCACAGTTCCGCGCAACCTTCGGGGCAACAATCCATTCACCTGGG	743	
DB	663	CAGAGCTGCAATACCCACAGTTCCGCGCAACCTTCGGGGCAACAATCCATTCACCTGGG	722	
QY	744	AGGAGTATTGAAATTCGAACACAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAAAGCCA	803	
DB	723	AGGAGTATTGAAATTCGAACACAGGTGCTTCGGGTGTTTGTCAATGTGACTGATCCAAAGCCA	782	
QY	804	AGTGAGCCATGGCACTGGCTTCAAGTCCCTTTGGCTTACTCAAACTC	849	
DB	783	AGTGAGCCATGGCACTGGCTTCAAGTCCCTTTGGCTTACTCAAACTC	828	
RESULT 15				
US-10-202-062-9				
; Sequence 9, Application US/10202062				
; Publication No. US20040038349A1				
; GENERAL INFORMATION:				
; APPLICANT: Human Genome Sciences, Inc.,				
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members				
; FILE REFERENCE: PF559				
; CURRENT APPLICATION NUMBER: US/10/202,062				
; CURRENT FILING DATE: 2002-07-25				
; PRIOR FILING DATE: 2001-07-27				
; NUMBER OF SEQ ID NOS: 42				
; SOFTWARE: PatentIn version 3.0				
; SEQ ID NO 9				
; LENGTH: 1803				
; TYPE: DNA				
; ORGANISM: human				
US-10-202-062-9				

```
Query Match      74.4%; Score 642.8; DB 16; Length 1803;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 204 TCCAAGAGGTTGGACACAGATAGAAGATGAAGGAATCTTCATGAAGATTTTGATTCAT 263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
183 TCATAGAAGGTTGGACACAGATAGAAGATGAAGGAATCTTCATGAAGATTTTGATTCAT 242
Qy 264 GAAACCGATACAGAGATCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
243 GAAACCGATACAGAGATCAACACAGGAGAAAGATCCTTATCCTTACTGAACTGTGAGGA 302
Qy 324 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
303 GATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 362
Qy 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTGCGGCACATGT 443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
363 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTGCGGCACATGT 422
Qy 444 CATAAGTGAGCCAGCAGCTAATAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 503
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
423 CATAAGTGAGCCAGCAGCTAATAACAAACATCTGTGTTACAGTGGGCTGAAAAGGATACTA 482
Qy 504 CACCATGAGCAACAACTTGGTAACCCCTGGRAAATGGGAAACAGCTGACCGTTAAAAGACA 563
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
483 CACCATGAGCAACAACTTGGTAACCCCTGGRAAATGGGAAACAGCTGACCGTTAAAAGACA 542
Qy 564 AGGACTCTATTATATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
543 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 602
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCGCCGGTAGATTCGAGAGAACTTTACT 683
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
603 AGCTCCATTTATAGCCAGCCTCTGCTAAAGTCCGCCGGTAGATTCGAGAGAACTTTACT 662
Qy 684 CAGAGCTGCAATACCCACAGTTCGCCCAACCTTGCGGCAACAAATCCATTCACCTTGGG 743
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
663 CAGAGCTGCAATACCCACAGTTCGCCCAACCTTGCGGCAACAAATCCATTCACCTTGGG 722
Qy 744 AGGAGTATTTGAATTGCAACCAAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
723 AGGAGTATTTGAATTGCAACCAAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 782
Qy 804 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 849
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
783 AGTGAGCCATGGCACTGGCTTCACGTCTCTTTGGCTTACTCAAACTC 828
```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C	1	641.2	74.2	786	9	AY416061 Homo sapi
	2	641.2	74.2	786	9	AY416062 Pan trogl
	3	570	66.0	767	6	CD638712 AGENCOURT
	4	505	58.4	806	6	CD521613 AGENCOURT
	5	450.8	52.2	783	9	AY416063 Mus muscu
	6	399.4	46.2	702	6	CD640741 AGENCOURT
	7	395.2	45.7	690	6	CD642064 AGENCOURT
	8	389	45.0	796	6	CD520208 AGENCOURT
	9	286.4	33.1	571	7	CNT794393
	10	246.4	28.5	740	7	CK834247
C	11	244	28.3	492	2	BF599437
	12	240	27.8	628	7	CNT786611
	13	169	19.6	398	2	AW486605
	14	137.4	15.9	636	7	COT702364
	15	108.4	12.5	847	7	CK777858
	16	78.6	9.1	727	5	BU294618
	17	78.6	9.1	731	5	BU373331
	18	71.4	8.3	638	1	AI982044
	19	59.6	6.9	268	6	CD727599
	20	58.4	6.8	997	9	CNS003TE
C	21	58	6.7	803	5	BU398104
	22	58	6.7	797	9	CL074154
	23	54.8	6.3	1302	9	AG311052
	24	54.6	6.3	1522	9	CL075364
	25	54.6	6.3	1522	9	CL075364
	26	54.6	6.3	1522	9	CL075364
	27	54.6	6.3	1522	9	CL075364
	28	54.6	6.3	1522	9	CL075364
	29	54.6	6.3	1522	9	CL075364
	30	54.6	6.3	1522	9	CL075364

Db 138 TCATAGAAGGCTGACAAAGATAGAGATGAAGAAATCTTCATGAAGATTTGTATTTCAT 197
Qy 264 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 323
Db 198 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 257
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGCGAA 383
Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGCGAA 317
Qy 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGACATGT 443
Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGACATGT 377
Qy 444 CATTAAGTGAGCCAGCAGTAAACCAACATCTGTCTTACAGTGGCTGAAAAGGATACTA 503
Db 378 CATTAAGTGAGCCAGCAGTAAACCAACATCTGTCTTACAGTGGCTGAAAAGGATACTA 437
Qy 504 CACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 497
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAACTTACT 683
Db 558 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAACTTACT 617
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACCTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACCTTGGG 677
Qy 744 AGGAGTATTTGAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803
Db 678 AGGAGTATTTGAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 737
Qy 804 AGTGAGCCATGGCAGTTCAGTCTCTTGGCTTACTCAAACTC 849
Db 738 AGTGAGCCATGGCAGTTCAGTCTCTTGGCTTACTCAAACTC 783

RESULT 2
AY416062 786 bp DNA linear GSS 17-DEC-2003
LOCUS Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416062
VERSION AY416062.1 GI:39772022
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
AUTHORS 1 (bases 1 to 786)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 786)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.
FEATURES Location/Qualifiers
source 1..786
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1..>786
/gene="TNFSF5"
/locus_tag="HCM5765"
ORIGIN
Query Match 74.2%; Score 641.2; DB 9; Length 786;
Best Local Similarity 99.5%; Pred. No. 1.7e-168;
Matches 643; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 204 TCCAAAGAGGTTGGACAAAGATAGAGATGAAGAAATCTTCATGAAGATTTGTATTTCAT 263
Db 138 TCATAGAAGGTTGGACAAAGATAGAGATGAAGAAATCTTCATGAAGATTTGTATTTCAT 197
Qy 264 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 323
Db 198 GAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCTTACTTGAACCTGTGAGGA 257
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGCGAA 383
Db 258 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTTAAACAAAGAGAGAGCGAA 317
Qy 384 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGACATGT 443
Db 318 GAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGACATGT 377
Qy 444 CATTAAGTGAGCCAGCAGTAAACCAACATCTGTCTTACAGTGGCTGAAAAGGATACTA 503
Db 378 CATTAAGTGAGCCAGCAGTAAACCAACATCTGTCTTACAGTGGCTGAAAAGGATACTA 437
Qy 504 CACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 438 CACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAGCTGACCGTTAAAAAGACA 497
Qy 564 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 623
Db 498 AGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCA 557
Qy 624 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAACTTACT 683
Db 558 AGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTTAGATTCGAGAGAACTTACT 617
Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACCTTGGG 743
Db 618 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACCTTGGG 677
Qy 744 AGGAGTATTTGAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 803
Db 678 AGGAGTATTTGAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCA 737
Qy 804 AGTGAGCCATGGCAGTTCAGTCTCTTGGCTTACTCAAACTC 849
Db 738 AGTGAGCCATGGCAGTTCAGTCTCTTGGCTTACTCAAACTC 783
RESULT 3
CD638712 767 bp mRNA linear EST 17-JUN-2003
LOCUS AGENCOURT_14532410 NIH_MGC_191 Homo sapiens cDNA clone
DEFINITION IMAGE:30416146 5', mRNA sequence.
ACCESSION CD638712
VERSION CD638712.1 GI:31804800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
 National Cancer Genomics
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM215 row: h column: 11
 High quality sequence stop: 564.
 Location/Qualifiers
 1..767
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30416146"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

FEATURES
 source
 Query Match 66.0%; Score 570; DB 6; Length 767;
 Best Local Similarity 97.8%; Pred. No. 1.6e-148;
 Matches 587; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 Qy 204 TCCAGAAGGTTGGACAAGATGAAAGGAATCTTCATGAAGATTGTGATTTCAT 263
 Db |||||
 Qy 264 GAAACGATACAGAGATCAACACAGGAGAAGATCCTTATCTTACTGAAGTGTGAGGA 323
 Db |||||
 Qy 324 GATTAAGCCAGTTTGAAGCTTTGTAAGATATATGTTAAACAAGGGAGACCAA 383
 Db |||||
 Qy 147 GATTAAGCCAGTTTGAAGCTTTGTAAGATATATGTTAAACAAGGGAGACCAA 206
 Db |||||
 Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCTCAATTCGGGCACATGT 443
 Db |||||
 Qy 207 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCTCAATTCGGGCACATGT 266
 Db |||||
 Qy 444 CATAGTGAGCGCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGATCTA 503
 Db |||||
 Qy 267 CATAGTGAGCGCCAGCAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGATCTA 326
 Db |||||
 Qy 504 CACCATGAGCAACACTTGGTAACTCGGAAATCGGAACAGCTGACCGTTAAAGACA 563
 Db |||||
 Qy 327 CACCATGAGCAACACTTGGTAACTCGGAAATCGGAACAGCTGACCGTTAAAGACA 386
 Db |||||
 Qy 564 AGGACTCTATTATATCTATGCCCCAGTCACTTCTGTTCATCGGGAAGCTTCGAGTCA 623
 Db |||||
 Qy 387 AGGACTCTATTATATCTATGCCCCAGTCACTTCTGTTCATCGGGAAGCTTCGAGTCA 446
 Db |||||

Qy 624 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 683
 Db |||||
 Qy 447 AGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGATCTTACT 506
 Db |||||
 Qy 684 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 743
 Db |||||
 Qy 507 CAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAACAATCCATTCACTTGGG 566
 Db |||||
 Qy 744 AGGAGTATTTCAATTGCAACAGGTGCTTCGGTGTTCATATGATGATGATCCAAAGCA 803
 Db |||||
 Qy 567 AGGAGTATTTCAATTGCAACAGGTGCTTCGGTGTTCATATGATGATGATCCAAAGCA 625
 Db |||||
RESULT 4
 CD521613 806 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT 14356206 NIH_MGC 191 Homo sapiens cDNA clone
 DEFINITION IMAGE:30413128 5', mRNA sequence.
 CD521613 GI:31453331
 ACCESSION CD521613
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 806)
 NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM207 row: j column: 17
 High quality sequence stop: 466.
 Location/Qualifiers
 1..806
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30413128"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC 191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.4%; Score 505; DB 6; Length 806;
 Best Local Similarity 96.7%; Pred. No. 2.8e-130;
 Matches 525; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
 Qy 204 TCCAGAAGGTTGCAAGATGAAAGGAATCTTCATGAAGATTGTGATTTCAT 263
 Db |||||

```
Db 232 TCATAGAAGGTTGACAAAGATAGAAGATGAAGAAGTCTTCATGAAGATTTGTATTTCAT 291
Qy 264 GAAACCGATACAGAGATCAACACAGGAGAAAGATCTTATCTTACTGAAGTCTGAGGA 323
Db 292 GAAACCGATACAGAGATCAACACAGGAGAAAGATCTTATCTTACTGAAGTCTGAGGA 351
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTATTAACAAGAGGAGACGAA 383
Db 352 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTATTAACAAGAGGAGACGAA 411
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 443
Db 412 GAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCANATTGGGCACATGT 471
Qy 444 CATAACTGAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAGAGATCTA 503
Db 472 CATAACTGAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAGAGATCTA 531
Qy 504 CACCATGAGCAACAACCTTGTTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 532 CACCATGAGCAACAACCTTGTTAAACCTCGAAAATGGGAAACAGCTGACCGTTAAAAAGACA 591
Qy 564 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 592 AAGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 651
Qy 624 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTCGAGAAATCTTACT 683
Db 652 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTCGAGAAATCTTACT 711
Qy 684 CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTT-GGGGCAACAATCCATTCACTGG 742
Db 712 CAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGCGGGCAACAATCCCTTCCCTTG 771
Qy 743 GAG 745
Db 772 GGG 774

RESULT 5
AY416063
LOCUS
DEFINITION Mus musculus TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY416063
VERSION AY416063.1 GI:39772023
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 783)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Gargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14571302
2 (bases 1 to 783)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Gargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
LOCATION/Qualifiers
1..783
/organism="Mus musculus"
```

```
gene
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>783
/gene="TNFSF5"
/locus_tag="HCM5765"

ORIGIN
Query Match 52.2%; Score 450.8; DB 9; Length 783;
Best Local Similarity 82.2%; Pred. No. 4.5e-115; Indels 3; Gaps 1;
Matches 531; Conservative 0; Mismatches 112;

Qy 204 TCCAAGAGGTTGACCAAGATAGAAGATGAAGAAGTCTTCATGAAGATTTGTATTTCAT 263
Db 138 TCATAGAAGATTGGATGAAGGTCGAAGAGAAAGTAAACCTTCATGAAGATTTGTATTTCAT 197
Qy 264 GAAACCGATACAGAGATGCAACACAGGAGAAAGATCTTATCTTACTGAAGTCTGAGGA 323
Db 198 AAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTTGTCTGAAGTCTGAGGA 257
Qy 324 GATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTATTAACAAGAGGAGACGAA 383
Db 258 GATGAGAAGGCAATTTGAAGACCTTTGCAAGGATATACGTTAAACAAAGAAAGA--GAA 314
Qy 384 GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGT 443
Db 315 AAAAGAAAAACAGCTTTGAAATGCAAAAGGTGATGAGGATCCTCAAAATGCGACACAGT 374
Qy 444 CATAACTGAGCCAGCAGTAAACCAACATCTGTGTGTACAGTGGGCTGAAAGAGATCTA 503
Db 375 TGTAAAGCGAAGCCAAACAGTAAATGCAAGTTCGTTCTACAGTGGGCCAAAGAAAGATATTA 434
Qy 504 CACCATGAGCAACAACCTTGTTAAACCTGGAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
Db 435 TACCATGAAAAGCAACTTGGTAATGCTTGAANAATGGGAAACAGCTGACCGTTAAAGAGA 494
Qy 564 AGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 495 AGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGGGAGCCTTCGAGTCA 554
Qy 624 AGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTCGAGAAATCTTACT 683
Db 555 ACGCCCATTTATCTGCTGGCCTCTGCTGAAGCCAGCAGTGGATCTGAGAGAAATCTTACT 614
Qy 684 CAGAGTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAACAATCCATTCACTTCGG 743
Db 615 CAAGCGCAAAATACCCACAGTTCCTCCAGCTTTGAGCAGCAGCTGTGTTCACTTCGG 674
Qy 744 AGGAGTATTTGAATTGCAATCCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAAGCCA 803
Db 675 CGGAGTGTGTAATTAACAAGCTGGTCTTCTGCTGTGTTGTCAACGCTGACTGAAGCAAGCCA 734
Qy 804 AGTGAGCATGGCACTGGCTTCAGTCTTTGGCTTTACTTCAAACTC 849
Db 735 AGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTC 780

RESULT 6
CD640741
LOCUS
DEFINITION AGENCOURT 14542170 NIH MGC 191 Homo sapiens cDNA clone IMAGE:30414715 5', mRNA sequence.
ACCESSION CD640741
VERSION CD640741.1 GI:31808911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
```

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: NDCM211 row: 1 column: 20
High quality sequence stop: 571.
Location/Qualifiers

FEATURES

source

1. .702
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30414715"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 46.2%; Score 399.4; DB 6; Length 702;
Best Local Similarity 95.9%; Pred. No. 1.2e-100;
Matches 421; Conservative 0; Mismatches 16; Indels 2; Gaps 1;
Qy 204 TCCAGAGAGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 263
Db 208 TCATAGAAGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 267
Qy 264 GAAACGATACAGATGCAACACAGGAGAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 268 GAAACGATACAGATGCAACACAGGAGAGATCCTTATCTTACTGAACTGTGAGGA 327
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTTAAACAAAGAGGAGACGAA 383
Db 328 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTTAAACAAAGAGGAGACGAA 387
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443
Db 388 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 447
Qy 444 CATAGTCAGCCAGCTTAAACACATCTGTGTACAGTGGGCTGAAAGGATCTA 503
Db 448 CATAGTCAGCCAGCTTAAACACATCTGTGTACAGTGGGCTGAAAGGATCTA 507
Qy 504 CACCATGAGCAACACTTGGTAACTCCGAAATGGGAAACAGCTGACCGTTTAAAGACA 563
Db 508 CACCATGAGCAACACTTGGTAACTCCGAAATGGGAAACAGCTGACCGTTTAAAGACA 567
Qy 564 AGGACTTATATATCTATGCCCAGTCACTCTTGTGTTCCAAATCGGGAAGCTTCGAGTCA 623
Db 568 AGGACTTATATATCTATGCCCAGTCACTCTTGTGTTCCAAATCGGGAAGCTTCGAGTCA 627
Qy 624 AGCTCCATTTATAGCCAGC 642
Db 628 --GCTCATTTATAGCCAGC 644

RESULT 7

CD642064

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD642064 690 bp mRNA linear EST 17-JUN-2003
AGNCOURT 14538852 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30418744 5', mRNA sequence.

CD642064
CD642064.1 GI:31811566
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 690)
NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: NDCM222 row: d column: 17

High quality sequence stop: 536.
Location/Qualifiers

FEATURES

source

1. .690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30418744"

/tissue_type="Pooled"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_191"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);

Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed

and directionally cloned. PBMC - Peripheral Blood

Mononuclear Cells. RNA was pooled from 3/6hour stimulation

with PMA adn Ionomycin. 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGCCCATTTATGCCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCCGAGCGCGGCACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.69

kb (range 0.70-5.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 45.7%; Score 395.2; DB 6; Length 690;
Best Local Similarity 99.0%; Pred. No. 1.7e-99;
Matches 397; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 204 TCCAGAGAGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 263
Db 213 TCATAGAAGTTGGACAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 272
Qy 264 GAAACGATACAGATGCAACACAGGAGAGATCCTTATCTTACTGAACTGTGAGGA 323
Db 273 GAAACGATACAGATGCAACACAGGAGAGATCCTTATCTTACTGAACTGTGAGGA 332
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTTAAACAAAGAGGAGACGAA 383
Db 333 GATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTTAAACAAAGAGGAGACGAA 392
Qy 384 GAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCACATGT 443

Db 393 GAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGGCGCACATGT 452
 QY 444 CATAAGTCAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 503
 Db 453 CATAAGTCAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 512
 QY 504 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
 Db 513 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 572
 QY 564 AGGACTCTATTATATCTATATGCCCCAAGTCACCTTCTGTGTTCCA 604
 Db 573 AGGACTCTATTATATCTATATGCCCCAAGTCACCTTCTGTGTTCCA 613

RESULT 8
 CD520208 796 bp mRNA linear EST 06-JUN-2003
 LOCUS AGENCOURT_14355767 NIH_MGC_191 Homo sapiens cDNA clone
 DEFINITION IMAGE:30412573 5', mRNA sequence.

ACCESSION CD520208
 VERSION CD520208.1 GI:31451926
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat

CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDCM206 row: C column: 14
 High quality sequence stop: 541.
 Location/Qualifiers

FEATURES
 source

1..796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30412573"
 /tissue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
 and directionally cloned. PMBC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCGCATTTAGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCGGCACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 45.0%; Score 389; DB 6; Length 796;
 Best Local Similarity 98.3%; Pred. No. 9.9e-98;
 Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 204 TCCAAGAAGGTGGCAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 263
 Db 205 TCATAGAAGGTGGCAAGATAGAAAGGAATCTTCATGAAGATTTTGTATTCAAT 264
 QY 264 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA 323
 Db 265 GAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCCTTACTGAACCTGTGAGGA 324
 QY 324 GATTAAAAGCCAGTTTGAAGCCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 383
 Db 325 GATTAAAAGCCAGTTTGAAGCCTTTGTGAAGGATATATGTTAAACAAAGAGGAGACGAA 384
 QY 384 GAAAAAACAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGGCGCACATGT 443
 Db 385 GAAAAAACAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTGGCGCACATGT 444
 QY 444 CATAAGTCAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 503
 Db 445 CATAAGTCAGCCAGCAGTAAACACACATCTGTGTACAGTGGGCTGAAAGGATACTA 504
 QY 504 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 563
 Db 505 CACCATGAGCAACAACTTGGTAACCTCGAAAAATGGGAAACAGCTGACCGTTAAAAAGACA 564
 QY 564 AGGACTCTATTATATCTATATGCCCCAAGTCA-CCTTCTGTGTTCCAATCGGGAA 612
 Db 565 AGGACTCTATTATATCTATATGCCCCAAGTCACCTTCTGTGTTCCAATCGGGAA 614

RESULT 9
 CN794193

LOCUS CN794193 571 bp mRNA linear EST 26-MAY-2004
 DEFINITION 4129335 BARC 8BOV Bos taurus cDNA clone 8BOV_50H03 5', mRNA
 sequence.

ACCESSION CN794193
 VERSION CN794193.1 GI:47690173
 KEYWORDS EST.

SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 571)
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
 Matukumalli,L.K.

TITLE Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Richard G. Baumann

Bovine Functional Genomics Lab
 ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt -, -trim_fasta. Vector identified
 by cross_match using options -minmatch 12 -minscore 18
 Plate: 50 row: H column: 03
 Seq primer: CCTATTAGGTGACACTATAGAAC

High quality sequence stop: 571.
 Location/Qualifiers

FEATURES
 source

1..571
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_50H03"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B Tona"
 /clone_lib="BARC 8BOV"

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 398)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGGACG
Plate: 34 row: F column: 23
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..398
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1B0V"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
ORIGIN
Query Match 19.6%; Score 169; DB 2; Length 398;
Best Local Similarity 88.0%; Pred. No. 4.3e-36;
Matches 184; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 204 TCCAGAGAGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 263
|||
Db 190 TCACAGAGATTGGACAAGATAGAGACGAAGGAATCTTCATGAAGATTTGTATTCAT 249
|||
Qy 264 GAAACGATACAGATGCACACAGGAGAAGATCCCTTACTGAACTGTGAGGA 323
|||
Db 250 GAAACGATACAGATGCATTAAGAGAGAGGGGTCCTTATCTTACTGAACTGTGAGGA 309
|||
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTCAAGATATATGTTAAACAAAGAGACGAA 383
|||
Db 310 AATTAGAAGCCGTTTGAAGACTTGTGCAGATATATGCAAAACAAAGAAAGTAAGAA 369
|||
Qy 384 GAAAGAAACAGCTTTGAAATCCAAAAAG 412
|||
Db 370 GAAAGAAAAAATTTGAATGCACAAAG 398
|||
RESULT 14
CO702364/c
LOCUS CO702364 636 bp mRNA linear EST 26-JUL-2004
DEFINITION DG32-liver Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO702364
VERSION CO702364.1 GI:50651032
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 636)

Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schluter
LION Bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.
Location/Qualifiers
1..636
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: Dog pBluescript LION"
ORIGIN
Query Match 15.9%; Score 137.4; DB 7; Length 636;
Best Local Similarity 87.7%; Pred. No. 3.7e-27;
Matches 150; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 204 TCCAGAGAGTTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 263
|||
Db 177 TCACAGAGATTGGACAAGATAGAGATGAAGGAATCTTCATGAAGATTTTGTATTCAT 118
|||
Qy 264 GAAACGATACAGATGCACACAGGAGAAGATCCCTTACTGAACTGTGAGGA 323
|||
Db 117 GAAACGTTACAGAAATGCACAAAGGGGGGTCCTTGTCTTACTGAACTGTGAGGA 58
|||
Qy 324 GATTAAGAGCCAGTTTGAAGGCTTTGTCAAGATATATGTTAAACAAAGA 374
|||
Db 57 AATTAAGAGCCATTTGAAGCCTTTCTCAAGGAGATATGCTTAACAAACGA 7
|||
RESULT 15
CK777858/c
LOCUS CK777858 847 bp mRNA linear EST 20-FEB-2004
DEFINITION 965004 MARC 3BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK777858
VERSION CK777858.1 GI:42730171
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 847)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 33 row: N column: 5

Seq primer: GTAATACGACTCACTATAGGG.

FEATURES

source
Location/Qualifiers
1..847
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN

Query Match 12.5%; Score 108.4; DB 7; Length 847;
Best Local Similarity 91.3%; Pred. NO. 5.5e-19;
Matches 115; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 724 CAACAATCCATTCTCTGGAGGAGTATTGAAATTCGAACCAACGAGGTTCGGTGTTC 783
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
847 CAGCAATCCATTCTCTAGGAGGAGTCTTGAATTCGAATCGGGTCTCGGTGTTC 788
Qy 784 AATGTGACTGATCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 843
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
787 AATGTGACTGATCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 728
Qy 844 AAATCTC 849
Db |||||
727 AAATCTC 722

Search completed: November 12, 2004, 12:49:36
Job time : 1899.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 11, 2004, 20:34:45 ; Search time 1965.86 Seconds
(without alignments)
16453.933 Million cell updates/sec

Title: US-09-687-864A-19
Perfect score: 684
Sequence: 1 aagcttgccgcgcgtctgta.....aactcgagtataatctaga 684

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hig.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	68.1	1566	6	AX455878
2	463.6	67.8	786	6	I87864
3	463.6	67.8	786	6	BD064000
4	463.6	67.8	786	6	BD064003
5	463.6	67.8	786	6	BD064005
6	463.6	67.8	786	6	BD064006
7	463.6	67.8	840	6	AR044779
8	463.6	67.8	840	6	AR076926
9	463.6	67.8	840	6	AR078316
10	463.6	67.8	840	6	AR085419
11	463.6	67.8	840	6	AR103375
12	463.6	67.8	840	6	AR106246
13	463.6	67.8	840	6	AR169232
14	463.6	67.8	840	6	AR171647
15	463.6	67.8	840	6	BD190674
16	463.6	67.8	840	6	I23893
17	463.6	67.8	840	6	I27345
18	463.6	67.8	840	6	I67828
19	463.6	67.8	840	6	AR216259

20	463.6	67.8	840	6	AR267621	Sequence
21	463.6	67.8	870	9	BC074950	BC074950 Homo sapi
22	463.6	67.8	879	6	AX254616	AX254616 Sequence
23	463.6	67.8	879	6	AX090039	AX090039 Sequence
24	463.6	67.8	879	9	HSGP39MR	Z15017 H.sapiens m
25	463.6	67.8	929	6	AR076932	AR076932 Sequence
26	463.6	67.8	929	6	AR078322	AR078322 Sequence
27	463.6	67.8	929	6	AR085425	AR085425 Sequence
28	463.6	67.8	929	6	AR103381	AR103381 Sequence
29	463.6	67.8	929	6	AR169238	AR169238 Sequence
30	463.6	67.8	929	6	I87867	I87867 Sequence 10
31	463.6	67.8	929	6	AR216265	AR216265 Sequence
32	463.6	67.8	1425	6	AR076929	AR076929 Sequence
33	463.6	67.8	1425	6	AR078319	AR078319 Sequence
34	463.6	67.8	1425	6	AR085422	AR085422 Sequence
35	463.6	67.8	1425	6	AR103378	AR103378 Sequence
36	463.6	67.8	1425	6	AR169235	AR169235 Sequence
37	463.6	67.8	1425	6	AR216262	AR216262 Sequence
38	463.6	67.8	1798	6	CQ725625	CQ725625 Sequence
39	463.6	67.8	1803	6	AR350226	AR350226 Sequence
40	463.6	67.8	1803	9	HSCD40	X67878 H.sapiens m
41	463.6	67.8	1816	6	BD187611	BD187611 Screening
42	463.6	67.8	1816	6	BD270930	BD270930 Use of CD
43	463.6	67.8	1816	6	AR254617	AR254617 Sequence
44	463.6	67.8	1816	9	HUMCD40L	L07414 Human CD40-
45	463.6	67.8	1822	9	HSTRAPA	X68550 H.sapiens T

ALIGNMENTS

RESULT 1
AX455878
LOCUS AX455878 1566 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 6 from Patent WO0202751.
ACCESSION AX455878
VERSION AX455878.1 GI:21714871
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Shirwan, H.
TITLE Alteration of cell membrane for new functions
JOURNAL Patent: WO 0202751-A 6 10-JAN-2002;
UNIVERSITY OF LOUISVILLE RESEARCH FOUNDATION, INC. (US)
FEATURES
source
Location/Qualifiers
1..1566
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="SA-CD40L"

ORIGIN	Query Match	68.1%;	Score 466;	DB 6;	Length 1566;
	Best Local Similarity	98.9%;	Pred. No. 2.4e-116;		
	Matches 469;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	200	CGGATCCAGAAAACAGCTTTCGAAATGCAAAAAGGTGATCAGATCCTCAAAATGGCGGAC	259		
Db	766	CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATGGCGGAC	825		
Qy	260	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT	319		
Db	826	ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT	885		
Qy	320	ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAAACAGCTGACCGTTAAAA	379		
Db	886	ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAAACAGCTGACCGTTAAAA	945		
Qy	380	GACAAGGACTTATATATATCTATGCCCCAAGTCACCTTCTGTCCAAATCGGAGNAGCTTCGA	439		
Db	946	GACAAGGACTTATATATATCTATGCCCCAAGTCACCTTCTGTCCAAATCGGAGNAGCTTCGA	1005		

```
QY      440  GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGATCT 499
Db      1006 GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGATCT 1065

QY      500  TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 559
Db      1066 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 1125

QY      560  TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db      1126 TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 1185

QY      620  GCCAAGTGAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCAGT 673
Db      1186 GCCAAGTGAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCAGT 1239

RESULT 2
187864
LOCUS      187864      786 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION Sequence 3 from patent US 5716805.
ACCESSION 187864
VERSION   187864.1 GI:3407804
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 786)
AUTHORS   Srinivasan,S. and Spriggs,M.K.
TITLE      Methods of preparing soluble, oligomeric proteins
JOURNAL    Patent: US 5716805-A 3 10-FEB-1998;
FEATURES   Location/Qualifiers
            source
            1..786
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      200  CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 259
Db      314  CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 373

QY      260  ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db      374  ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 433

QY      320  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db      434  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 493

QY      380  GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db      494  GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 553

QY      440  GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAACTCT 499
Db      554  GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAACTCT 613

QY      500  TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 559
Db      614  TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 673

QY      560  TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db      674  TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 733

QY      620  GCCAAGTGAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db      734  GCCAAGTGAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 783
```

```
RESULT 3
BD064000
LOCUS      BD064000      786 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Novel expression vectors containing accessory molecule ligand genes
            and their use for immuno-modulation and treatment of malignancies
            and autoimmune disease.
ACCESSION  BD064000
VERSION     BD064000.1 GI:22609603
KEYWORDS   JP 2001505782-A/1.
SOURCE      synthetic construct
            artificial sequences.
            1. (bases 1 to 786)
REFERENCE   Kipps,T.J., Sharma,S. and Cantwell,M.
            Novel expression vectors containing accessory molecule ligand genes
            and their use for immuno-modulation and treatment of malignancies
            and autoimmune disease
JOURNAL     Patent: JP 2001505782-A 1 08-MAY-2001;
            UNIVERSITY OF CALIFORNIA
COMMENT     PN JP 2001505782-A/1
            PD 08-MAY-2001
            PR 08-DEC-1997 JP 1998526956
            PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI
            THOMAS J KIPPS,SANJAI SHAERMA,MARK CANTWELL,
            PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/525,C07K14/705,
            PC C12N15/86,
            PC A61K48/00,A61K38/17,A61K35/12
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers.
FEATURES    Location/Qualifiers
            source
            1..786
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      200  CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 259
Db      314  CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 373

QY      260  ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db      374  ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 433

QY      320  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db      434  ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 493

QY      380  GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db      494  GACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 553

QY      440  GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAACTCT 499
Db      554  GTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGATTCGAGAGAACTCT 613

QY      500  TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 559
Db      614  TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGGGGCAACAATCCATTCACT 673

QY      560  TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 619
Db      674  TGGGAGGAGTATTTGAATTGCAACAGAGTGTCTCGGTGTTTGTCAATGTGACTGATCCAA 733

QY      620  GCCAAGTGAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
```

Db 734 GCCAAGTGAGCCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAAACTC 783

RESULT 4
BD064003
LOCUS
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.
BD064003
ACCESSION
VERSION BD064003.1 GI:22609606
KEYWORDS JP 2001505782-A/4.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 786)
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease
JOURNAL Patent: JP 2001505782-A 4 08-MAY-2001;
UNIVERSITY OF CALIFORNIA
COMMENT PN JP 2001505782-A/4
PD 08-MAY-2001
PF 08-DEC-1997 JP 1998526956
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI
THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/705,
PC C12N15/86,
PC A61K48/00,A61K38/17,A61K35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1..786
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 67.8%; Score 463.6; DB 6; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTTGGGCAC 259
Db 314 CGAAGAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTTGGGCAC 373

Qy 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db 374 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 433

Qy 320 ACTACACCATGAGCAACAACTTGTGTAACCTCGAAATGGGAAACAGCTGACCGTTAAA 379
Db 434 ACTACACCATGAGCAACAACTTGTGTAACCTCGAAATGGGAAACAGCTGACCGTTAAA 493

Qy 380 GACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 439
Db 494 GACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 553

Qy 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 499
Db 554 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 613

Qy 500 TACTCAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 614 TACTCAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 673

Qy 560 TGGGAGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db 674 TGGGAGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

Qy 620 GCCAAGTGAGCCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAAACTC 669

Db 734 GCCAAGTGAGCCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAAACTC 783

RESULT 5
BD064005
LOCUS
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.
BD064005
ACCESSION
VERSION BD064005.1 GI:22609608
KEYWORDS JP 2001505782-A/6.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 786)
AUTHORS Kipps,T.J., Sharma,S. and Cantwell,M.
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease
JOURNAL Patent: JP 2001505782-A 6 08-MAY-2001;
UNIVERSITY OF CALIFORNIA
COMMENT PN JP 2001505782-A/6
PD 08-MAY-2001
PF 08-DEC-1997 JP 1998526956
PR 09-DEC-1996 US 60/032145,01-DEC-1997 US 08/982272 PI
THOMAS J KIPPS,SANJAI SHARMA,MARK CANTWELL
PC C12N15/12,C12N15/62,C07K14/48,C07K14/52,C07K14/705,
PC C12N15/86,
PC A61K48/00,A61K38/17,A61K35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1..786
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 67.8%; Score 463.6; DB 6; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTTGGGCAC 259
Db 314 CGAAGAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTTGGGCAC 373

Qy 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db 374 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 433

Qy 320 ACTACACCATGAGCAACAACTTGTGTAACCTCGAAATGGGAAACAGCTGACCGTTAAA 379
Db 434 ACTACACCATGAGCAACAACTTGTGTAACCTCGAAATGGGAAACAGCTGACCGTTAAA 493

Qy 380 GACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 439
Db 494 GACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 553

Qy 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 499
Db 554 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 613

Qy 500 TACTCAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 614 TACTCAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 673

Qy 560 TGGGAGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db 674 TGGGAGGAGTATTTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 733

QY 620 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 669
|||||
Db 734 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 783

RESULT 6
LOCUS BD064006 786 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease.
ACCESSION BD064006
VERSION BD064006.1 GI:22609609
KEYWORDS JP 2001505782-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 786)
AUTHORS Kipps T.J., Sharma, S. and Cantwell, M.
TITLE Novel expression vectors containing accessory molecule ligand genes and their use for immuno-modulation and treatment of malignancies and autoimmune disease
JOURNAL Patent: JP 2001505782-A 7 08-MAY-2001;
UNIVERSITY OF CALIFORNIA
COMMENT PN JP 2001505782-A/7
PD 08-MAY-2001
PF 08-DEC-1997 JP 1998526956
PR 09-DEC-1996 US 60/032145, 01-DEC-1997 US 08/982272 PI
THOMAS J KIPPS, SANJAI SHARMA, MARK CANTWELL
PC C12N15/12, C12N15/62, C07K14/48, C07K14/52, C07K14/525, C07K14/705,
PC C12N15/86,
PC A61K48/00, A61K38/17, A61K35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1..786
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 67.8%; Score 463.6; DB 6; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
|||||
Db 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 373
|||||

QY 260 ATGTCATAAGTGAGCGCAGCACTGTTGATGTTTACAGTGGGCTGAAAAGGAT 319
|||||
Db 374 ATGTCATAAGTGAGCGCAGCACTGTTGATGTTTACAGTGGGCTGAAAAGGAT 433
|||||

QY 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
|||||
Db 434 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 493
|||||

QY 380 GACAGGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439
|||||
Db 494 GACAGGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 553
|||||

QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAACTCT 499
|||||
Db 554 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAACTCT 613
|||||

QY 500 TACTCAGAGCTCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAACAATCCATTCACT 559
|||||
Db 614 TACTCAGAGCTCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAACAATCCATTCACT 673
|||||

QY 560 TGGGAGGAGTATTGAAATGCAACCAAGTGTCTTCGGTGTTCCTCAATGTGACTGATCCAA 619
|||||
Db 674 TGGGAGGAGTATTGAAATGCAACCAAGTGTCTTCGGTGTTCCTCAATGTGACTGATCCAA 733
|||||

QY 620 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 669
|||||
Db 734 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 783

RESULT 7
LOCUS AR044779 840 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION AR044779.1 GI:5966244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Kehry, M. and Castle, B.
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 3 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
|||||
Db 335 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 394
|||||

QY 260 ATGTCATAAGTGAGCGCAGCACTGTTGATGTTTACAGTGGGCTGAAAAGGAT 319
|||||
Db 395 ATGTCATAAGTGAGCGCAGCACTGTTGATGTTTACAGTGGGCTGAAAAGGAT 454
|||||

QY 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
|||||
Db 455 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 514
|||||

QY 380 GACAGGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439
|||||
Db 515 GACAGGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 574
|||||

QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAACTCT 499
|||||
Db 575 GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAACTCT 634
|||||

QY 500 TACTCAGAGCTCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAACAATCCATTCACT 559
|||||
Db 635 TACTCAGAGCTCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAACAATCCATTCACT 694
|||||

QY 560 TGGGAGGAGTATTGAAATGCAACCAAGTGTCTTCGGTGTTCCTCAATGTGACTGATCCAA 619
|||||
Db 695 TGGGAGGAGTATTGAAATGCAACCAAGTGTCTTCGGTGTTCCTCAATGTGACTGATCCAA 754
|||||

QY 620 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 669
|||||
Db 755 GCCAAGTGAGCATGGCACTGGCTTCAGTCCCTTTGGCTTACTCAAACTC 804
|||||

RESULT 8
LOCUS AR076926 840 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 11 from patent US 5961974.
ACCESSION AR076926
VERSION AR076926.1 GI:10003672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.


```
Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS  Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE     Monoclonal antibodies to CD40 ligand, pharmaceutical composition
          comprising the same and hybridomas producing the same
JOURNAL   Patent: US 5961974-A 11 05-OCT-1999;
FEATURES  Location/Qualifiers
           source
           1..840
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 259
Db  |||
Db 359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 418
Qy 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db  |||
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 478
Qy 320 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db  |||
Db 479 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
Qy 380 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 439
Db  |||
Db 539 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 598
Qy 440 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 499
Db  |||
Db 599 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAAATCCATTCAC 559
Db  |||
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAAATCCATTCAC 718
Qy 560 TGGGAGGAGTATTGAAATGCAACCCAGCTGCTTGGTGTGTTGTCATGTGATGATCCAA 619
Db  |||
Db 719 TGGGAGGAGTATTGAAATGCAACCCAGCTGCTTGGTGTGTTGTCATGTGATGATCCAA 778
Qy 620 GCCAAGTGAGCCATGGCAGTGGCTTACGCTCTTTGGCTTACTCAAACTC 669
Db  |||
Db 779 GCCAAGTGAGCCATGGCAGTGGCTTACGCTCTTTGGCTTACTCAAACTC 828

RESULT 10
AR085419
LOCUS     AR085419
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION   AR085419.1 GI:10012188
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS  Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
          Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE     DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL   Patent: US 5981724-A 11 09-NOV-1999;
FEATURES  Location/Qualifiers
           source
           1..840
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 259
Db  |||
Db 359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 418
Qy 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db  |||
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 478
Qy 320 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db  |||
Db 479 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
Qy 380 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 439
Db  |||
Db 539 GACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 598
Qy 440 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 499
Db  |||
Db 599 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAAATCCATTCAC 559
Db  |||
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAAATCCATTCAC 718
Qy 560 TGGGAGGAGTATTGAAATGCAACCCAGCTGCTTGGTGTGTTGTCATGTGATGATCCAA 619
Db  |||
Db 719 TGGGAGGAGTATTGAAATGCAACCCAGCTGCTTGGTGTGTTGTCATGTGATGATCCAA 778
Qy 620 GCCAAGTGAGCCATGGCAGTGGCTTACGCTCTTTGGCTTACTCAAACTC 669
Db  |||
Db 779 GCCAAGTGAGCCATGGCAGTGGCTTACGCTCTTTGGCTTACTCAAACTC 828

RESULT 9
AR078316
LOCUS     AR078316
DEFINITION Sequence 11 from patent US 5962406.
ACCESSION AR078316
VERSION   AR078316.1 GI:10005062
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS  Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
          Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE     Recombinant soluble CD40 ligand polypeptide and pharmaceutical
          composition containing the same
JOURNAL   Patent: US 5962406-A 11 05-OCT-1999;
FEATURES  Location/Qualifiers
           source
           1..840
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
```

```
Db 539 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 499
Db 599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 718
Qy 560 TGGGAGGAGTATTTGAATTGCAACACAGTCTTCCGTTGTTTGTCAATGTGACTGATCCAA 619
Db 719 TGGGAGGAGTATTTGAATTGCAACACAGTCTTCCGTTGTTTGTCAATGTGACTGATCCAA 778
Qy 620 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 828

RESULT 11
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 JUL-2000;
FEATURES
source
Location/Qualifiers
1..840
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.8%; Score 463.6; DB 6; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.1e-115;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCAC 259
Db 359 CGAAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCAC 418
Qy 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db 419 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 478
Qy 320 ACTACACCATGAGCAACAACCTTGGTAAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 479 ACTACACCATGAGCAACAACCTTGGTAAACCTCGGAAAATGGGAAACAGCTGACCGTTAAAA 538
Qy 380 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 539 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 499
Db 599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 718
Qy 560 TGGGAGGAGTATTTGAATTGCAACACAGTCTTCCGTTGTTTGTCAATGTGACTGATCCAA 619
Db 719 TGGGAGGAGTATTTGAATTGCAACACAGTCTTCCGTTGTTTGTCAATGTGACTGATCCAA 778
Qy 620 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 828

RESULT 13
LOCUS AR169232 840 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6290972.
ACCESSION AR169232
VERSION AR169232.1 GI:17907047
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
```

Db	335	CGAAGAAGAAAAACAGCTTTTGAATATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC	394
Qy	260	ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT	319
Db	395	ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT	454
Qy	320	ACTACACATGAGCAACAACTTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA	379
Db	455	ACTACACATGAGCAACAACTTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA	514
Qy	380	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA	439
Db	515	GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCGGGAAGCTTCGA	574
Qy	440	GTCAAGCTCCAAATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT	499
Db	575	GTCAAGCTCCAAATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT	634
Qy	500	TACTCAGAGCTGCAAAATACCCACAGTTCCGGCAAACTTTGGGGCAACAATCCATTCACT	559
Db	635	TACTCAGAGCTGCAAAATACCCACAGTTCCGGCAAACTTTGGGGCAACAATCCATTCACT	694
Qy	560	TGGGAGAGTATTTGAATTGCAACACAGTGTCTTGGTGTTCATGTGACTGATCCAA	619
Db	695	TGGGAGAGTATTTGAATTGCAACACAGTGTCTTGGTGTTCATGTGACTGATCCAA	754
Qy	620	GCCAAGTGAGCCATGGGCACCTGGCTTCAGTCTCTTTGGCTTACTCAAATC	669
Db	755	GCCAAGTGAGCCATGGGCACCTGGCTTCAGTCTCTTTGGCTTACTCAAATC	804
RESULT 15			
BD190674			
LOCUS	BD190674	840 bp	DNA linear PAT 17-JUL-2000
DEFINITION	Method of activating dendritic cells.		
ACCESSION	BD190674		
VERSION	BD190674.1 GI:330000413		
KEYWORDS	JP 2002514047-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 840)		
TITLE	Marauskovsky, E. and McKenna, H.J.		
JOURNAL	Method of activating dendritic cells		
COMMENT	Patent: JP 2002514047-A 1 14-MAY-2002; IMMUNEX CORP		
FEATURES	OS	Homo sapiens (human)	
	PN	JP 2002514047-A/1	
	PD	14-MAY-2002	
	PF	09-JUL-1997 JP 1998505349	
	PR	10-JUL-1996 US 08/677762,12-DEC-1996 US 08/763995 PI	
	PC	EUGENE MARASKOVSKY, HILARY J MCKENNA	
	CC	C12N5/00, C12N15/63, C12N15/09, A61K48/00	
	CC	Strandedness: Single;	
	CC	Topology: Linear;	
	Key	Location/Qualifiers	
source	FT	CDS	46..831.
		Location/Qualifiers	
		1..840	
		/organism="Homo sapiens"	
ORIGIN		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
	Query Match	67.8%;	Score 463.6; DB 6; Length 840;
	Best Local Similarity	99.1%;	Pred. No. 1.1e-115;
	Matches 466;	Conservative 0;	Mismatches 4; Indels 0; Gaps 0
Qy	200	CGATCCAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC	259
Db	359	CGAAGAAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC	418

```
Qy 260 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db 419 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
Qy 320 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 479 ACTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
Qy 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAATCGGGAAGCTTCGA 439
Db 539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAATCGGGAAGCTTCGA 598
Qy 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAGTCCCCCGGTAGATTTCGAGAGAACTCT 499
Db 599 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAGTCCCCCGGTAGATTTCGAGAGAACTCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTGGGGGCAACAATCCCATTTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTGGGGGCAACAATCCCATTTCACT 718
Qy 560 TGGGAGGAGTATTTGAATTGCAACCAAGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAA 619
Db 719 TGGGAGGAGTATTTGAATTGCAACCAAGTGCTTCGGTGTTTTGTCAATGTGACTGATCCAA 778
Qy 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 828
```

Search completed: November 12, 2004, 07:54:39
Job time : 1966.86 secs

PA (HAYD/) HAYDEN-LEDBETTER M S.
XX Ledbetter JA, Hayden-Ledbetter MS;
FI WPI; 2001-281790/29.
DR P-PSDB; AAB62340.
XX
XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
XX Example 1; Fig 2B; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
CC CD154 short form extracellular domain fusion protein linked by ProAspPro
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 684 BP; 216 A; 154 C; 147 G; 167 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 684; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.4e-193;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTGGCGCATCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60
DB 1 AAGCTTGGCGCATCTGTATACCTCTCAGCTGTTAGGACTACTTCTGTTTGGATCTCG 60
QY 61 GCTTCGAGATCTGTAGTAATTAATTTGTACAGACCACCAATACAGAGAGGTTA 120
DB 61 GCTTCGAGATCTGTAGTAATTAATTTGTACAGACCACCAATACAGAGAGGTTA 120
QY 121 TCTATAGACACGAGGAGAGCTTTTATCGAAGAGAAACATAATAGGAGATATAGACAA 180
DB 121 TCTATAGACACGAGGAGAGCTTTTATCGAAGAGAAACATAATAGGAGATATAGACAA 180
QY 181 GCACATTGTAACATTAGTCCGGATCCAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAG 240
DB 181 GCACATTGTAACATTAGTCCGGATCCAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAG 240
QY 241 AATCTCTAAATTCGGGCACATGTCTAAGTAGGAGCCAGCAGTAAACACATCTGTGTTA 300
DB 241 AATCTCTAAATTCGGGCACATGTCTAAGTAGGAGCCAGCAGTAAACACATCTGTGTTA 300
QY 301 CAGTGGGCTGAAAAGGATCTACACCATGAGCAACACTTGGTAACCTCGMAAATGGG 360
DB 301 CAGTGGGCTGAAAAGGATCTACACCATGAGCAACACTTGGTAACCTCGMAAATGGG 360
QY 361 AAACAGCTGACCGTTTAAAGAGCAAGGACTCTATTATATATATGCCCCAAGTCACCTTCTGT 420
DB 361 AAACAGCTGACCGTTTAAAGAGCAAGGACTCTATTATATATATGCCCCAAGTCACCTTCTGT 420
QY 421 TCCAAATCGGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCGCC 480
DB 421 TCCAAATCGGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCGCC 480
QY 481 GGTAGATTCGAGAGATCTTACTCAGAGTGCATAATACCCAGTTCCGCCAAACCTTGC 540
DB 481 GGTAGATTCGAGAGATCTTACTCAGAGTGCATAATACCCAGTTCCGCCAAACCTTGC 540
QY 541 GGGCAACATCCATTCACTTGGGAGGAGTATTGTAATTCGAACACAGGTGCTTCGGTGTGT 600
DB 541 GGGCAACATCCATTCACTTGGGAGGAGTATTGTAATTCGAACACAGGTGCTTCGGTGTGT 600
QY 601 GTCAATGTGATGTATCCAGCAAGCAAGTGCAGTGGCTTCAAGTCTTTCGGCTTGA 660
DB 601 GTCAATGTGATGTATCCAGCAAGCAAGTGCAGTGGCTTCAAGTCTTTCGGCTTGA 660
QY 661 CTCAACTCGAGTGATATCTAGA 684

DB 661 CTCAACTCGAGTGATATCTAGA 684
RESULT 2
AAF82934
ID AAF82934 standard; cDNA; 726 BP.
XX
XX AAF82934;
XX
XX 11-SEP-2003 (revised)
XX 29-JUN-2001 (first entry)
XX HIV-1 gp120 V3 loop-CD154 short form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX
XX Human immunodeficiency virus 1.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 13..726
FT CDS /*tag= a
FT sig_peptide 13..72
FT /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..198
FT /*tag= c
FT /note= "HIV-1 gp120 V3 loop coding sequence"
FT misc_feature 199..249
FT /*tag= d
FT /note= "[Gly4Ser]3 linker coding sequence"
FT misc_feature 250..726
FT /*tag= e
FT /note= "human CD154 short form extracellular domain coding sequence"
XX
XX WO200126608-A2.
XX
XX 19-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028414.
XX
XX 14-OCT-1999; 99US-0159690P.
XX
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
XX Ledbetter JA, Hayden-Ledbetter MS;
XX
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62339.
XX
XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
XX Example 1; Fig 2B; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
CC CD154 short form extracellular domain fusion protein linked by (Gly4Ser)3
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 726 BP; 220 A; 159 C; 171 G; 176 T; 0 U; 0 Other;
SQ
Query Match 92.2%; Score 630.4; DB 4; Length 726;

Best Local Similarity 94.1%; Pred. No. 1.4e-177;
Matches 683; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

QY 1 AAGCTTGCCGCGCATGCTGTATACCTCTCAGCTGTGTAGGACTACTTCTGTGTGTGGATCTCG 60
DB 1 AAGCTTGCCGCGCATGCTGTATACCTCTCAGCTGTGTAGGACTACTTCTGTGTGTGGATCTCG 60

QY 61 GCTTCGAGATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAAGAAAGAGTTA 120
DB 61 GCTTCGAGATCTGTAGTAATTAATTTGTACAAGACCCCAACAATACAAGAAAGAGTTA 120

QY 121 TCTATAGGACCGGAGAGACATTTATGCAAGAGAAACATATAGGAGATATAGACAA 180
DB 121 TCTATAGGACCGGAGAGACATTTATGCAAGAGAAACATATAGGAGATATAGACAA 180

QY 181 GCACATTGTAAACATTA-----GT 198
DB 181 GCACATTGTAAACATTAAGTGGTGGCGGTGCTCAGGAGCGGTGGATCTGGCGGTGAGGT 240

QY 199 CCGGATCCAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATCGGCA 258
DB 241 TCGGATCCAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATCGGCA 300

QY 259 CATGTCATAAGTGAGCCAGCAGTAACAAACATCTGTGTACAGTGGCTGAAAAAGGA 318
DB 301 CATGTCATAAGTGAGCCAGCAGTAACAAACATCTGTGTACAGTGGCTGAAAAAGGA 360

QY 319 TACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAA 378
DB 361 TACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAA 420

QY 379 AGACAAGGACTCTATTATATATATGATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCG 438
DB 421 AGACAAGGACTCTATTATATATATGATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCG 480

QY 439 AGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAATC 498
DB 481 AGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGATTGAGAGAATC 540

QY 499 TTACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTGGGGCAACAAATCCATTAC 558
DB 541 TTACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAAAACCTTGGGGCAACAAATCCATTAC 600

QY 559 TTGGGAGGAGTATTTCAATTTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCA 618
DB 601 TTGGGAGGAGTATTTGAAATTTGCAACACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCA 660

QY 619 ACCCAAGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTCGAGTGATAA 678
DB 661 ACCCAAGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTCGAGTGATAA 720

QY 679 TCTAGA 684
DB 721 TCTAGA 726

RESULT 3
ID AAF82931 standard; cDNA; 2028 BP.
XX AAF82931;
AC AAF82931;
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 13..2028
FT /*tag= a
FT sig_peptide 13..72
FT /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542
FT /*tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1551
FT /*tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 1552..2028
FT /*tag= e
FT /note= "human CD154 short form extracellular domain coding sequence"
XX WO200126608-A2.
PN 19-APR-2001.
PD 13-OCT-2000; 2000WO-US028414.
PR 14-OCT-1999; 99US-0159690P.
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
PI Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
DR P-PSDB; AAB62336.
XX DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.
PT Example 1; Fig 3B; 55pp; English.
XX The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154 short form extracellular domain fusion protein linked by a ProAspPro linker. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 2028 BP; 727 A; 378 C; 425 G; 498 T; 0 U; 0 Other;
Query Match 72.5%; Score 496.2; DB 4; Length 2028;
Best Local Similarity 92.4%; Pred. No. 2.5e-137;
Matches 522; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 120 ATCTATAGGACCGGAGAGCATTTTATGCAAGAGAAACAATATAGGAGATATAAGACA 179
DB 1464 ATATAAAGTAGTAAGAAATTGAACCAATAGGAGTAGCACCCACCGGCAAGAGAAGAAC 1523

QY 180 AGCAGATTTGAACATTAGTCCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCA 239
DB 1524 AGTGCAAAAGAGAAAAAGACCGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCA 1583

QY 240 GAATCCTCAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGT 299
DB 1584 GAATCCTCAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGT 1643

QY 300 ACAGTGGCTGAAAAAGGATACCTACCATGAGCAACAACTTGGTAACCTGGAAAAATGG 359
DB 1644 ACAGTGGCTGAAAAAGGATACCTACCATGAGCAACAACTTGGTAACCTGGAAAAATGG 1703

QY 360 GAAACAGCTGACCGTTAAAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTG 419
DB 360 GAAACAGCTGACCGTTAAAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTG 419

Db 1704 GAAACAGCTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTTGTG 1763
Qy 420 TTCCAAATCGGAGAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCC 479
Db 1764 TTCCAAATCGGAGAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCC 1823
Qy 480 CGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCGCAACCTTG 539
Db 1824 CGGTAGATTTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGCGCAACCTTG 1883
Qy 540 CGGGCAACAATCCATTCATCTTGGGAGGAGTATTTGAATGCAACAGAGTCTTCGGTGT 599
Db 1884 CGGGCAACAATCCATTCATCTTGGGAGGAGTATTTGAATGCAACAGAGTCTTCGGTGT 1943
Qy 600 TGTCNAATGTGACTGATCCAAAGCAAGTCAGCATGGCAGTGGCTTCACGTCTCTTGGCTT 659
Db 1944 TGTCNAATGTGACTGATCCAAAGCAAGTCAGCATGGCAGTGGCTTCACGTCTCTTGGCTT 2003
Qy 660 ACTCAAACTCGAGTGATAATCTAGA 684
Db 2004 ACTCAAACTCGAGTGATAATCTAGA 2028

RESULT 4
AAF82933
ID AAF82933 standard; cDNA; 865 BP.
AC AAF82933;
XX
XX 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX
DE HIV-1 gp120 V3 loop-CD154 long form extracellular domain fusion cDNA.
XX
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX
OS Human immunodeficiency virus 1.
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FH CDS 13..865
FT /*tag= a
FT sig_peptide 13..72
FT /*cdg= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..198
FT /*tag= c
FT /note= "HIV-1 gp120 V3 loop coding sequence"
FT misc_feature 199..207
FT /*tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 208..865
FT /*tag= e
FT /note= "human CD154 long form extracellular domain coding sequence"
XX
XX WO200126608-A2.
XX
XX 19-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028414.
XX
XX 14-OCT-1999; 99US-0159690P.
XX
XX (LEDB/) LEDBETTER J A.
XX (HAYD/) HAYDEN-LEDBETTER M S.
XX
XX Ledbetter JA, Hayden-Ledbetter MS;
XX WPI; 2001-281790/29.
XX P-PSDB; AAB62338.

XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
XX Example 1; Fig 2A; 55pp; English.
XX
XX The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
CC CD154 long form extracellular domain fusion protein linked by ProAspPro
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 865 BP; 290 A; 174 C; 192 G; 209 T; 0 U; 0 Other;
SQ
Query Match 72.2%; Score 494; DB 4; Length 865;
Best Local Similarity 79.2%; Pred. No. 8e-137;
Matches 684; Conservative 0; Mismatches 0; Indels 180; Gaps 1;
Qy 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Db 1 AAGCTTGGCGCATGCTGTATACCTCTCAGCTGTAGGACTACTTCTGTTTGGATCTCG 60
Qy 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCACCAACAATACAAGAGAGTTA 120
Db 61 GCTTCGAGATCTGTAGTAATTAATTGTACAAGACCACCAACAATACAAGAGAGTTA 120
Qy 121 TCTATAGGACCAGGAGAGCAATTTTATGCAAGAGAAACATAAATAGGAGATATAAGACAA 180
Db 121 TCTATAGGACCAGGAGAGCAATTTTATGCAAGAGAAACATAAATAGGAGATATAAGACAA 180
Qy 181 GCACATTGTATACATTAGTCCGATCC----- 206
Db 181 GCACATTGTATACATTAGTCCGATCCAAAGAGTTGGACAAGATAGAAAGAAAT 240
Qy 207 ----- 206
Db 241 CTTCAATGAAGATTTTGTATTTCATGNAACGATACAGATGCACACAGGAGAGAAATCC 300
Qy 207 ----- 206
Db 301 TTATCCTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATA 360
Qy 207 -----AGAAACAGCTTTGAAATGCAGGAGGATCATCAG 240
Db 361 ATGTTAAACAAAGAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAGGAGGATCATCAG 420
Qy 241 AATCCTCAAAATTCGGGCACATGTATAGTGCAGGCGCAGGATGAAACACATCTCTGTGTTA 300
Db 421 AATCCTCAAAATTCGGGCACATGTATAGTGCAGGCGCAGGATGAAACACATCTCTGTGTTA 480
Qy 301 CAGTGGGCTGAAAAGAGGATCTTACACCATGAGCAACAACTTGGTAACTCCCTGGAATGGG 360
Db 481 CAGTGGGCTGAAAAGAGGATCTTACACCATGAGCAACAACTTGGTAACTCCCTGGAATGGG 540
Qy 361 AAAAGAGTGCAGGTTAAAAGACAAGGACTCTTATATATATATGCCCCAGTCACTTCTGT 420
Db 541 AAAAGAGTGCAGGTTAAAAGACAAGGACTCTTATATATATGCCCCAGTCACTTCTGT 600
Qy 421 TCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCC 480
Db 601 TCCAAATCGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCC 660
Qy 481 GGTAGATTTCGAGAGAAATCTTACTCAGAGTGCAGGATGCAATACCCAGTTCGCGCAACCTTGC 540
Db 661 GGTAGATTTCGAGAGAAATCTTACTCAGAGTGCAGGATGCAATACCCAGTTCGCGCAACCTTGC 720
Qy 541 GGGCAACAATCCATTCACCTTGGAGAGGATTTGAAATGCAACAGGTCCTTCGGTGT 600
Db 721 GGGCAACAATCCATTCACCTTGGAGAGGATTTGAAATGCAACAGGTCCTTCGGTGT 780

QY 601 GTCAATGTGACTGATCCCAAGCCAGTGGACATGGCGTTCACGTCTTGGCTTA 660
 |||||
 Db 781 GTCAATGTGACTGATCCCAAGCCAGTGGACATGGCGTTCACGTCTTGGCTTA 840
 |||||
 QY 661 CTCAAACTCGAGTGATTAATCTAGA 684
 |||||
 Db 841 CTCAAACTCGAGTGATTAATCTAGA 864
 |||||

RESULT 5
 AAF82930
 ID AAF82930 standard; cDNA; 2070 BP.
 XX
 AC AAF82930;
 XX
 DT 11-SEP-2003 (revised)
 DT 29-JUN-2001 (first entry)
 XX
 DE HIV-1 gp120-human CD154 short form extracellular domain fusion cDNA.
 XX
 KW Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
 KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
 KW HIV-1; gp120; human; CD154; fusion protein; ss.
 XX

OS Human immunodeficiency virus 1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 13..2070
 FT /*tag= a
 FT sig_peptide 13..72
 FT /*tag= b
 FT misc_feature 73..1542
 FT /*note= "synthetic secretory signal peptide"
 FT /*tag= c
 FT misc_feature 1543..1593
 FT /*tag= d
 FT /*note= "[Gly4Ser]3 linker coding sequence"
 FT misc_feature 1594..2070
 FT /*tag= e
 FT /*note= "human CD154 short form extracellular domain coding sequence"

WO200126608-A2.
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028414.
 XX
 PR 14-OCT-1999; 99US-0159690P.
 XX
 PA (LEDB/) LEDBETTER J A.
 PA (HAYD/) HAYDEN-LEDBETTER M S.
 XX
 PI Ledbetter JA, Hayden-Ledbetter MS;
 XX
 DR WPI; 2001-281790/29.
 DR P-P5DB; AAB62335.
 XX
 PT DNA vaccine for improving antigen-specific humoral and cellular immune responses, comprising one or more antigens linked to a domain that binds at least one receptor.
 PT
 XX Example 1; Fig 3B; 55pp; English.
 PS
 CC The invention provides a vaccine comprising one or more antigens linked to a domain that binds at least one receptor to improve the antigen-specific humoral and cellular immune response. The DNA vaccines induce strong antigen-specific humoral and cellular immune responses. The vaccine can be used against acquired immunodeficiency syndrome (AIDS). The present sequence represents a cDNA encoding a HIV-1 gp120-human CD154

CC short form extracellular domain fusion protein linked by (Gly4Ser)3
 CC linker. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 2070 BP; 733 A; 380 C; 450 G; 507 T; 0 U; 0 Other;

Query Match 70.9%; Score 485; DB 4; Length 2070;
 Best Local Similarity 100.0%; Pred. No. 5.5e-134;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGCAC 259
 |||||
 Db 1586 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGCAC 1645
 |||||
 QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAAGGAT 319
 |||||
 Db 1646 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGAAAAAGGAT 1705
 |||||
 QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTGGRAAATGGGAACAGCTGACCGTTAAAA 379
 |||||
 Db 1706 ACTACACCATGAGCAACAACCTTGGTAACCTGGRAAATGGGAACAGCTGACCGTTAAAA 1765
 |||||
 QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
 |||||
 Db 1766 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1825
 |||||
 QY 440 GTCAAGTCTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 499
 |||||
 Db 1826 GTCAAGTCTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGATTCGAGAGAATCT 1885
 |||||
 QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCCT 559
 |||||
 Db 1886 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAACAATCCATTCCT 1945
 |||||
 QY 560 TGGGAGGAGTATTGAAATTGCAACCCAGGTGCTTCGGTGTGTCAATGTACTGATCCAA 619
 |||||
 Db 1946 TGGGAGGAGTATTGAAATTGCAACCCAGGTGCTTCGGTGTGTCAATGTACTGATCCAA 2005
 |||||
 QY 620 GCCAAGTGAGCCATGGCAGTCTGCCTTCAAGTCCCTTTGGCTTACTCAAACTCGAGTGAAT 679
 |||||
 Db 2066 GCCAAGTGAGCCATGGCAGTCTGCCTTCAAGTCCCTTTGGCTTACTCAAACTCGAGTGAAT 2065
 |||||
 QY 680 CTAGA 684
 |||||
 Db 2066 CTAGA 2070

RESULT 6

ABK89858
 ID ABK89858 standard; DNA; 1290 BP.
 XX
 AC ABK89858;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Synthetic mouse/human chimeric fusion gene #6.
 XX
 KW Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
 KW neuroprotective; gene therapy; single chain antibody; variable fragment;
 KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
 KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
 KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
 KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
 KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
 KW ulcerative colitis; inflammatory bowel disease; immunological effector;
 KW cell mediated cytotoxicity; complement dependent cytotoxicity;
 KW complement fixation; gene; ds; mouse; human.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers

```
FT misc_feature 1. .808
FT /tag= b
FT /note= "Murine anti-human CD20 single chain antibody
FT variable fragment (scFv)"
FT CDS
FT 13. .1281
FT /tag= a
FT /product= "Mouse/human chimeric fusion protein"
FT 814. .1275
FT /tag= c
FT /note= "Human extracellular domain short form CD154"
XX
XX WO200256910-A1.
XX
XX 25-JUL-2002.
XX
XX 17-JAN-2002; 2002WO-US001487.
XX
XX 17-JAN-2001; 2001US-00765208.
XX (GENE-) GENE-CRAFT INC.
XX
XX Ledbetter JA, Hayden-Ledbetter M;
XX
XX WPI; 2002-599691/64.
XX P-PSDB; ABG31032.
XX
XX New human binding domain-immunoglobulin fusion protein useful for
XX treating a subject having or suspected of having a B-cell disorder or
XX malignant condition e.g. rheumatoid arthritis.
XX
XX Disclosure; Fig 7C-D; 136pp; English.
XX
XX The invention describes a binding domain-immunoglobulin fusion protein
XX that is capable of at least one immunological activity, comprising a
XX binding domain polypeptide fused to an immunoglobulin hinge region
XX polypeptide capable of specifically binding to an antigen, or an
XX immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
XX to the hinge region polypeptide or to the CH2 constant region
XX polypeptide. The fusion protein is useful for treating a subject having
XX or suspected of having a B-cell disorder or malignant condition e.g.
XX rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
XX thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
XX erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,
XX psoriasis, scleroderma, cancer and inflammatory bowel disease such as
XX Chron's disease and ulcerative colitis. The fusion protein retains the
XX ability to participate in well known immunological effector activities
XX including antibody dependent cell mediated cytotoxicity and/or complement
XX fixation in complement dependent cytotoxicity, despite having structures
XX that would not be expected to be capable of promoting the effector
XX activities. It can be produced in substantial quantities that are
XX typically greater than those routinely attained with single-chain
XX antibody constructs. This sequence encodes a chimeric fusion protein
XX created from the mouse anti-human CD20 single chain antibody variable
XX fragment (scFv) and the human extracellular domain short form CD154
XX
XX Sequence 1290 BP; 336 A; 324 C; 321 G; 309 T; 0 U; 0 Other;
XX
XX Query Match 70.7%; Score 483.4; DB 6; Length 1290;
XX Best Local Similarity 99.8%; Pred. NO. 1.4e-133;
XX Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 200 CGGATCCGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 259
XX
XX 806 CTGATCCGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCTCAAAATGGCGCAC 865
XX
XX 260 ATGTCATAGTGAGCCGACGAGTAAACAAATCTGTGTACAGTGGGCTGAAAGGAT 319
XX
XX 866 ATGTCATAGTGAGCCGACGAGTAAACAAATCTGTGTACAGTGGGCTGAAAGGAT 925
XX
XX 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTAAAA 379
XX
XX 926 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAAAACAGCTGACCGTTAAAA 985
```

```
Qy 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTGA 439
Dy 986 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTGA 1045
Qy 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 499
Dy 1046 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 1105
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAACCTTGGCGGCAACAATCCATTCACT 559
Dy 1106 TACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAACCTTGGCGGCAACAATCCATTCACT 1165
Qy 560 TGGGAGGAGTATTTGAATTCGAACACAGTGCTTCGGTGTTCGATGTGCTGATCCAA 619
Dy 1166 TGGGAGGAGTATTTGAATTCGAACACAGTGCTTCGGTGTTCGATGTGCTGATCCAA 1225
Qy 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCGAGTGATAAT 679
Dy 1226 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCGAGTGATAAT 1285
Qy 680 CTAGA 684
Dy 1286 CTAGA 1290
XX
XX RESULT 7
XX ADD25461
XX ID ADD25461 standard; DNA; 1290 BP.
XX AC ADD25461;
XX
XX 15-JAN-2004 (first entry)
XX
XX Binding domain-immunoglobulin fusion protein-associated DNA #12.
XX
XX ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
XX antiarthritic; immunosuppressive; antidiabetic; antithyroid;
XX neuroprotective; hinge region; immunoglobulin heavy chain;
XX CH2 constant region; CH3 constant region; IgG1;
XX antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX Unidentified.
XX
XX US2003118592-A1.
XX
XX 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
XX
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0385691P.
XX
XX (GENE-) GENE-CRAFT INC.
XX
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
XX WPI; 2003-801317/75.
XX
XX New binding domain-immunoglobulin fusion protein, useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 22; 157pp; English.
XX
XX Unidentified
XX
XX Sequence 1290 BP; 336 A; 324 C; 321 G; 309 T; 0 U; 0 Other;
XX
XX Query Match 70.7%; Score 483.4; DB 10; Length 1290;
```

	Best Local Similarity	99.8%;	Pred. No. 1.4e-133;	Matches 484;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	200	CGGATCCAGAAAAACAGCTTTTGAATGCAGAAAGGTGATCAGAATTCCTCAAAATTCGGCGCAC	259					
Db	806	CTGATCCAGAAAACAGCTTTTGAATGCAGAAAGGTGATCAGAATTCCTCAAAATTCGGCGCAC	865					
Qy	260	ATGTCATAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319					
Db	866	ATGTCATAAGTGAGGCCAGCAGTAATAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	925					
Qy	320	ACTACACCATCAGCAACAACCTTGCTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAAA	379					
Db	926	ACTACACCATCAGCAACAACCTTGCTAACCTTGGAAATGGGAAACAGCTGACCGTTAAAAA	985					
Qy	380	GACAAGGACTCTATTATATCTATATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGA	439					
Db	986	GACAAGGACTCTATTATATCTATATGCCCAAGTCACCTTCTGTTCCTCAATCGGGAAAGCTTCGA	1045					
Qy	440	GTCAGCTCCATTTATATAGCAGCCTCTGCCTAAAGTCCCCGGTAGATATCGAGAGAAATCT	499					
Db	1046	GTCAGCTCCATTTATATAGCAGCCTCTGCCTAAAGTCCCCGGTAGATATCGAGAGAAATCT	1105					
Qy	500	TACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTCGGGCGCAACAATCCATTCACCT	559					
Db	1106	TACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTCGGGCGCAACAATCCATTCACCT	1165					
Qy	560	TGGGAGGAGTATTTGAATTCGCAACCGAGTGCTTCGGTGTGTTGTCCAATGTGACCTGATCCAA	619					
Db	1166	TGGGAGGAGTATTTGAATTCGCAACCGAGTGCTTCGGTGTGTTGTCCAATGTGACCTGATCCAA	1225					
Qy	620	GCCAAGTGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAAATCGAGTGATAAT	679					
Db	1226	GCCAAGTGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAAATCGAGTGATAAT	1285					
Qy	680	CTAGA 684						
Db	1286	CTAGA 1290						
RESULT 8								
ADD25590	ID	ADD25590	standard; DNA; 1290 BP.					
XX	AC	ADD25590;						
XX	DT	15-JAN-2004	(first entry)					
XX	DE	Binding domain-immunoglobulin fusion protein-associated DNA #79.						
KW	ds;	Binding domain; immunoglobulin; fusion protein; cytostatic;						
KW	antiarthritic;	immunosuppressive; antidiabetic; antithyroid;						
KW	neuroprotective;	hinge region; immunoglobulin heavy chain;						
KW	CH2 constant region;	CH3 constant region; IgG1;						
KW	antibody dependent cell-mediated cytotoxicity;	ADCC; complement fixation;						
KW	malignant condition;	B-cell disorder; melanoma; sarcoma;						
KW	rheumatoid arthritis;	myasthenia gravis; Grave's disease;						
KW	type I diabetes mellitus;	multiple sclerosis; autoimmune disease.						
XX	OS	Unidentified.						
XX	PN	US2003118592-A1.						
XX	PD	26-JUN-2003.						
XX	PF	25-JUL-2002; 2002US-00207655.						
XX	PR	17-JAN-2001; 2001US-0367358P.						
XX	PR	17-JAN-2002; 2002US-0005353O.						
XX	PA	03-JUN-2002; 2002US-0385691P.						
XX	XX	(GENE-) GENE-CRAFT INC.						

FT sig_peptide /*tag= a
 FT 13..72 /*tag= b
 FT /note= "synthetic secretory signal peptide"
 FT 73..198
 FT misc_feature /*tag= c
 FT /note= "HIV-1 gp120 V3 loop coding sequence"
 FT 199..249
 FT misc_feature /*tag= d
 FT /note= "[Gly4Ser]3 linker coding sequence"
 FT 250..906
 FT misc_feature /*tag= e
 FT /note= "human CD154 long form extracellular domain coding
 FT sequence"
 FT
 PN WO200126608-A2.
 XX
 XX 19-APR-2001.
 XX
 XX 13-OCT-2000; 2000WO-US028414.
 XX
 XX 14-OCT-1999; 99US-0159690P.
 XX
 XX (LEDB/) LEDBETTER J A.
 XX (HAYD/) HAYDEN-LEDBETTER M S.
 XX
 XX Ledbetter JA, Hayden-Ledbetter MS;
 XX
 XX WPI; 2001-281790/29.
 XX P-PSDB; AAB62337.
 XX
 XX DNA vaccine for improving antigen-specific humoral and cellular immune
 XX responses, comprising one or more antigens linked to a domain that binds
 XX at least one receptor.
 XX
 XX Example 1; Fig 2A; 55pp; English.
 XX
 XX The invention provides a vaccine comprising one or more antigens linked
 XX to a domain that binds at least one receptor to improve the antigen-
 XX specific humoral and cellular immune response. The DNA vaccines induce
 XX strong antigen-specific humoral and cellular immune responses. The
 XX vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
 XX present sequence represents a cDNA encoding a HIV-1 gp120 V3 loop- human
 XX CD154 long form extracellular domain fusion protein linked by (Gly4Ser)3
 XX linker. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 906 BP; 294 A; 179 C; 216 G; 217 T; 0 U; 0 Other;
 XX
 XX Query Match 70.0%; Score 478.6; DB 4; Length 906;
 XX Best Local Similarity 99.2%; Pred. No. 3.2e-132;
 XX Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 200 CGGATCCAGAAACAGCTTGAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
 DB 422 CGAAGAAGAAACAGCTTGAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 481
 QY 260 ATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTGAAAAGGAT 319
 DB 482 ATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGGCTGAAAAGGAT 541
 QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTAAAA 379
 DB 542 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTAAAA 601
 QY 380 GACAGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTCCAAATCGGAAGCTTGA 439
 DB 602 GACAGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTCCAAATCGGAAGCTTGA 661
 QY 440 GTCAGGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
 DB 662 GTCAGGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGGTAGATTTCGAGAGAATCT 721
 QY 500 TACTCAGAGCTGCAATAATACCCACAGTTCGGCAAACTTGGGGGCAACAATCCATTCCTACT 559

Db 722 TACTCAGAGCTGCAATAATACCCACAGTTCGGCAAACTTGGGGGCAACAATCCATTCCTACT 781
 QY 560 TGGGAGGAGTATTTCGAATTGCAACCCAGGTGCTTCGGTGTCTTCTCAATGTGACTGATCCAA 619
 Db 782 TGGGAGGAGTATTTCGAATTGCAACCCAGGTGCTTCGGTGTCTTCTCAATGTGACTGATCCAA 841
 QY 620 GCCAAGTCAGGCATGGGCACCTGGCTTCACGTCTCTTGGCTTACTCAAACTCGAGTGATTAAT 679
 Db 842 GCCAAGTCAGGCATGGGCACCTGGCTTCACGTCTCTTGGCTTACTCAAACTCGAGTGATTAAT 901
 QY 680 CTAGA 684
 Db 902 CTAGA 906
 Db
 RESULT 11
 ABK89857
 ID ABK89857 standard; DNA; 1470 BP.
 XX
 AC ABK89857;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Synthetic mouse/human chimeric fusion gene #5.
 XX
 KW Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
 KW neuroprotective; gene therapy; single chain antibody; variable fragment;
 KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
 KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
 KW Grave's disease; Hashimoto's thyroiditis; type 1 diabetes mellitus;
 KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
 KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
 KW ulcerative colitis; inflammatory bowel disease; immunological effector;
 KW cell mediated cytotoxicity; complement dependent cytotoxicity;
 KW complement fixation; gene; ds; mouse; human.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..808
 FT /*tag= b
 FT /note= "Murine anti-human CD20 single chain antibody
 FT variable fragment (scFv)"
 FT 13..1461
 FT CDS /*tag= a
 FT /product= "Mouse/human chimeric fusion protein"
 FT 814..1455
 FT misc_feature /*tag= c
 FT /note= "Human extracellular domain long form CD154"
 FT WO200256910-A1.
 XX
 XX 25-JUL-2002.
 XX
 XX 17-JAN-2002; 2002WO-US001487.
 XX
 XX 17-JAN-2001; 2001US-00765208.
 XX
 XX (GENE-) GENE-CRAFT INC.
 XX
 XX Ledbetter JA, Hayden-Ledbetter M;
 XX
 XX WPI; 2002-599691/64.
 XX P-PSDB; ABG31031.
 XX
 XX New human binding domain-immunoglobulin fusion protein useful for
 XX treating a subject having or suspected of having a B-cell disorder or
 XX malignant condition e.g. rheumatoid arthritis.

PS Disclosure; Fig 7A-B; 136pp; English.

XX The invention describes a binding domain-immunoglobulin fusion protein that is capable of at least one immunological activity, comprising a binding domain polypeptide fused to an immunoglobulin hinge region polypeptide capable of specifically binding to an antigen, or an immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused to the hinge region polypeptide or to the CH2 constant region polypeptide. The fusion protein is useful for treating a subject having or suspected of having a B-cell disorder or malignant condition e.g. rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura, psoriasis, scleroderma, cancer and inflammatory bowel disease such as Chron's disease and ulcerative colitis. The fusion protein retains the ability to participate in well known immunological effector activities including antibody dependent cell mediated cytotoxicity and/or complement fixation in complement dependent cytotoxicity, despite having structures that would not be expected to be capable of promoting the effector activities. It can be produced in substantial quantities that are typically greater than those routinely attained with single-chain antibody constructs. This sequence encodes a chimeric fusion protein created from the mouse anti-human CD20 single chain antibody variable fragment (scFv) and the human extracellular domain long form CD154

XX Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;

Query Match 70.0%; Score 478.6; DB 6; Length 1470;
Best Local Similarity 99.2%; Pred. No. 3.9e-132;
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
DB 986 CGAAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 1045

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
DB 1046 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 1105

QY 320 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 1106 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 1165

QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCCAGTGTGATAAT 439
DB 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCCAGTGTGATAAT 1225

QY 440 GTCAGAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 499
DB 1226 GTCAGAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 1285

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAAATCCATTCACT 559
DB 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAAATCCATTCACT 1345

QY 560 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGCTCAATGTGATGATCCAA 619
DB 1346 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGCTCAATGTGATGATCCAA 1405

QY 620 GCCAAGTGGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCCAGTGTGATAAT 679
DB 1406 GCCAAGTGGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCCAGTGTGATAAT 1465

QY 680 CTAGA 684
DB 1466 CTAGA 1470

RESULT 12
ADD25460
ID ADD25460 standard; DNA; 1470 BP.
XX
AC ADD25460;

XX 15-JAN-2004 (first entry)

XX Binding domain-immunoglobulin fusion protein-associated DNA #11.

DE ds; Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid;

XX neuroprotective; hinge region; immunoglobulin heavy chain;

KW CH2 constant region; CH3 constant region; IgG1;

KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;

KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;

KW rheumatoid arthritis; myasthenia gravis; Grave's disease;

KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

OS US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUN-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

XX 17-JAN-2002; 2002US-00053530.

XX 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENE-CRAFT INC.

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

XX Disclosure; SEQ ID NO 21; 157pp; English.

XX Unidentified

XX Sequence 1470 BP; 410 A; 344 C; 366 G; 350 T; 0 U; 0 Other;

Query Match 70.0%; Score 478.6; DB 10; Length 1470;
Best Local Similarity 99.2%; Pred. No. 3.9e-132;
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
DB 986 CGAAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 1045

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
DB 1046 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAGGAT 1105

QY 320 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 1106 ACTACACCATGAGCAACAACTTGGTAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 1165

QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCCAGTGTGATAAT 439
DB 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAATCCAGTGTGATAAT 1225

QY 440 GTCAGAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 499
DB 1226 GTCAGAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCGAGAGAATCT 1285

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAAATCCATTCACT 559
DB 1286 TACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGGGCAACAAATCCATTCACT 1345

QY 560 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGCTCAATGTGATGATCCAA 619
DB 1346 TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGCTCAATGTGATGATCCAA 1405

QY 620 GCCAAGTGGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCCAGTGTGATAAT 679
DB 1406 GCCAAGTGGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTCCAGTGTGATAAT 1465

QY 680 CTAGA 684
DB 1466 CTAGA 1470

RESULT 12
ADD25460
ID ADD25460 standard; DNA; 1470 BP.
XX
AC ADD25460;

comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The fusion protein is capable of at least one immunological activity such as antibody dependent cell-mediated cytotoxicity and complement fixation, and is capable of specifically binding to an antigen. The hinge region polypeptide is selected from a mutated hinge region polypeptide that contains no cysteine residues (and that is derived from a wild-type immunoglobulin hinge region polypeptide having one or more cysteine residues) and a mutated hinge region polypeptide that contains one or more cysteine residues (and that is derived from a wild-type immunoglobulin hinge region polypeptide having two or more cysteine residues), a wild-type human immunoglobulin (Ig)A hinge region polypeptide, a mutated human IgA hinge region polypeptide that contains no cysteine residues (and that is derived from a wild-type human IgA region polypeptide) and a mutated human IgA hinge region polypeptide that contains one cysteine residue (and that is derived from a wild-type human IgA region polypeptide). Also included are an isolated polynucleotide encoding the novel fusion protein, a recombinant expression construct comprising the polynucleotide, a host cell transformed or transfected with the expression construct, producing the novel fusion protein (comprising immunoglobulin hinge region polypeptide, immunoglobulin heavy chain CH2 constant region polypeptide, immunoglobulin heavy chain CH3 constant region polypeptide, and immunoglobulin heavy chain CH1 constant region polypeptide) under conditions that permit expression of the novel fusion protein and isolating the binding domain-immunoglobulin fusion protein from the host cell culture), a pharmaceutical composition comprising the novel fusion protein in combination with a carrier and treating a subject having or suspected of having a malignant condition or a B-cell disorder (comprising administering to the patient an amount of the novel fusion protein). The mutated hinge region polypeptide exhibits a reduced ability to dimerize, relative to a wild-type human immunoglobulin G hinge region polypeptide. The binding domain polypeptide comprises at least one immunoglobulin variable region polypeptide selected from an immunoglobulin light chain variable region polypeptide and an immunoglobulin heavy chain variable region polypeptide, and optionally at least one linker peptide that is fused to the immunoglobulin variable region polypeptide. The immunoglobulin variable and constant region polypeptides are derived from a human immunoglobulin. The immunoglobulin heavy chain constant region CH2 and CH3 polypeptides are of an isotype selected from human IgG and human IgA. The antigen is selected from CD19, CD20, CD37, CD40 and L6. The binding domain polypeptide comprises a CD154 extracellular domain, and optionally, at least one immunoglobulin variable region polypeptide (e.g. mouse V1 and Vh regions forming single chain antibodies which bind to one of the above antigens). The composition and methods are useful in treating malignant conditions (e.g. cancer) and B-cell disorders, including diseases characterised by autoantibody production, such as rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune diseases. The present sequence encodes a fusion protein of the invention comprising mouse antibody V1 and Vh regions fused to either human Immunoglobulin sequence or CD154 extracellular domain.

Query Match 70.0%; Score 478.6; DB 11; Length 1470; Best Local Similarity 99.2%; Pred. No. 3.9e-132; Mismatches 481; Conservative 0; Gaps 0; Indels 0; Gaps 0;

200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 259
986 CGAAGAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 1045
260 ATGTCATAGTGAGCCAGCAGTAAACAACTGTGTTCAGTGGGCTGAAAAGGAT 319
1046 ATGTCATAGTGAGCCAGCAGTAAACAACTGTGTTCAGTGGGCTGAAAAGGAT 1105
320 ACTACACCATGACCAACTTGGTAACCTCGAAATGGGAACAGCTGACCGTTAAA 379
1106 ACTACACCATGACCAACTTGGTAACCTCGAAATGGGAACAGCTGACCGTTAAA 1165
380 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTTGTTCCAATCGGGAAGCTTGA 439

Db 1166 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTTGTTCCAATCGGGAAGCTTGA 1225
Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
Db 1226 GTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 1285
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAAACTTCGGGGCAACAATCCATTCACT 559
Db 1286 TACTCAGAGCTGCAAAATACCCACAGTTCCGCGCAAACTTCGGGGCAACAATCCATTCACT 1345
Qy 560 TGGGAGGAGTATTGAAATTCGAACACAGTGCTTCGGTGTTCGTTCAATGTGACTGATCAA 619
Db 1346 TGGGAGGAGTATTGAAATTCGAACACAGTGCTTCGGTGTTCGTTCAATGTGACTGATCAA 1405
Qy 620 GCCAAGTCAGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTCGAGTGTATAAT 679
Db 1406 GCCAAGTCAGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTCGAGTGTATAAT 1465
Qy 680 CTAGA 684
Db 1466 CTAGA 1470

RESULT 15
AAF82929
ID AAF82929 standard; cDNA; 2209 BP.
AC AAF82929;
XX
DT 11-SEP-2003 (revised)
DT 29-JUN-2001 (first entry)
XX HIV-1 gp120-human CD154 long form extracellular domain fusion CDNA.
XX Antigen; receptor; humoral; cellular; immune response; DNA vaccine;
KW acquired immunodeficiency syndrome; AIDS; immunostimulant; anti-HIV;
KW HIV-1; gp120; human; CD154; fusion protein; ss.
XX Human immunodeficiency virus 1.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..2209 /*tag= a
FT sig_peptide 13..72 /*tag= b
FT /note= "synthetic secretory signal peptide"
FT misc_feature 73..1542 /*tag= c
FT /note= "HIV-1 gp120 domain coding sequence"
FT misc_feature 1543..1551 /*tag= d
FT /note= "ProAspPro linker coding sequence"
FT misc_feature 1552..2209 /*tag= e
FT /note= "human CD154 long form extracellular domain coding sequence"
XX
PN WO200126608-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028414.
XX
PR 14-OCT-1999; 99US-0159690P.
XX (LEDB/) LEDBETTER J A.
PA (HAYD/) HAYDEN-LEDBETTER M S.
XX
PI Ledbetter JA., Hayden-ledbetter MS;
XX
DR WPI; 2001-281790/29.
DR P-PSDB; AAB62334.

XX DNA vaccine for improving antigen-specific humoral and cellular immune
PT responses, comprising one or more antigens linked to a domain that binds
PT at least one receptor.
XX
XX
PS Example 1; Fig 3A; 55pp; English.
XX
CC The invention provides a vaccine comprising one or more antigens linked
CC to a domain that binds at least one receptor to improve the antigen-
CC specific humoral and cellular immune response. The DNA vaccines induce
CC strong antigen-specific humoral and cellular immune responses. The
CC vaccine can be used against acquired immunodeficiency syndrome (AIDS). The
CC present sequence represents a cDNA encoding a HIV-1 gp120-human CD154
CC long form extracellular domain fusion protein linked by a ProAspPro
CC linker. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2209 BP; 801 A; 398 C; 470 G; 540 T; 0 U; 0 Other;

Query Match 70.0%; Score 478.6; DB 4; Length 2209;
Best Local Similarity 99.2%; Pred. No. 4.6e-132;
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTCAAAATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 259
DB 1724 CGAAGAAAGAAAACAGCTTTGAATATGCAAAAAGGTGATCAGAACTCCTCAAAATTCGGGCAC 1783

QY 260 ATGTCATAAGTGAGGCCAGCAGTAAGAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
DB 1784 ATGTCATAAGTGAGGCCAGCAGTAAGAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 1843

QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 1844 ACTACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 1903

QY 380 GACAAGGACTCTATTATATCTATGCCAAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 439
DB 1904 GACAAGGACTCTATTATATCTATGCCAAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA 1963

QY 440 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGGTAGATTGAGAGAAATCT 499
DB 1964 GTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGGTAGATTGAGAGAAATCT 2023

QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559
DB 2024 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 2083

QY 560 TGGGAGGAGTATTGAAATTGCAATCCAGTGTTCGGTGTCTTGTCAATGTGACTGATCCAA 619
DB 2084 TGGGAGGAGTATTGAAATTGCAATCCAGTGTTCGGTGTCTTGTCAATGTGACTGATCCAA 2143

QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCGAGTGATAAT 679
DB 2144 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAACTCGAGTGATAAT 2203

QY 680 CTAGA 684
DB 2204 CTAGA 2208

Search completed: November 12, 2004, 01:29:50
Job time : 226.368 secs

THIS PAGE BLANK

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:10:25 ; Search time 39.9199 Seconds
(without alignments)
12178.890 Million cell updates/sec

Title: US-09-687-864A-19
Perfect score: 684
Sequence: 1 aagcttgccgcacgtcgtgta.....aactcgagtgataatctaga 684

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.6	67.8	786	1	US-08-446-922-3
2	463.6	67.8	786	5	PCT-US93-10034-3
3	463.6	67.8	840	1	US-07-940-605A-1
4	463.6	67.8	840	1	US-08-184-422-7
5	463.6	67.8	840	1	US-08-360-923A-1
6	463.6	67.8	840	1	US-08-431-055-3
7	463.6	67.8	840	2	US-08-690-096-1
8	463.6	67.8	840	2	US-08-249-189-11
9	463.6	67.8	840	2	US-08-484-624A-11
10	463.6	67.8	840	2	US-08-477-733B-11
11	463.6	67.8	840	3	US-08-763-995-1
12	463.6	67.8	840	3	US-09-088-913A-11
13	463.6	67.8	840	3	US-08-589-771B-7
14	463.6	67.8	840	3	US-08-763-819-11
15	463.6	67.8	840	3	US-08-770-974-11
16	463.6	67.8	840	3	US-08-858-197-3
17	463.6	67.8	840	3	US-08-770-981-11
18	463.6	67.8	840	4	US-09-399-106-11
19	463.6	67.8	840	4	US-09-430-448-1
20	463.6	67.8	879	4	US-09-645-926A-1
21	463.6	67.8	929	1	US-08-446-922-10
22	463.6	67.8	929	2	US-08-249-189-20
23	463.6	67.8	929	2	US-08-484-624A-20
24	463.6	67.8	929	2	US-08-477-733B-20
25	463.6	67.8	929	3	US-09-088-913A-20
26	463.6	67.8	929	3	US-08-769-819-20
27	463.6	67.8	929	3	US-08-770-974-20

28	463.6	67.8	929	3	US-08-770-981-20	Sequence 20, Appl
29	463.6	67.8	929	4	US-08-399-106-20	Sequence 20, Appl
30	463.6	67.8	1425	2	US-08-249-189-15	Sequence 15, Appl
31	463.6	67.8	1425	2	US-08-484-624A-15	Sequence 15, Appl
32	463.6	67.8	1425	2	US-08-477-733B-15	Sequence 15, Appl
33	463.6	67.8	1425	3	US-09-088-913A-15	Sequence 15, Appl
34	463.6	67.8	1425	3	US-08-769-819-15	Sequence 15, Appl
35	463.6	67.8	1425	3	US-08-770-974-15	Sequence 15, Appl
36	463.6	67.8	1425	3	US-08-770-981-15	Sequence 15, Appl
37	463.6	67.8	1425	4	US-09-399-106-15	Sequence 15, Appl
38	463.6	67.8	1803	4	US-09-099-595-3	Sequence 3, Appl
39	463.6	67.8	1816	4	US-09-645-926A-5	Sequence 5, Appl
40	448.4	55.6	839	4	US-09-023-655-919	Sequence 919, App
41	366.4	53.6	633	4	US-09-322-409-77	Sequence 77, Appl
c 42	366.4	53.6	633	4	US-09-322-409-79	Sequence 79, Appl
c 43	366.4	53.6	633	4	US-09-451-527-77	Sequence 77, Appl
c 44	366.4	53.6	633	4	US-09-451-527-79	Sequence 79, Appl
45	366.4	53.6	780	4	US-09-322-409-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-446-922-3
; Sequence 3, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: 1..783
US-08-446-922-3

Query Match 67.8%; Score 463.6; DB 1; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.3e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGGATCCGAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
Db |||
Qy 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 373
Db |||
Qy 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db |||
Qy 374 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 433
Db |||
Qy 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
Db |||
Qy 434 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 493
Db |||
Qy 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTGTTCCTCAATCGGGAAGCTTCGA 439
Db |||
Qy 494 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTGTTCCTCAATCGGGAAGCTTCGA 553
Db |||
Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
Db |||
Qy 554 GTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 613
Db |||
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAATCCATTCACT 559
Db |||
Qy 614 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAATCCATTCACT 673
Db |||
Qy 560 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAA 619
Db |||
Qy 674 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAA 733
Db |||
Qy 620 GCCAAGTGAGCCATGGCAGCTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db |||
Qy 734 GCCAAGTGAGCCATGGCAGCTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 783
Db |||

RESULT 2
PCT-US93-10034-3
; Sequence 3, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
PCT-US93-10034-3

Query Match 67.8%; Score 463.6; DB 5; Length 786;
Best Local Similarity 99.1%; Pred. No. 1.3e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGGATCCGAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
Db |||
Qy 314 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 373
Db |||
Qy 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db |||
Qy 374 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAGGAT 433
Db |||
Qy 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
Db |||
Qy 434 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 493
Db |||
Qy 380 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTGTTCCTCAATCGGGAAGCTTCGA 439
Db |||
Qy 494 GACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTGTTCCTCAATCGGGAAGCTTCGA 553
Db |||
Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
Db |||
Qy 554 GTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 613
Db |||
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAATCCATTCACT 559
Db |||
Qy 614 TACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAACAATCCATTCACT 673
Db |||
Qy 560 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAA 619
Db |||
Qy 674 TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCATGTGACTGATCCAA 733
Db |||
Qy 620 GCCAAGTGAGCCATGGCAGCTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
Db |||
Qy 734 GCCAAGTGAGCCATGGCAGCTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 783
Db |||

RESULT 3
US-07-940-605A-1
; Sequence 1, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pernie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22...807

US-07-940-605A-1

Query Match 67.8%; Score 463.6; DB 1; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC	259
Db	335	CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC	394
Qy	260	ATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTCTACAGTGGGCTGAAAAAGGAT	319
Db	395	ATGTCATAGTGAGGCCAGCAGTAAACCAACATCTGTCTACAGTGGGCTGAAAAAGGAT	454
Qy	320	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCCGTTAAAA	379
Db	455	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCCGTTAAAA	514
Qy	380	GACAAGGACTCTATTATATCTATGATCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA	439
Db	515	GACAAGGACTCTATTATATCTATGATCCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA	574
Qy	440	GTCAGCTCCATTATATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTGAGAGAATCT	499
Db	575	GTCAGCTCCATTATATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTGAGAGAATCT	634
Qy	500	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAAATCCATTCACT	559
Db	635	TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCAACAAATCCATTCACT	694
Qy	560	TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGATCAATCAAA	619
Db	695	TGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAATGTGATCAATCAAA	754
Qy	620	GCCAAAGTCAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC	669
Db	755	GCCAAAGTCAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC	804

RESULT 4

US-08-184-422-7
Sequence 7, Application US/08184422
Patent No. 5565321
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSHAW, WILLIAM
APPLICANT: RENSHAW, BLAIR

APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
Prior Application DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831

US-08-184-422-7

Query Match 67.8%; Score 463.6; DB 1; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	200	CGGATCCAGAAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC	259
Db	359	CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC	418
Qy	260	ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTCTTACAGTGGGCTGAAAAAGGAT	319
Db	419	ATGTCATAAGTGAGGCCAGCAGTAAACCAACATCTGTCTTACAGTGGGCTGAAAAAGGAT	478
Qy	320	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCCGTTAAAA	379
Db	479	ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAAATGGGAAACAGCTGACCCGTTAAAA	538
Qy	380	GACAAGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA	439
Db	539	GACAAGGACTCTATTATATCTATGCCCAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGA	598
Qy	440	GTCAGCTCCATTATATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTGAGAGAATCT	499
Db	599	GTCAGCTCCATTATATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTGAGAGAATCT	658


```
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
; US-08-431-055-3

Query Match      67.8%; Score 463.6; DB 1; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCTCTCAAATTCGGGCAC 259
Db 335 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCTCTCAAATTCGGGCAC 394
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 454
QY 320 ACTACACCATGACCAACACTTGGTAACCTCGGAAATGGAAACAGCTGACCGTTAAAA 379
Db 455 ACTACACCATGACCAACACTTGGTAACCTCGGAAATGGAAACAGCTGACCGTTAAAA 514
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGA 439
Db 515 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGA 574
QY 440 GTCAAGCTCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCT 499
Db 575 GTCAAGCTCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCT 634
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAACAAATCCATTCCACT 559
Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAACAAATCCATTCCACT 694
QY 560 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db 695 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 754
QY 620 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
Db 755 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 804

RESULT 7
US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUPFO, ALEJANDRO
; APPLICANT: HOLLENAUGH, DIANE
; APPLICANT: HOLLENAUGH, DIANE
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
; US-08-431-055-3

Query Match      67.8%; Score 463.6; DB 1; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCTCTCAAATTCGGGCAC 259
Db 335 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCTCTCAAATTCGGGCAC 394
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db 395 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 454
QY 320 ACTACACCATGACCAACACTTGGTAACCTCGGAAATGGAAACAGCTGACCGTTAAAA 379
Db 455 ACTACACCATGACCAACACTTGGTAACCTCGGAAATGGAAACAGCTGACCGTTAAAA 514
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGA 439
Db 515 GACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAATCGGGAAGCTTCGA 574
QY 440 GTCAAGCTCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCT 499
Db 575 GTCAAGCTCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGATTCGAGAGAATCT 634
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAACAAATCCATTCCACT 559
Db 635 TACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAACAAATCCATTCCACT 694
QY 560 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db 695 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA 754
QY 620 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 669
Db 755 GCCAAGTGAGCCATGGCAGCTGGCTTCACGTCCTTTGGCTTACTCAAACCTC 804

RESULT 8
US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
```

[illegible]

TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11

Query Match 67.8%; Score 463.6; DB 2; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
DB 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 418
QY 260 ATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
DB 419 ATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 479 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
QY 380 GACAGGAGCTCTATTATATCTATGATCCCAAGTCACCTCTGTTCCCAATCGGGAAGCTTCGA 439
DB 539 GACAGGAGCTCTATTATATCTATGATCCCAAGTCACCTCTGTTCCCAATCGGGAAGCTTCGA 598
QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
DB 599 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT 658
QY 500 TACTCAGAGTCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 559
DB 659 TACTCAGAGTCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 718
QY 560 TGGGAGGAGTATTGAAATGCAACAGGCTTCGGTGTGTTGTCATGTGACTGATCCAA 619
DB 719 TGGGAGGAGTATTGAAATGCAACAGGCTTCGGTGTGTTGTCATGTGACTGATCCAA 778
QY 620 GCCAAGTGAGCCATGGCAGCTGCTTCAAGTCTTTGGCTTACTCAAACTC 669
DB 779 GCCAAGTGAGCCATGGCAGCTGCTTCAAGTCTTTGGCTTACTCAAACTC 828

RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-477-733B-11

Query Match 67.8%; Score 463.6; DB 2; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
DB 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 418
QY 260 ATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
DB 419 ATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 479 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
QY 380 GACAGGAGCTCTATTATATCTATGATCCCAAGTCACCTCTGTTCCCAATCGGGAAGCTTCGA 439
DB 539 GACAGGAGCTCTATTATATCTATGATCCCAAGTCACCTCTGTTCCCAATCGGGAAGCTTCGA 598
QY 440 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
DB 599 GTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAATCT 658
QY 500 TACTCAGAGTCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 559

Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGCAACAATCCATTCACT 718

Qy 560 TGGGAGGAGTATTGAAATGCAACAGAGTGTCTGCGTGTGTTGTCGAATGAGTATCAACAA 619

Db 719 TGGGAGGAGTATTGAAATGCAACAGAGTGTCTGCGTGTGTTGTCGAATGAGTATCAACAA 778

Qy 620 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTC 669

Db 779 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTC 828

RESULT 11

US-08-763-995-1

; Sequence 1, Application US/08763995

; Patent No. 6017527

; GENERAL INFORMATION:

; APPLICANT: MARASKOVSKY, EUGENE

; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMUNEX CORPORATION

; STREET: 51 UNIVERSITY STREET

; CITY: SEATTLE

; STATE: WASHINGTON

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Power Macintosh 7200/90

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/763,995

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/677,762

; FILING DATE: 10 JUL 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2845-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 840 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: CD40-L

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 46..831

US-08-763-995-1

Query Match

Best Local Similarity 67.8%; Score 463.6; DB 3; Length 840;

Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 200 CGGATCCGAAACAGCTTTGAAATGCAAAAGGATCAGAAATCTCAAAATTCGGGCAC 259

Db 359 CGAAGAAAGAAACAGCTTTGAAATGCAAAAGGATCAGAAATCTCAAAATTCGGGCAC 418

Qy 260 ATGTCTAAGTAGAGCCAGCAGTAGTAAAAACAACATCTGTGTTACAGTGGGCTCAAAAAGGAT 319

Db 419 ATGTCTAAGTAGAGCCAGCAGTAGTAAAAACAACATCTGTGTTACAGTGGGCTCAAAAAGGAT 478

Qy 320 ACTACACCATGAGCAACAACCTTGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 379

Db 479 ACTACACCATGAGCAACAACCTTGTAAACCTTGGAAAATGGGAAAACAGCTGACCGTTAAAA 538

Qy 380 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTGTGTTCCAAATCGGGAAGCTTCGA 439

Db 539 GACAAGGACTCTATTATATCTATGCCAAGTCACCTTGTGTTCCAAATCGGGAAGCTTCGA 598

Qy 440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCGCGTAGATTCCGAGAGAACTCT 499

Db 599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCGCGTAGATTCCGAGAGAACTCT 658

Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGGCAACAATCCATTCACT 559

Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGGCAACAATCCATTCACT 718

Qy 560 TGGGAGGAGTATTGAAATTCGAATTCGAACAGGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619

Db 719 TGGGAGGAGTATTGAAATTCGAATTCGAACAGGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778

Qy 620 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTC 669

Db 779 GCCAAGTCAGCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAACTC 828

RESULT 12

US-09-088-913A-11

; Sequence 11, Application US/09088913A

; Patent No. 6087329

; GENERAL INFORMATION:

; APPLICANT: ARMITAGE, RICHARD

; APPLICANT: FANSLOW, WILLIAM

; APPLICANT: SPRIGGS, MELANIE

; APPLICANT: SRINIVASAN, SUBHASHINI

; APPLICANT: GIBSON, MARYLOU

; APPLICANT: MORRIS, ARVIA E.

; APPLICANT: MCGREW, JEFFERY

; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMUNEX CORPORATION

; STREET: 51 UNIVERSITY STREET

; CITY: SEATTLE

; STATE: WASHINGTON

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/088,913A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/484,624

; FILING DATE:

; APPLICATION NUMBER: 08/477,733

; FILING DATE: June 07, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,703

; FILING DATE: October 23, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/805,723

; FILING DATE: December 5, 1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/783,707

; FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-09-088-913A-11

Query Match 67.8%; Score 463.6; DB 3; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
DB |||
QY 359 CGAAGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 418
DB |||
QY 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
DB |||
QY 419 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 478
DB |||
QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB |||
QY 479 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
DB |||
QY 380 GACAAGGACTCTATTATATCTATGCGCCAGTCACCTTCTGTTCATCGGGAAGCTTCGA 439
DB |||
QY 539 GACAAGGACTCTATTATATCTATGCGCCAGTCACCTTCTGTTCATCGGGAAGCTTCGA 598
DB |||
QY 440 GTCAAGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
DB |||
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCCAATTCCT 559
DB |||
QY 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCCAATTCCT 718
DB |||
QY 560 TGGGAGGAGTATTGAAATGCAACAGAGTCTTGGGTGTTGTCATGTGATGATCAAA 619
DB |||
QY 719 TGGGAGGAGTATTGAAATGCAACAGAGTCTTGGGTGTTGTCATGTGATGATCAAA 778
DB |||
QY 620 GCCAAGTCAGCATGGCAGCTGCTTCAGTCTCTTGGGCTTACTCAAACTC 669
DB |||
QY 779 GCCAAGTCAGCATGGCAGCTGCTTCAGTCTCTTGGGCTTACTCAAACTC 828
DB |||

RESULT 13
US-08-589-771B-7
Sequence 7, Application US/08589771B
Patent No. 6106832
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLON, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-08-589-771B-7

Query Match 67.8%; Score 463.6; DB 3; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
DB |||
QY 359 CGAAGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 418
DB |||
QY 260 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 319
DB |||
QY 419 ATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT 478
DB |||
QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 379
DB |||
QY 479 ACTACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGGAAACAGCTGACCGTTAAAA 538
DB |||
QY 380 GACAAGGACTCTATTATATCTATGCGCCAGTCACCTTCTGTTCATCGGGAAGCTTCGA 439
DB |||
QY 539 GACAAGGACTCTATTATATCTATGCGCCAGTCACCTTCTGTTCATCGGGAAGCTTCGA 598
DB |||
QY 440 GTCAAGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
DB |||
QY 599 GTCAAGCTCCATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTTCGAGAGAATCT 658
DB |||
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAACAAATCCCAATTCCT 559
DB |||

Db 659 TACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGGGCAACAATCCATTCACT 718
Qy 560 TGGGAGGAGTATTGAAATGCAACACAGTGCTTCGGTGTGTTGTCATGTAAGTGAATGCAAC 619
Db 719 TGGGAGGAGTATTGAAATGCAACACAGTGCTTCGGTGTGTTGTCATGTAAGTGAATGCAAC 778
Qy 620 GCCAAGTCAGCAGTCAGGCTGCTTACGTCCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTCAGCAGTCAGGCTGCTTACGTCCTTTGGCTTACTCAAACTC 828

RESULT 14

US-08-769-819-11
; Sequence 11, Application US/08769819
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:

; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
US-08-769-819-11
Query Match 67.8%; Score 463.6; DB 3; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 200 CGGATCCAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 259
Db 359 CGAAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATTCGGGCAC 418
Qy 260 ATGTCATAAGTGAGGCCAGCAGTAGTAAACCAACATCTGTGTTACAGTGGGCTCAAAAAGGAT 319
Db 419 ATGTCATAAGTGAGGCCAGCAGTAGTAAACCAACATCTGTGTTACAGTGGGCTGAAAAGGAT 478
Qy 320 ACTACACCATGAGCAACAACCTTGGTAAACCCCTGGAAAAATGGGAAAACAGCTGACCCGTAAAAA 379
Db 479 ACTACACCATGAGCAACAACCTTGGTAAACCCCTGGAAAAATGGGAAAACAGCTGACCCGTAAAAA 538
Qy 380 GACAAGGACTCTATTATATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 539 GACAAGGACTCTATTATATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
Qy 440 GTCAAGCTCCATTATATAGCCAGCCTCTGCGCTAAAGTCCCGGTAGATTTCGAGAGAATCT 499
Db 599 GTCAAGCTCCATTATATAGCCAGCCTCTGCGCTAAAGTCCCGGTAGATTTCGAGAGAATCT 658
Qy 500 TACTCAGAGCTGCAAAATACCCACAGTTTCGCCCAACCTTGGGGGCAACAATCCATTCACT 559
Db 659 TACTCAGAGCTGCAAAATACCCACAGTTTCGCCCAACCTTGGGGGCAACAATCCATTCACT 718
Qy 560 TGGGAGGAGTATTGAAATGCAACACAGTGCTTCGGTGTGTTGTCATGTAAGTGAATGCAAC 619
Db 719 TGGGAGGAGTATTGAAATGCAACACAGTGCTTCGGTGTGTTGTCATGTAAGTGAATGCAAC 778
Qy 620 GCCAAGTCAGCAGTCAGGCTGCTTACGTCCTTTGGCTTACTCAAACTC 669
Db 779 GCCAAGTCAGCAGTCAGGCTGCTTACGTCCTTTGGCTTACTCAAACTC 828

RESULT 15

US-08-770-974-11
; Sequence 11, Application US/08770974
; Patent No. 6290972
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,974
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733

Search completed: November 12, 2004, 12:57:46
Job time : 41.1199 secs

;; FILING DATE: 02-AUG-1995
;; APPLICATION NUMBER: 08/249,189
;; FILING DATE: May 24, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/969,703
;; FILING DATE: October 23, 1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/805,723
;; FILING DATE: December 5, 1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/783,707
;; FILING DATE: October 25, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia A.
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2802-D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 2065870430
;; TELEFAX: 2065870606
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 840 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; CLONE: CD40-L
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 46...831
US-08-770-974-11

Query Match 67.8%; Score 463.6; DB 3; Length 840;
Best Local Similarity 99.1%; Pred. No. 1.4e-137;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	200	CGGATCCGAGAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCAC	259
Db	359	CGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCTCAAAATTCGGGCAC	418
QY	260	ATGTCATAAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT	319
Db	419	ATGTCATAAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGAT	478
QY	320	ACTACACCATGAGCAACAACTTGGTAAACCTCGGAAAAATGGGAAAACAGCTGACCGTTAAAA	379
Db	479	ACTACACCATGAGCAACAACTTGGTAAACCTCGGAAAAATGGGAAAACAGCTGACCGTTAAAA	538
QY	380	GACAGGACTCTATTATATCTATGCGCCAGTCACTCTCTGTTCCTCAATCGGAGCTTCGA	439
Db	539	GACAGGACTCTATTATATCTATGCGCCAGTCACTCTCTGTTCCTCAATCGGAGCTTCGA	598
QY	440	GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAACTCT	499
Db	599	GTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTTCGAGAGAACTCT	658
QY	500	TACTCAGAGCTCAAAATACCCACAGTTCGCGCAAAACCTTTGCGGGCAACAAATCCATTCACT	559
Db	659	TACTCAGAGCTCAAAATACCCACAGTTCGCGCAAAACCTTTGCGGGCAACAAATCCATTCACT	718
QY	560	TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA	619
Db	719	TGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGTCAATGTGACTGATCCAA	778
QY	620	GCCAAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGGCTTACTCAAACTC	669
Db	779	GCCAAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGGCTTACTCAAACTC	828

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

OV 200 CCGATCCAGAAAACAGCTTTGAAAATGCCAAAAGGTGATCAGAAATCCTCAAAATTGCGGCAC 259

	Query Match	70.0%;	Score 478.6;	DB 15;	Length 1470;
	Best Local Similarity	99.2%;	Pred. No. 3.4e-133;		
	Matches 481;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	200	CGGATCCGAAAAACAGCTTTTGAAATGCAAAAAAGGTGATCAGAAATCTTCAAAATTCGGGCAC	259		
Db	986	CGAAGAAGAAAAACAGCTTTTGAAATGCAAAAAAGGTGATCAGAAATCTTCAAAATTCGGGCAC	1045		
Qy	260	ATGTCATAAGTGAGCGCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	319		
Db	1046	ATGTCATAAGTGAGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT	1105		
Qy	320	ACTACACATGAGCAACAACCTTGTTAAACCTCGGAAAAATGGAAACACGCTGACCGTTAAAAA	379		
Db	1106	ACTACACATGAGCAACAACCTTGTTAAACCTCGGAAAAATGGAAACACGCTGACCGTTAAAAA	1165		
Qy	380	GACAAGACCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	439		
Db	1166	GACAAGACCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA	1225		
Qy	440	GTCAAGTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGAATTCGAGAGAAATCT	499		
Db	1226	GTCAAGTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGAATTCGAGAGAAATCT	1285		

Db 1406 GCCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGCTTACTCAAACTCGAGTGATAAT 1465
QY 680 CTAGA 684
Db 1466 CTAGA 1470

RESULT 6

US-10-053-530-21
; Sequence 21, Application US/10053530
; Publication No. US20030133939A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey, Martha
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053.530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 21
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MOUSE-HUMAN HYBRID
; NAME/KEY: misc feature
; LOCATION: (1)..(808)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV
; NAME/KEY: misc feature
; LOCATION: (814)..(1455)
; OTHER INFORMATION: HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154
US-10-053-530-21

Query Match 70.0%; Score 478.6; DB 15; Length 1470;
Best Local Similarity 99.2%; Pred. No. 3.4e-133; Indels 0; Gaps 0;
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 259
Db 986 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 1045
QY 260 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db 1046 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 1105
QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 1106 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAA 1165
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 1166 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1225
QY 440 GTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACT 499
Db 1226 GTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACT 1285
QY 500 TACTCAGAGCTGCAAAATCCCAAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 1286 TACTCAGAGCTGCAAAATCCCAAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1345
QY 560 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTTCGTAATGTGACTGATCCAA 619
Db 1346 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTTCGTAATGTGACTGATCCAA 1405
QY 620 GCCAAGTGAGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAAACTCGAGTGATAAT 679
Db 1406 GCCAAGTGAGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAAACTCGAGTGATAAT 1465
QY 680 CTAGA 684

Db 1466 CTAGA 1470

RESULT 7

US-10-312-245-6
; Sequence 6, Application US/10312245
; Publication No. US20030219419A1
; GENERAL INFORMATION:
; APPLICANT: University of Louisville Research Foundation, Inc.
; APPLICANT: Shirwan, Haval
; TITLE OF INVENTION: Methods and Compositions for Altering Cell Membrane Function.
; FILE REFERENCE: 1160.015W01
; CURRENT APPLICATION NUMBER: US/10/312.245
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/215,580
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1566
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SA-CD40L
US-10-312-245-6

Query Match 68.1%; Score 466; DB 15; Length 1566;
Best Local Similarity 98.9%; Pred. No. 2.2e-129; Indels 0; Gaps 0;
Matches 469; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 259
Db 766 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 825
QY 260 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 319
Db 826 ATGTCATAAGTGAGCCAGCAGTAACAACATCTGTGTACAGTGGGCTGAAAAGGAT 885
QY 320 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
Db 886 ACTACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAGCTGACCGTTAAAA 945
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db 946 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 1005
QY 440 GTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACT 499
Db 1006 GTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGATTTCGAGAGAACT 1065
QY 500 TACTCAGAGCTGCAAAATCCCAAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 559
Db 1066 TACTCAGAGCTGCAAAATCCCAAGTTCGCCAAACCTTGGGGCAACAATCCATTCACT 1125
QY 560 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTTCGTAATGTGACTGATCCAA 619
Db 1126 TGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTTCGTAATGTGACTGATCCAA 1185
QY 620 GCCAAGTGAGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAAACTCGAGT 673
Db 1186 GCCAAGTGAGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAAACTCGAAT 1239

RESULT 8

US-09-365-940-11
; Sequence 11, Application US/09365940
; Publication No. US20030091564A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI


```
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-294-176-1

Query Match      67.8%; Score 463.6; DB 14; Length 840;
Best Local Similarity 99.1%; Pred. No. 8.5e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

200 CGGATCCAGAAAAACAGCTTTTCAAAATGCAAAAAGGTGATCAGAAATCCCTCAAAATTCGGGCAC 259
Db      |||
359 CGAAGAAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCCTCAAAATTCGGGCAC 418
      |||
260 ATGTCTATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db      |||
419 ATGTCTATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
      |||
320 ACTACACCATGAGCAACAACCTTGTGTAACCTTGGAAAAATGGAAAAACAGCTGACCGTTAAAA 379
Db      |||
479 ACTACACCATGAGCAACAACCTTGTGTAACCTTGGAAAAATGGAAAAACAGCTGACCGTTAAAA 538
      |||
380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db      |||
539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
      |||
440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
Db      |||
599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 658
      |||
500 TACTCAGAGCTGCAAAATACCAACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACT 559
Db      |||
659 TACTCAGAGCTGCAAAATACCAACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACT 718
      |||
560 TGGGAGGAGTATTGAAATGCAACACAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db      |||
719 TGGGAGGAGTATTGAAATGCAACACAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778
      |||
620 GCCAAGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 669
      |||
779 GCCAAGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 828
      |||

RESULT 10
US-10-200-242-11
; Sequence 11, Application US/10200242
; Publication No. US2003014182A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11

; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-294-176-1

Query Match      67.8%; Score 463.6; DB 14; Length 840;
Best Local Similarity 99.1%; Pred. No. 8.5e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

200 CGGATCCAGAAAAACAGCTTTTCAAAATGCAAAAAGGTGATCAGAAATCCCTCAAAATTCGGGCAC 259
Db      |||
359 CGAAGAAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCCTCAAAATTCGGGCAC 418
      |||
260 ATGTCTATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
Db      |||
419 ATGTCTATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
      |||
320 ACTACACCATGAGCAACAACCTTGTGTAACCTTGGAAAAATGGAAAAACAGCTGACCGTTAAAA 379
Db      |||
479 ACTACACCATGAGCAACAACCTTGTGTAACCTTGGAAAAATGGAAAAACAGCTGACCGTTAAAA 538
      |||
380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 439
Db      |||
539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAATCGGGAAGCTTCGA 598
      |||
440 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 499
Db      |||
599 GTCAAGCTCCATTATAGCCAGCCTCTGCCTTAAAGTCCCCCGGTAGATTTCGAGAGAATCT 658
      |||
500 TACTCAGAGCTGCAAAATACCAACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACT 559
Db      |||
659 TACTCAGAGCTGCAAAATACCAACAGTTCGCGCAAAACCTTGGCGGCAACAATCCATTCACT 718
      |||
560 TGGGAGGAGTATTGAAATGCAACACAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
Db      |||
719 TGGGAGGAGTATTGAAATGCAACACAGTCTTCGGTGTGTTGTCAATGTGACTGATCCAA 778
      |||
620 GCCAAGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 669
      |||
779 GCCAAGTGAGCCATGGCAGTGGCTTCAGCTCCTTTGGCTTACTCAAACTC 828
      |||

RESULT 11
US-10-200-242-11
; Sequence 11, Application US/10200242
; Publication No. US20040006006A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(831)
; OTHER INFORMATION:
US-10-200-242-11
```

Query Match 67.8%; Score 463.6; DB 16; Length 840;
Best Local Similarity 99.1%; Pred. No. 8.5e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
DB |||||
DB 359 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 418
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
DB |||||
DB 419 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 478
QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAACAGCTGACCGTTAAAA 379
DB |||||
DB 479 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAACAGCTGACCGTTAAAA 538
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 439
DB |||||
DB 539 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 598
QY 440 GTCAAGCTCCATTATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 499
DB |||||
DB 599 GTCAAGCTCCATTATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 658
QY 500 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559
DB |||||
DB 659 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 718
QY 560 TGGGAGGAGTATTGAAATGCAACAGTCTTGGGTGTTGTCAATGTGACTGATCCAA 619
DB |||||
DB 719 TGGGAGGAGTATTGAAATGCAACAGTCTTGGGTGTTGTCAATGTGACTGATCCAA 778
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
DB |||||
DB 779 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 828

RESULT 12
US-10-242-212-1
; Sequence 1, Application US/10242212
; Publication No. US200300996441
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEEMA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242,212
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/09/645,926
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-212-1

Query Match 67.8%; Score 463.6; DB 14; Length 879;
Best Local Similarity 99.1%; Pred. No. 8.7e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 259
DB |||||
DB 335 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTCGGGCAC 394
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 319
DB |||||
DB 395 ATGTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGAT 454
QY 320 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAACAGCTGACCGTTAAAA 379
DB |||||

Db 455 ACTACACCATGAGCAACAACTTGGTAACCCCTGGAATAATGGGAACAGCTGACCGTTAAAA 514
QY 380 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 439
DB |||||
DB 515 GACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTTCCAAATCGGGAAGCTTCGA 574
QY 440 GTCAAGCTCCATTATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 499
DB |||||
DB 575 GTCAAGCTCCATTATTATAGCCAGCTCTGCCTAAAGTCCCGGTAGATTCCAGAGAATCT 634
QY 500 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 559
DB |||||
DB 635 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACT 594
QY 560 TGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTGTTGTCAATGTGACTGATCCAA 619
DB |||||
DB 695 TGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTGTTGTCAATGTGACTGATCCAA 754
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
DB |||||
DB 755 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 804

RESULT 13
US-09-365-940-20
; Sequence 20, Application US/09365940
; Publication No. US200300915641
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,940
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Human CD40-L trimer
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 65..142
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 65..886
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 143..886
;
US-09-365-940-20

Query Match      67.8%; Score 463.6; DB 10; Length 929;
Best Local Similarity 99.1%; Pred. No. 9e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGGGCAC 259
DB 414 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGGGCAC 473
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTTACAGTGGGCTGAAAAGGAT 319
DB 474 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTTACAGTGGGCTGAAAAGGAT 533
QY 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 534 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 593
QY 380 GACAAGGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 439
DB 594 GACAAGGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 653
QY 440 GTCAGAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 499
DB 654 GTCAGAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 713
QY 500 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 559
DB 714 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 773
QY 560 TGGGAGGAGTATTTGAAATGCAACAGAGTGTCTGGTGTGTTGTCAATGTGACTGATCCAA 619
DB 774 TGGGAGGAGTATTTGAAATGCAACAGAGTGTCTGGTGTGTTGTCAATGTGACTGATCCAA 833
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
DB 834 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 883

RESULT 14
US-10-200-242-20
; Sequence 20, Application US/10200242
; Publication No. US20030144182A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
; FILE REFERENCE: 2802-N
; CURRENT APPLICATION NUMBER: US/10/200,242
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 09/365,940
```

```
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 08/769,819
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 08/484,624
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/249,189
; PRIOR FILING DATE: 1994-05-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (65)..(883)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (143)..( )
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (65)..(142)
; OTHER INFORMATION:
;
US-10-200-242-20

Query Match      67.8%; Score 463.6; DB 15; Length 929;
Best Local Similarity 99.1%; Pred. No. 9e-129;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 200 CGGATCCAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGGGCAC 259
DB 414 CGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGGGCAC 473
QY 260 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTTACAGTGGGCTGAAAAGGAT 319
DB 474 ATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTTACAGTGGGCTGAAAAGGAT 533
QY 320 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 379
DB 534 ACTACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAGCTGACCGTTAAAA 593
QY 380 GACAAGGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 439
DB 594 GACAAGGACTCTATTATATCTATGATGCCAAGTCACTTCTGTTCCTCAATCGGGAAGCTTCGA 653
QY 440 GTCAGAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 499
DB 654 GTCAGAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGATTCGAGAGAATCT 713
QY 500 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 559
DB 714 TACTCAGAGCTGCAAAATACCAACAGTTCGGCCAAACCTTGGGGCAACAAATCCATTCACT 773
QY 560 TGGGAGGAGTATTTGAAATGCAACAGAGTGTCTGGTGTGTTGTCAATGTGACTGATCCAA 619
DB 774 TGGGAGGAGTATTTGAAATGCAACAGAGTGTCTGGTGTGTTGTCAATGTGACTGATCCAA 833
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 669
DB 834 GCCAAGTGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAACTC 883

RESULT 15
US-10-200-242-20
; Sequence 20, Application US/10200242
; Publication No. US20040006006A9
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, Richard, J.
; APPLICANT: FANSLAW, III, William, C.
; APPLICANT: SPRIGGS, Melanie, K.
; TITLE OF INVENTION: CD40-LIGAND LACKING NATIVE-PATTERN GLYCOSYLATION
```

Search completed: November 12, 2004, 19:50:43
Job time : 238.902 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2004, 00:05:05 ; Search time 1501.63 Seconds
(without alignments)
16598.440 Million cell updates/sec

Title: US-09-687-864A-19
Perfect score: 684
Sequence: 1 aactgtcgccatgtgtgta.....aactcgagtgataatctaga 684

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.6	67.8	786	9 AY416061	AY416061 Homo sapi
2	463.6	67.8	786	9 AY416062	AY416062 Pan trogl
3	390.8	57.1	767	6 CD638712	CD638712 AGENCOURT
4	330.2	48.3	783	9 AY416063	AY416063 Mus muscu
5	325.8	47.6	806	6 CD521613	CD521613 AGENCOURT
6	286.4	41.9	571	7 CN794193	CN794193 4129335 B
7	240	35.1	628	7 CN786611	CN786611 4120632 B
8	220.2	32.2	702	6 CD640741	CD640741 AGENCOURT
9	216	31.6	690	6 CD642064	CD642064 AGENCOURT
10	209.8	30.7	795	6 CD520208	CD520208 AGENCOURT
11	108.4	15.8	847	7 CK777858	CK777858 965004 MA
12	98.6	14.4	740	7 CK834247	CK834247 4058618 B
13	96.6	14.1	492	2 BF599437	BF599437 263218 MA
14	78.6	11.5	727	5 BU294618	BU294618 603603621
15	78.6	11.5	731	5 BU373331	BU373331 603589056
16	71.4	10.4	638	1 AI982044	AI982044 pat. pk007
17	59.6	8.7	268	6 CD727599	CD727599 4032503 1
18	58	8.5	803	5 BU398104	BU398104 603535227
19	46.6	6.8	878	9 CNS0187R	AI108993 Drosophil
20	46	6.7	389	6 CA432817	CA432817 UI-H-COO-
21	46	6.7	997	9 CNS005TE	AL060767 Drosophil
22	45.2	6.6	1286	9 AG280276	AG280276 Mus muscu
23	44.2	6.5	861	5 BX367066	BX367066 BX367066
24	43.6	6.4	948	9 CNS000D4A	AL060208 Drosophil

C 25	43.6	6.4	1247	9	AG278972	Mus muscu
C 26	43.2	6.3	1343	9	AG310713	Mus muscu
C 27	42.8	6.3	739	5	BW379682	BW379682
C 28	42.6	6.2	1135	8	CC233138	CC233138
C 29	42.2	6.2	507	9	CNS01852	CH261-192
C 30	41.8	6.1	787	9	CNS007XT	AL108996 Drosophil
C 31	41.8	6.1	982	9	CNS06JLK	AL050371 Drosophil
C 32	41.8	6.1	1076	9	CNS026ZE	AL401742 T7 end of
C 33	41.8	6.1	1225	9	AG311152	AL184019 Tetraodon
C 34	41.4	6.1	894	8	BH151765	AG311152 Mus muscu
C 35	41.4	6.1	900	8	BH159228	BH151765 ENTPH12TF
C 36	41.4	6.1	935	1	AL536095	BH159228 ENTPH51TR
C 37	41.2	6.0	369	6	CD068937	AL536095 AL536095
C 38	41.2	6.0	415	5	BX312454	CD068937 MA2-0006U
C 39	41.2	6.0	799	9	CNS011SA	BX312454 BX312454
C 40	41.2	6.0	1059	5	BH060397	AL100660 Drosophil
C 41	41.2	6.0	1182	9	CL019530	BH060397 AGENCOURT
C 42	41.2	6.0	1373	9	AG347201	CL019530 CH216-SH1
C 43	41	6.0	1370	9	AG280286	AG347201 Mus muscu
C 44	40.8	6.0	572	6	CD851963	AG280286 Mus muscu
C 45	40.6	5.9	480	9	CE527096	CD851963 DH0ALL202
						CE527096 tigr-gas-

ALIGNMENTS

RESULT 1
LOCUS AY416061 786 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens TNFSP5 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY416061
VERSION AY416061.1 GI:39772021
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 786)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 786)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..786
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>786
/gene="TNFSP5"
/locus_tag="HCM5765"
ORIGIN
Query Match 67.8%; Score 463.6; DB 9; Length 786;
Best Local Similarity 99.1%; Pred. No. 2.2e-126;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 200 CGATCCAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCTCAATTCGGCAC 259
|||||

Db 314 CGAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 373
QY 260 ATGTCATAAGTGGAGCCAGAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db 374 ATGTCATAAGTGGAGCCAGAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGAT 433
QY 320 ACTACACCATGAGCAACAACCTTGTAAACCCCTGGAAAAATGGAAACAGCTGACCCGTTAAAA 379
Db 434 ACTACACCATGAGCAACAACCTTGTAAACCCCTGGAAAAATGGAAACAGCTGACCCGTTAAAA 493
QY 380 GACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGA 439
Db 494 GACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGA 553
QY 440 GTCAAGTCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 499
Db 554 GTCAAGTCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 613
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 559
Db 614 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 673
QY 560 TGGAGAGGATTTTGAATTTGCAACACAGGTCTTCGGTGTGTTGTCATGTGACTGATCCAA 619
Db 674 TGGAGAGGATTTTGAATTTGCAACACAGGTCTTCGGTGTGTTGTCATGTGACTGATCCAA 733
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 669
Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 783

RESULT 2
AY416062
LOCUS AY416062 786 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes TNFSF5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416062
VERSION AY416062.1 GI:39772022
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 786)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 786)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..786
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>786
/gene="TNFSF5"
/locus_tag="HCM5765"
gene
ORIGIN
Query Match 67.8%; Score 463.6; DB 9; Length 786;

Best Local Similarity 99.1%; Pred. No. 2.2e-126;
Matches 466; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 200 CGATCCAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 259
Db 314 CGAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCTCAAAATTCGGGCAC 373
QY 260 ATGTCATAAGTGGAGCCAGAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGAT 319
Db 374 ATGTCATAAGTGGAGCCAGAGTAAACACATCTGTGTTACAGTGGGCTGAAAAGGAT 433
QY 320 ACTACACCATGAGCAACAACCTTGTAAACCCCTGGAAAAATGGAAACAGCTGACCCGTTAAAA 379
Db 434 ACTACACCATGAGCAACAACCTTGTAAACCCCTGGAAAAATGGAAACAGCTGACCCGTTAAAA 493
QY 380 GACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGA 439
Db 494 GACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTCTGTTCCAAATCGGGAAGCTTCGA 553
QY 440 GTCAAGTCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 499
Db 554 GTCAAGTCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCT 613
QY 500 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 559
Db 614 TACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTGGGGCAACAATCCATTCACT 673
QY 560 TGGAGAGGATTTTGAATTTGCAACACAGGTCTTCGGTGTGTTGTCATGTGACTGATCCAA 619
Db 674 TGGAGAGGATTTTGAATTTGCAACACAGGTCTTCGGTGTGTTGTCATGTGACTGATCCAA 733
QY 620 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 669
Db 734 GCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAACTC 783
RESULT 3
CD638712
LOCUS CD638712 767 bp mRNA linear EST 17-JUN-2003
DEFINITION AGENCOURT 14532410 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30416146 5', mRNA sequence.
ACCESSION CD638712
VERSION CD638712.1 GI:31804800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM215 row: h column: 11
High quality sequence stop: 564.
FEATURES
Location/Qualifiers
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30416146"
/tissue_type="Pooled"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM207 row: j column: 17

High quality sequence stop: 466.

FEATURES
source

Location/Qualifiers

1..806

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30413128"

/tissue_type="pooled"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 191"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);

Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed

and directionally cloned. PMC - Peripheral Blood

Mononuclear Cells. RNA was pooled from 3/6hour stimulation

with PMA adn Ionomycin. 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGAGCGCGACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.69

kb (range 0.70-5.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 47.6%; Score 325.8; DB 6; Length 806;

Best Local Similarity 94.6%; Pred. No. 2.2e-85;

Matches 347; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 200 CGGATCCAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCAAAATTGGCGCAC 259

DB 408 CGAAGAAAGANACAGCTTTGAAATGCAAAAGGTGATCAGAACTCTCANATTGGCGCAC 467

QY 260 ATGTCATAAGTGAGCGCCAGCAGTAAACACATCTGTGTTACAGTGGCTGAAAAAGGAT 319

DB 468 ATGTCATAAGTGAGCGCCAGCAGTAAACACATCTGTGTTACAGTGGCTGAAAAAGGAT 527

QY 320 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAA 379

DB 528 ACTACACCATGAGCAACAACTTGGTAAACCTGGAAAAATGGGAAACAGCTGACCGTTAAA 587

QY 380 GACAGGAGCTCTATTATATCTATGCCCCAGTCACCTCTGTTCCCAATCGGGAAGCTTGA 439

DB 588 GACAAGAGCTCTATTATATCTATGCCCCAGTCACCTCTGTTCCCAATCGGGAAGCTTGA 647

QY 440 GTCAAGCTCTCAATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 499

DB 648 GTCAAGCTCTCAATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGATTTCGAGAGAATCT 707

QY 500 TACTCAGAGCTCGAAATACCCACAGTTCGCCCAAAACCTTTCGCGGCAACAACTTCATTAC 558

DB 708 TACTCAGAGCTCGAAATACCCCAAGTTCGCCCAACCTTTCGCGGCAACAACTTCCTTTCC 767

QY 559 TTGGGAG 565

768 CTTGGGG 774

RESULT 6

CN794193

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 571)

Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and

Matukumalli,L.K.

Construction and Analysis of a cDNA Library Generated From

Intestinal Muscle and Epithelial Tissues of Holstein Cattle

Unpublished (2004)

Contact: Richard G. Baumann

Bovine Functional Genomics Lab

ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt -trim fasta. Vector identified

by cross match using options -minmatch 12 -minscore 18

Plate: 50 row: H column: 03

Seq primer: CTTATTAGTGACACATATAGAAC

High quality sequence stop: 571.

Location/Qualifiers

1..571

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clone="8BOV_50H03"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stage="Lactating, Neonatal"

/lab_host="DH10B Tona"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:

NotI; Site 2: EcoRI; Normalized cow cDNA intestinal

library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources, 4 lactating intestinal, 1

neonatal intestinal 4/5 Lactating, Proximal Duodenum,

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal

Duodenum, Jejenum, Distal Ileum"

ORIGIN

Query Match

Best Local Similarity

Matches 308; Conservative

0; Mismatches

0; Gaps

0;

QY 326 CCATCAGCAACAACTTGGTAAACCTCGAAATGGGAAACAGCTGACCGTTAAAGACAAG 385

DB 1 CCTTAAGCAACAACTTGGTAAACCTCGAAACGGGAAACAGCTGCGCGTGAAGACAAG 60

QY 386 GACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAG 445

DB 61 GATTCTATCAGCTCTACACCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAG 120

QY 446 CTCCTATTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 505

DB 121 CTCCTATTATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAATCTTACTCA 180

QY 506 GAGCTGCAATACCCACAGTTCGGCCAAACCTTGGGGCAACAATCCATTCACTTGGGAG 565
 Db 181 GAGCTGCAAAACCCACAGTTCCTTCCAAACCACTGGGGCAGCAATCCATTCACTTAGGAG 240
 QY 566 GAGTATTGAATTGCAACACAGGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGCCAAAG 625
 Db 241 GAGCTTTGNAATTGCAATCGGTGTCTTCGGTGTGTTGTCAATGTGACTGATCCAAAGTCAAG 300
 QY 626 TGAGCCATGGCACTGGCTTCAGTCTCTTGGTGTGTTGTCAATCAAACTC 669
 Db 301 TGAGCCACGGGACGGGCTTCACATCATTTGGCTTACTCAAACTC 344

RESULT 7
 CN786611 4120632 BARC 8BOV Bos taurus cDNA clone 8BOV_29K22 5', mRNA linear EST 26-MAY-2004
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 SOURCE
 EST.
 ORGANISM
 Bos taurus (cow)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 628)
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
 Matukumalli,L.K.
 Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 Unpublished (2004)
 Contact: Richard G. Baumann
 Bovine Functional Genomics Lab
 ANRI
 BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744
 Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim alt -' -trim fasta. Vector identified
 by cross_match using options -mismatch 12 -minscore 18
 Plate: 29 row: K column: 22
 Seq primer: CCTATTAGGTGACACTATAGAAC
 High quality sequence stop: 628.

FEATURES
 source
 1..628
 Location/Qualifiers
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_29K22"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B Tona"
 /clone_lib="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
 Not1; Site 2: EcoRI; Normalized cow cDNA intestinal
 library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
 Duodenum, Jejunum, Distal Ileum"

ORIGIN
 Query Match 35.1%; Score 240; DB 7; Length 628;
 Best Local Similarity 89.7%; Pred. NO. 6.8e-60;
 Matches 280; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

QY 358 GGGAAACAGCTGACCGTTAAAGACAGGACTCTATTATCTATGCGCAAGTCACTTC 417
 Db 11 GGGAAACAGCTGGCGCGTGAAGAC-AGGATTCTATTATCTACACCAAGTCACTTC 69

QY 418 TGTTCCAATCGGAAAGCTTCGAGTCAAGCTCCATTATATAGCAGCCTCTGCCTAAAGTCC 477
 Db 70 TGTTC-ATCGGAAACTTGGTCAAGCTCCATTATATAGCAGCCTCTGCCTGAAGTCC 128
 QY 478 CCCGTAGATTTCGAGAGATCTTACTCAGAGCTGCAATACCCACAGTTCGCCCAACCT 537
 Db 129 CAAAGTGTAGCAGAGAGATCTTACTGAGAGCTGCAACACCCACAGTTCCTTCCAAACCA 188
 QY 538 TCGGGCAACAATCCATTCACTTGGGAGGAGTATTGAATTGCAACCAAGGTCTTCGGTG 597
 Db 189 TCGGGCAGCAATCCATTCACTTAGGAGGAGTCTTTGAATTGCAATCGGTCTTCGGTG 248
 QY 598 TTTGTCAATGTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTACGTCCTTTGGC 657
 Db 249 TTTGTCAATGTGACTGATCCAAAGTCAAGTGAGCCAGCGGCTTCACATCATTTGGC 308
 QY 658 TTACTCAAACTC 669
 Db 309 TTACTCAAACTC 320

CD640741 702 bp mRNA linear EST 17-JUN-2003
 AGNCOURT_14542170 NIH_MGC_191 Homo sapiens cDNA clone
 IMAGE:30414715 5', mRNA sequence.
 CD640741
 CD640741.1 GI:31808911
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 702)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NCI
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDCM211 row: 1 column: 20
 High quality sequence stop: 571.

FEATURES
 source
 1..702
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30414715"
 /tissue_type="Pooled"
 /lab_host="DH10B (Tl phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pBMR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctctggcc); Library is oligo-dT primed
 and directionally cloned. PMBC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CAGCGCCATTATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,


```

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN
Query Match      14.4%; Score 98.6; DB 7; Length 740;
Best Local Similarity 85.3%; Pred. No. 8.4e-18;
Matches 110; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 207 AGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCAAAATTCGGGCACATGTCAT 266
    |||||
Db 612 AGAAAAAATTTGAAATGCAAAAGGTGATCAGAGCCTCAGATAGCGGCACATGTCAT 671
    |||||

QY 267 AAGTGAGCGCCAGCACTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTACAC 326
    |||||
Db 672 CAGTGAGCGCCAGTAGTAAACCAACCTCTGTCTCCAGTGGGCCCCCAAGGATACTACAC 731
    |||||

QY 327 CATGAGCAA 335
    |||||
Db 732 CCTAAGCAA 740

RESULT 13
BF599437
LOCUS      263218 MARC 3BOV Bos taurus cdna 5', mRNA linear EST 25-APR-2001
DEFINITION
ACCESSION BF599437
VERSION    BF599437.1 GI:11695919
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus

REFERENCE
AUTHORS    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pettea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keefe,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cdna
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
JOURNAL    21180013
MEDLINE
PUBMED     11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACACAGCTATGACCAT
            BACKWARD: GTTTCCTCCAGTCACGAG
            Plate: 33 row: N column: 5
            Seq primer: ATTAGGTGACACTATAG.
            Location/Qualifiers
            1..492
            /organism="Bos taurus"
            /mol_type="mRNA"
            /db_xref="taxon:9913"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /clone_lib="MARC 3BOV"
            /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
            Library made from pooled tissue from marrow, alveolar
            macrophage, ovary, fetal semitendinosus muscle, and fetal
            longissimus muscle."

ORIGIN
Query Match      14.1%; Score 96.6; DB 2; Length 492;
Best Local Similarity 85.3%; Pred. No. 7.4e-12;
Matches 108; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 207 AGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCAAAATTCGGGCACATGTCAT 266
    |||||
Db 366 AGAAAAAATTTGAAATGCAAAAGGTGATCAGAGCCTCAGATAGCGGCACATGTCAT 425
    |||||

QY 267 AAGTGAGCGCCAGCACTAAACCAACATCTGTGTACAGTGGGCTGAAAAGGATACTACAC 326
    |||||
Db 426 CAGTGAGCGCCAGTAGTAAACCAACCTCTGTCTCCAGTGGGCCCCCAAGGATACTACAC 485
    |||||

QY 327 CATGAGC 333
    |||||
Db 486 CCTAAGC 492

RESULT 14
BU294618
LOCUS      603603621P1 CSEQHN55 Gallus gallus cdna clone CHEST58216 5', mRNA
DEFINITION
ACCESSION BU294618
VERSION    BU294618.1 GI:25744254
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus

REFERENCE
AUTHORS    Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
            A Comprehensive Collection of Chicken cDNAs
            Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL    22335534
MEDLINE    12445392
PUBMED
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
            1..727
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="Compton Line 151"
            /db_xref="taxon:9031"
            /clones="CHEST58216"
            /sex="Female"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="CSEQHN55"
            /note="Organ: kidney + adrenal; Vector: pBluescript II
            KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
            library was constructed from 1 million independent clones.
            cDNA synthesis was initiated using an oligo(dT) primer.
            using methylated C in the first strand reaction, double-stranded cDNA.
            Following this first strand reaction, digested with
            EcoRI, size-selected, and cloned into the NotI and EcoRI
            compatible sites of a custom modified MCS of the
            pBluescript (KS+) vector. The library was normalized in 2
            rounds using conditions adapted from Soares et al., PNAS
            (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
            (1996): 791, except that a significantly longer
            reannealing hybridization was used."

ORIGIN
Query Match      11.5%; Score 78.6; DB 5; Length 727;
Best Local Similarity 57.3%; Pred. No. 7.4e-12;

```


Matches	185;	Conservative	0;	Mismatches	129;	Indels	9;	Gaps	2;
Qy	356	ATGGGAACAGCTCACCGTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCT	415						
Db	248	ATGAGGGGAAGCTGAAGGTGGAGAAAGCAGGGCTCTACTCATCTCTCTACAAGTCAGCT	307						
Qy	416	TCGTGTTCCAATCGGGGAAGCTTCGAGTCGAGTCCGATTTATATAGCCAGGCTCTGCGCTAAAGT	475						
Db	308	TCTGCACCAAGCGCGCGGCTTCG-----GGCCCAITTCACCTCTATATTTATTGTGACC	361						
Qy	476	CCCCCGGTAGATTCCGAGAGAATCTTACTCTAGAGCTGCAAAATACCCACAGTTTCGCCCAAAC	535						
Db	362	TCCCCATGGGAAGGACCGGCTCTGATGAAGGGAGCTTGCACGACAGCACTTCCACGG	421						
Qy	536	CT---TCGGGGCAACAATCCATTCACTTTGGGAGGAGTATTTGAATTCGCAACGAGTGCTT	592						
Db	422	CTCTCTGTGAGCTCCAGTCCATCCGGGAGGCGGTGCTTCGAGCTGGCGCAGGGCGACA	481						
Qy	593	CGGTGTTTGTCAATGTGACTGATCCAAGCCAAAGTAGGCCATGGGCATGGCTTCAAGTCCT	652						
Db	482	TGGTCTTTGTCAATGTGACGAGCTCAACAGCAGTGAACGTCACCCCTGGCAACACCTTACT	541						
Qy	653	TTGGCTTACTCAAACTCGAGTGA	675						
Db	542	TTGGCATGTTCAAGCTGTAGAGA	564						

RESULT	15
BU373331	
LOCUS	
DEFINITION	731 bp mRNA linear EST 28-NOV-2002 60359056F1 CSEQCHN74 Gallus gallus CDNA clone CHEST549pl3 5', mRNA sequence.
ACCESSION	BU373331
VERSION	BU373331.1
KEYWORDS	EST
SOURCE	GI:25681332
ORGANISM	Gallus gallus (chicken)
REFERENCE	Gallus gallus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 731) Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs <i>Curr. Biol.</i> 12 (22), 1965-1969 (2002) 22335534
AUTHORS	Contract: Simon Hubbard
TITLE	
JOURNAL	
MEDLINE	
PUBMED	12445392
COMMENT	

FEATURES
SOURCE

ECORI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match	11.5%	Score 78.6	DB 5	Length 731
Best Local Similarity	57.3%	Pred. No. 7.4e-12		
Matches 185	Conservative 0	Mismatches 129	Indels 9	Gaps 2
Qy	356	ATCGGAAACAGCTGACCGCTTAAAGACAGGAGCTCTATTATATCTATATCTATGCCCCAACGTCACCT	415	
Db	250	ATGAGGGGAAGCTGGAAGGTGGAGAAAGAGGGCTCTACTACATCTTACTACAAGTCAGCT	309	
Qy	416	TCCTGTTTCCAATCGGGAAGCTTTCGAGTCAAGCTCCATTTATPAGCCAGCCTCTGCCTAAAGT	475	
Db	310	TCCTGCACCAAGCGCGCGCTTCG-----GGCCATTACCCCTCTATATTTATTTGTACC	363	
Qy	476	CCCCGGTAGATTGAGAGAGAACTTACTAGAGCTGCAATACCCACAGTTCGCCCAAC	535	
Db	364	TCGCCATGGAAGAGGACCGGCTCCTGATGAAGGCACTTGACACGCACAGCACCTCCACGG	423	
Qy	536	CT---TGCGGGCAACAATCCATTCCTTGGGAGGAGTATTGGAATTGCAACCAAGGTGCTT	592	
Db	424	CTCTGTGAGCTCCAGTCCATCCGGAGGGCGGTGTCTTCGAGCTGCGCAGGGCGACA	483	
Qy	593	CGGTGTTTGTGCAATGTGACTGTATGATCCAAAGCCAAAGTGAGCCATGGCATCTGGCTTCACGTCCT	652	
Db	484	TGTCCTTTGTCAATGTGACGGACTCAACGACGTGAACGTCGCAACCTGGGCAACACCTACT	543	
Qy	653	TTGCGTTACTCAAACTCGAGTGA	675	
Db	544	TTGGCATGTTCAAGCTGTAGAGA	566	

Search completed: November 12, 2004, 12:49:38
Job time : 1503.63 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)